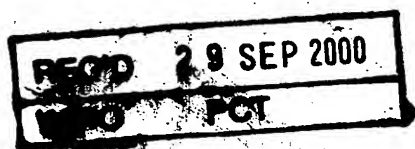




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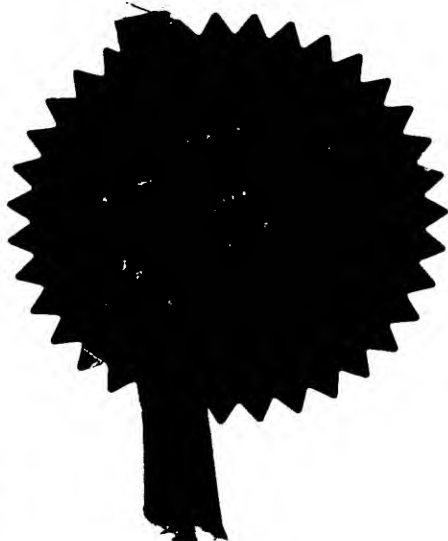
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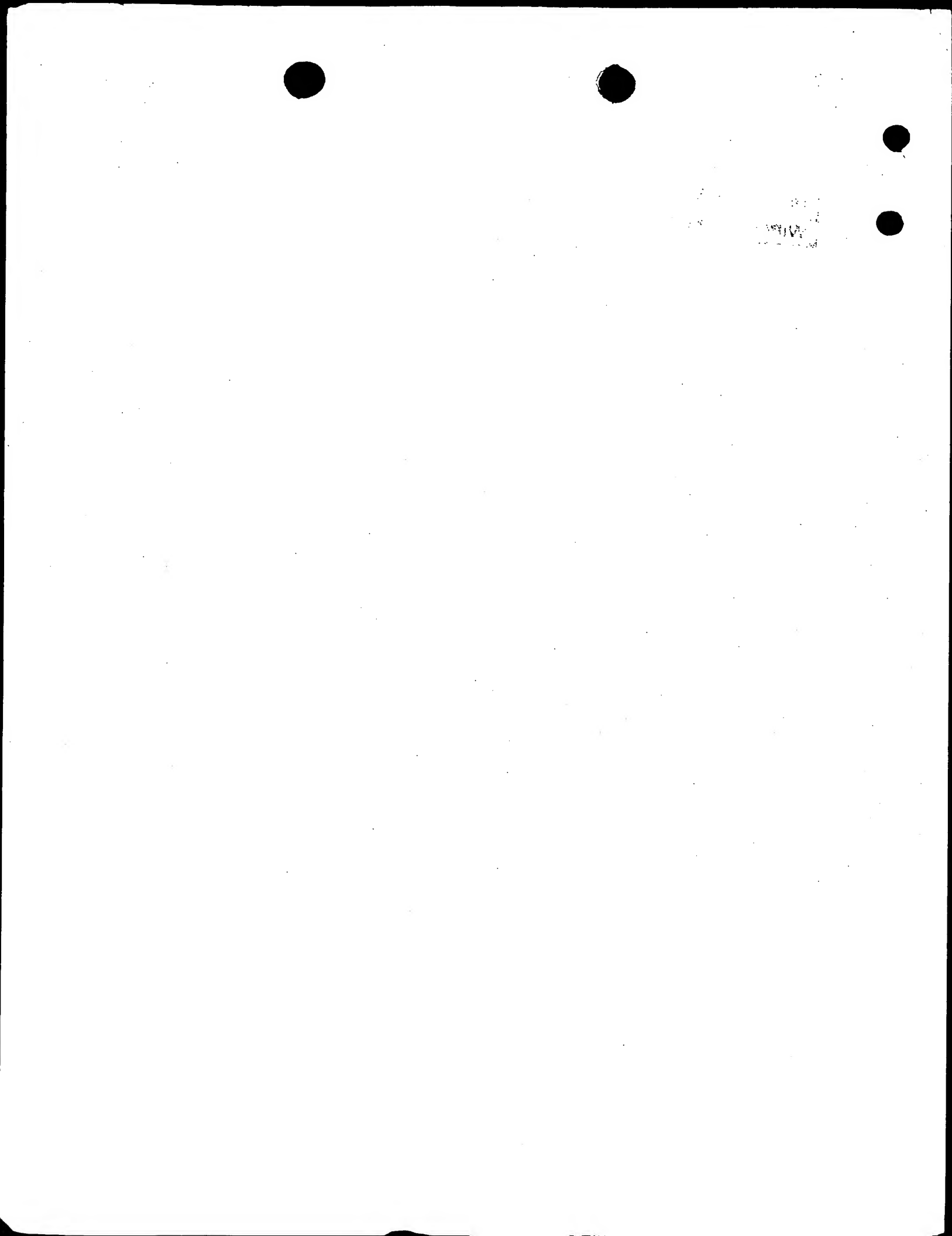
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3. Full name, address and postcode of the or of each applicant (underline all surnames)

NEUROPA LIMITED  
ROBERTSON BUILDING  
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GLASGOW G11 6NU

SECTION 30(1)(A) APPLICATION FILED 21/8/2000

Patents ADP number (if you know it)

If the applicant is a corporate body, give the country/state of its incorporation

7288202001

4. Title of the invention

"ESSENTIAL GENES AND ASSAYS RELATING THERETO"

5. Name of your agent (if you have one)

CRUIKSHANK & FAIRWEATHER

"Address for service" in the United Kingdom to which all correspondence should be sent (including the postcode)

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ESSENTIAL GENES AND ASSAYS RELATING THERETO

The present invention relates to screening assays particularly for pesticides based on the use of essential genes/proteins, as well as the novel genes/proteins themselves. It also relates to screening assays for compounds with therapeutic use in cancer therapy.

Crop destruction by pests such as insects results in a considerable economic loss and serious reduction in productivity. Chemical pesticides are typically used in order to control the pests and reduce crop loss. However pesticide development has generally been less than controlled or focussed, such that the biochemical or genetical functions of the pesticide have not been a major concern, but rather simply whether or not the pesticide was effective ie. killed the pests.

However, increasing environmental concerns and development of resistance to existing pesticides has led to a more rational approach to pesticide development being voiced.

It is amongst the objects of the present invention to provide a more rational approach to pesticide development by providing pesticide screening assays based on the identification of genes/proteins which are considered to be essential to the pest.

Each of the genes identified are shown to be essential for cell or organism survival and/or reproduction based on the evidence of the effect of a complete loss of gene function caused by a mutation. Since the action of the protein encoded by such a gene is essential for cell and/or organism survival or reproduction, it follows that chemical interference with the action or production of the protein will mimic the effect of mutation and result in the death of cells and the organism (or failure to reproduce). Thus chemical interference with the action of each essential gene and protein represents a way to kill cells and organisms, and specifically insects.

The present inventors have used genetic techniques in order to study a model pest, namely *Drosophila*. As a result of these studies, the present inventors have identified a considerable number of essential genes/proteins, which may be used in functional and/or ligand binding assays for screening for pesticides.

Thus, in a first aspect the present invention provides a screening assay for identifying compounds which have a physiological effect on an organism, the assay comprising the steps of:

- a) reacting a test compound with a protein encoded by an essential gene from the organism; and
- b) detecting any physiological effect the compound has on the protein.

A physiological effect is one which alters the function and/or activity of the protein. Typically the assay is designed to be used to screen for compounds which are harmful or pesticidal. However, the assay may be used to screen for other effects, such as beneficial or therapeutic effects.

An essential gene is one for which it has been determined that the expression of a functional protein is necessary in order to avoid a lethal or semi-lethal phenotype. A lethal phenotype is defined as a phenotype characterised by organism death due to cellular or system failure at some developmental stage, or by the failure of adults that do occur to leave any viable offspring. A semi-lethal phenotype is characterised by low fecundity (the tendency to produce few offspring compared to wildtype), and frequently by short lifespan.

Studies carried out by the present inventors have identified over 900 distinct fly lines, in the model organism, *Drosophila*, which display a lethal or semi-lethal phenotype. Fly lines which display such a lethal or semi-lethal phenotype have been generated using the technique of P-element transposon-tagged insertion (1) Torok, T.G. Tick, M. Alvarado and I. Kiss, 1993 P-lacW Insertional

Mutagenesis on the second chromosome of *Drosophila melanogaster*: Isolation of lethals with different overgrowth phenotypes. Genetics 135: 71 - 80; (2) Dèak, P., M.M. Omar, R.D.C. Saunders, M. Pal, O. Komonyi, J. Szidonya, P. Maroy, Y. Zhang, M. Ashburner, P. Benos, C. Savakis, I. Siden-Kiamos, C. Louis, V.N. Bolshakov, F.C. Kafatos, E. Madueno, J. Modolell and D.M. Glover, 1998 P element insertion alleles of essential gens on the third chromosome of *Drosophila melanogaster*: Correlation of physical and cytogenetics maps in chromosomal region 86E-87F. Genetics 14: 1697 - 1722). Using the technique of transposon rescue, it has been possible to determine the nucleotide sequence surrounding the site of transposon insertion. The partial sequences of regions surrounding the P-element insertion site from distinct fly lines are identified herein as SEQ ID NOS. 1 - 902. It is immediately evident to one skilled in the art how to use this information to clone a larger portion of nucleic acid containing the complete gene and thereafter express the encoded protein. Such techniques are disclosed for example in Sambrook et al (1989). It will be appreciated that the P-element may be inserted within a particular gene, or in regulatory sequences associated with a gene, such that P-element insertion affects expression of the gene, resulting in the lack of the expressed protein or expression of a dysfunctional form.

In a further aspect the present invention provides a polynucleotide fragment comprising nucleotides capable of encoding or partially encoding an essential gene for use in assays of the present invention. More particular the present invention provides means for obtaining essential proteins for use in assays of the present invention.

"Polynucleotide fragment" as used herein refers to a chain of nucleotides such as deoxyribose nucleic acid (DNA) and transcription products thereof, such as RNA. Naturally, the skilled addressee will appreciate the whole naturally occurring PoEV genome is not included in the

definition of polynucleotide fragment.

The polynucleotide fragment can be isolated in the sense that it is substantially free of biological material with which the whole genome is normally associated *in vivo*. The isolated polynucleotide fragment may be cloned to provide a recombinant molecule comprising the polynucleotide fragment. Thus, "polynucleotide fragment" includes double and single stranded DNA, RNA and polynucleotide sequences derived therefrom, for example, subsequences of said fragment and which are of any desirable length. Where a nucleic acid is single stranded then both a given strand and a sequence complementary thereto is within the scope of the present invention.

In general, the term "expression product" refers to both transcription and translation products of said polynucleotide fragments. When the expression product is a "polypeptide" (i.e. a chain or sequence of amino acids displaying a biological activity substantially similar to the biological activity of an essential protein, it does not refer to a specific length of the product as such. Thus, the skilled addressee will appreciate that "polypeptide" encompasses *inter alia* peptides, polypeptides and proteins. The polypeptide if required, can be modified *in vivo* and *in vitro*, for example by glycosylation, amidation, carboxylation, phosphorylation and/or post-translational cleavage.

The present invention further provides an isolated polynucleotide fragment capable of specifically hybridising to a related polynucleotide sequence from another species. In this manner, the present invention provides probes and/or primers for use in *ex vivo* and/or *in situ* detection and expression studies. Typical detection studies include polymerase chain reaction (PCR) studies, hybridisation studies, or sequencing studies. In principle any specific polynucleotide sequence from the identified sequences may be used in detection and/or expression studies.



"Capable of specifically hybridising" is taken to mean that said polynucleotide fragment preferably hybridises to a related or similar polynucleotide sequence in preference to unrelated or dissimilar polynucleotide sequences.

The invention includes polynucleotide sequence(s) which are capable of specifically hybridising to an essential polynucleotide sequence or to a part thereof without necessarily being completely complementary to said related polynucleotide sequence or fragment thereof. For example, there may be at least 50% preferably at least 75%, most preferably at least 90% or at least 95% complementarity. Of course, in some cases the sequences may be exactly complementary (100% complementary) or nearly so (e.g. there may be less than 10, preferably less than 5 mismatches). Thus, the present invention also provides anti-sense or complementary nucleotide sequence(s) which is/are capable of specifically hybridising to the disclosed DNA sequence. If a specific polynucleotide is to be used as a primer in PCR and/or sequencing studies, the polynucleotide must be capable of hybridising to related nucleic acid and capable of initiating chain extension from 3' end of the polynucleotide, but not able to correctly initiate chain extension from unrelated sequences.

If a polynucleotide sequence of the present invention is to be used in hybridisation studies to obtain a related sequence from another organism the polynucleotide sequence should preferably remain hybridised to a sample polynucleotide under stringent conditions. If desired, either the test or sample polynucleotide may be immobilised. Generally the test polynucleotide sequence is at least 10 or at least 50 bases in length. It may be labelled by suitable techniques known in the art. Preferably the test polynucleotide sequence is at least 200 bases in length and may even be several kilobases in length. Thus, either a denatured sample or test sequence can be first bound to a support. Hybridization can be effected at a temperature of between 50 and 70°C in double

strength SSC (2xNaCl 17.5g/l and sodium citrate (SC) at 8.8g/l) buffered saline containing 0.1% sodium dodecyl sulphate (SDS). This can be followed by rinsing of the support at the same temperature but with a buffer having a reduced SSC concentration. Depending upon the degree of stringency required, and thus the degree of similarity of the sequences, such reduced concentration buffers are typically single strength SSC containing 0.1%SDS, half strength SSC containing 0.1%SDS and one tenth strength SSC containing 0.1%SDS. Sequences having the greatest degree of similarity are those the hybridisation of which is least affected by washing in buffers of reduced concentration. It is most preferred that the sample and inventive sequences are so similar that the hybridisation between them is substantially unaffected by washing or incubation in standard sodium citrate (0.1 x SSC) buffer containing 0.1%SDS.

Oligonucleotides may be designed to specifically hybridise to essential nucleic acid. They may be synthesised, by known techniques and used as primers in PCR or sequencing reactions or as probes in hybridisations designed to detect the presence of related material in a sample. The oligonucleotides may be labelled by suitable labels known in the art, such as, radioactive labels, chemiluminescent labels or fluorescent labels and the like. Thus, the present invention also provides oligonucleotide probes and primers for use in detecting essential genes.

The term "oligonucleotide" is not meant to indicate any particular length of sequence and encompasses nucleotides of preferably at least 10b (e.g. 10b to 1kb) in length, more preferably 12b-500b in length and most preferably 15b to 100b.

The oligonucleotides may be determined from the sequences shown in SEQ ID Nos. 1-902 and may be manufactured according to known techniques. They may have substantial sequence identity (e.g. at least 50%, at least 75%, at least 90% or at least 95% sequence identity) with

one of the strands shown therein or an RNA equivalent, or with a part of such a strand. Preferably such a part is at least 10, at least 30, at least 50 or at least 200 bases long. It may be an ORF or a part thereof.

Oligonucleotides which are generally greater than 30 bases in length should preferably remain hybridised to a sample polynucleotide under one or more of the stringent conditions mentioned above. Oligonucleotides which are generally less than 30 bases in length should also preferably remain hybridised to a sample polynucleotide but under different conditions of high stringency. Typically the melting temperature of an oligonucleotide less than 30 bases may be calculated according to the formula of;  $2^{\circ}\text{C}$  for every A or T, plus  $4^{\circ}\text{C}$  for every G or C, minus  $5^{\circ}\text{C}$ . Hybridization may take place at or around the calculated melting temperature for any particular oligonucleotide, in 6 x SSC and 1% SDS. Non specifically hybridised oligonucleotides may then be removed by stringent washing, for example in 3 x SSC and 0.1% SDS at the same temperature. Only substantially similar matched sequences remain hybridised i.e. said oligonucleotide and corresponding PoEV nucleic acid.

When oligonucleotides of generally less than 30 bases in length are used in sequencing and/or PCR studies, the melting temperature may be calculated in the same manner as described above. The oligonucleotide may then be allowed to anneal or hybridise at a temperature around the oligonucleotides calculated melting temperature. In the case of PCR studies the annealing temperature should be around the lower of the calculated melting temperatures for the two priming oligonucleotides. It is to be appreciated that the conditions and melting temperature calculations are provided by way of example only and are not intended to be limiting. It is possible through the experience of the experimenter to vary the conditions of hybridisation and thus anneal/hybridise oligonucleotides at temperatures above their calculated melting temperature. Indeed this

can be desirable in preventing so-called non-specific hybridisation from occurring.

It is possible when conducting PCR studies to predict an expected size or sizes of PCR product(s) obtainable using an appropriate combination of two or more PoEV oligonucleotides, based on where they would hybridise to the sequences SEQ ID Nos. 1-902. If, on conducting such a PCR on a sample of PoEV DNA, a fragment of the predicted size is obtained, then this is predictive that the DNA is PoEV.

The partial sequences of the essential genes, identified as SEQ ID NOS. 1 - 902, have been analysed in order to ascertain if there is any homology to previously identified sequences contained in nucleotide sequence databases such as the GENBANK and EMBL databases. Database searching has ascertained that a number of the nucleotide sequences have been previously identified. However, the lack of the gene/protein associated with the sequence may not have been suggested to result in a lethal/semi-lethal phenotype. Moreover, a number of the sequences appear to show no significant database matches and others match only sequences for which no putative function has been ascribed.

Table 1 discloses details of the sequences identified by the present invention which display a match with sequences already deposited in a nucleic acid database.

As described above, genes described herein generally fall into two classes:

- A. Genes encoding proteins with recognizable similarity to proteins of known functional class e.g. protein kinases, neurotransmitter receptors; and
- B. Genes encoding proteins of unknown function.

Assays for proteins of known function are known in the art. A list of typical assays for some of the major classes of protein that are estimated to represent likely insecticide targets is exemplified herein. Where a functional assay is available, it is to be preferred to a ligand binding assay.

Assays for proteins of unknown function rely on assessment of ligand binding only.

The typical purpose of the assays described herein is to select for pesticides/insecticides, though in some cases lead compounds may have therapeutic activity, such as in inducing cell death which may be applicable in cancer therapy. A relative specificity of action based on species groups or species may be achieved based on differences in protein sequence and structure, differences in protein expression, variations in development role and/or variations in degree of redundancy with related proteins.

The information disclosed herein teaches that the loss of the function of each of the proteins encoded by the genes comprising the partial sequences identified by SEQ 1D Nos. 1-902, causes death of insects at some point during development, or causes reproductive failure. An insecticidal chemical compound will therefore be a compound that strongly modulates, either agonistically or antagonistically, the activity of such a protein. Thus, where the purpose of the assay is selection of insecticides, chemicals will be sought that interfere with the normal function of the protein.

For proteins of known function with available functional assays, application of these assays will rapidly select a set of chemicals having the desired effect on the protein in the appropriate assay system.

In a second step, each member of the set of chemicals may then be tested directly for killing activity on insects. *Drosophila* itself is a convenient assay insect. In a typical fly killing assay, young flies are kept without fluid for a time, then transferred to vials containing filter paper dosed with a solution of the chemical to be tested. A range of chemical concentrations is used. After a defined treatment, flies are returned to normal conditions and observed. Rate of killing and percentage lethality are the parameters assessed.

In a third step, compounds with very effective killing activity on *Drosophila* are then tested on pest species or accepted model pest related insects. For example, aphid species may be maintained on isolated lettuce plants: the time of death and the numbers of aphids falling dead onto paper traps beneath the plants after spraying with defined doses of the candidate chemical is assessed. As another example, lepidopteran pest larvae may be maintained on artificial media or plant leaves, which are treated with defined doses of chemicals, and survival is assessed.

For proteins of unknown function, the ligand binding assays outlined herein will also define a group of candidate chemicals. However, this group is likely to be large, since binding may occur to a number of different sites on the exposed surface of the protein, and binding alone does not predict the effect of ligand binding on the activity of the protein. Stringent selection among the candidate chemicals for those with the greatest affinity will define a set of chemicals small enough to be tested for insect killing. The use of *Drosophila* as a test organism enables large numbers of compounds to be assessed. Therefore the same procedure may be used as for proteins for which functional assays are available.

An alternative or additional procedure is to use a cellular killing assay as an intermediate step. For example, a gene of unknown function can be examined for location and timing of gene expression in tissues throughout development. The primary sites of tissue death may be determined by apoptosis assays or direct observation. In many cases, particular cell types e.g. nerve cells, can be defined as subject to death when the protein is not expressed. Appropriate cell types can be isolated from the appropriate tissue and developmental stage of *Drosophila* or a larger insect. Effects of candidate chemicals from the binding assay screen on survival of these cells in culture may then be ascertained, using commercially available live/dead cell assessment

methods.

A further alternative or additional procedure is to express the protein target in a cell which has been manipulated genetically to contain a sensor for calcium ions, cyclic AMP or other components of cell signaling pathways. This may be achieved, for example, by generating transgenic *Drosophila* containing the gene encoding the protein with its expression driven by a promoter that is utilized in the cell type of choice. Alternatively, permanent cell lines of any suitable origin may be transfected, and lines expressing the protein permanently selected. In many cases, expression of an unknown protein will cause a shift in the level of cell signaling components, which will be detected by the sensor and can be read, for example, as a fluorescent or luminescent signal. The difference between the protein-expressing cells and control cells forms the basis of the assay. Effects of chemicals on the difference between protein expressing and control lines are assessed.

Proteins for all the assays described can be produced by cloning the gene into plasmid vectors that allow high expression in a system of choice e.g. insect cell culture, yeast, animal cells, *Escherichia coli*. To enable effective purification of the protein, a vector may be used that incorporates an epitope tag onto the protein on synthesis. A number of such vectors and purification systems are commercially available.

The polynucleotide fragment can be molecularly cloned into a prokaryotic or eukaryotic expression vector using standard techniques and administered to a host. The expression vector is taken up by cells and the polynucleotide fragment of interest expressed, producing protein.

The cloning and expression of a recombinant "essential" polynucleotide fragment also facilitates in producing anti-"essential" antibodies and fragments thereof (particularly monoclonal antibodies).

It will be understood that for the particular polypeptides embraced herein, natural variations can exist between individuals or between members of the family. These variations may be demonstrated by (an) amino acid difference(s) in the overall sequence or by deletions, substitutions, insertions, inversions or additions of (an) amino acid(s) in said sequence. All such derivatives showing active polymerase and/or envelope polypeptide physiological and/or immunological activity are included within the scope of the invention. For example, for the purpose of the present invention conservative replacements may be made between amino acids within the following groups:

- (I) Alanine, serine, threonine;
- (II) Glutamic acid and aspartic acid;
- (III) Arginine and leucine;
- (IV) Asparagine and glutamine;
- (V) Isoleucine, leucine and valine;
- (VI) Phenylalanine, tyrosine and tryptophan

Moreover, recombinant DNA technology may be used to prepare nucleic acid sequences encoding the various derivatives outlined above.

As is well known in the art, the degeneracy of the genetic code permits substitution of bases in a codon resulting in a different codon which is still capable of coding for the same amino acid, e.g. the codon for amino acid glutamic acid is both GAT and GAA. Consequently, it is clear that for the expression of polypeptides from nucleotide sequences shown in SEQ. ID Nos. 1-902 or fragments thereof, use can be made of a derivative nucleic acid sequence with such an alternative codon composition different from the nucleic acid sequence shown in said Figure 1.



The polynucleotide fragment of the present invention are preferably linked to regulatory control sequences. Such control sequences may comprise promoters, operators, inducers, enhancers, ribosome binding sites, terminators etc. Suitable control sequences for a given host may be selected by those of ordinary skill in the art.

A polynucleotide fragment according to the present invention can be ligated to various expression controlling sequences, resulting in a so called recombinant nucleic acid molecule. Thus, the present invention also includes an expression vector containing an expressible nucleic acid molecule. The recombinant nucleic acid molecule can then be used for the transformation of a suitable host. Such hybrid molecules are preferably derived from, for example, plasmids or from nucleic acid sequences present in bacteriophages or viruses and are termed vector molecules.

Specific vectors which can be used to clone nucleic acid sequences according to the invention are known in the art (e.g. Rodriguez, R.L. and Denhardt, D.T., Edit., Vectors: a survey of molecular cloning vectors and their uses, Butterworths, 1988).

The methods to be used for the construction of a recombinant nucleic acid molecule according to the invention are known to those of ordinary skill in the art and are inter alia set forth in Sambrook, et al. (Molecular Cloning: a laboratory manual Cold Spring Harbour Laboratory, 1989).

The present invention also relates to a transformed cell containing the polynucleotide fragment in an expressible form. "Transformation", as used herein, refer to the introduction of a heterologous polynucleotide fragment into a host cell. The method used may be any known in the art, for example, direct uptake, transfection transduction or electroporation (Current Protocols in Molecular Biology, 1995. John Wiley and Sons Inc.). The heterologous polynucleotide fragment may be maintained through autonomous replication or alternatively, may be

integrated into the host genome. The recombinant nucleic acid molecules preferably are provided with appropriate control sequences compatible with the designated host which can regulate the expression of the inserted polynucleotide fragment, e.g. tetracycline responsive promoter, thymidine kinase promoter, SV-40 promoter and the like.

Suitable hosts for the expression of recombinant nucleic acid molecules may be prokaryotic or eukaryotic in origin. Hosts suitable for the expression of recombinant nucleic acid molecules may be selected from bacteria, yeast, insect cells and mammalian cells.

#### 1. Binding assays for proteins of unknown function

Ligands for any protein may be discovered by direct binding assays. In order to select true lead chemicals for insecticide or therapeutic development, these must be followed by insect killing assays or other functional assays as indicated in pages 8 and 9 above.

In binding assays one partner molecule is immobilized, and the other is labeled in some fashion (e.g. using a fluorescent tag, or by the incorporation of a radioactive isotope) and added free in solution. After incubation to allow molecular interaction, and a wash step, the amount of bound ligand is measured using an appropriate detection system. This may be used in a qualitative mode at first. Ligands showing significant binding may then be studied further by ensuring that the protein is in excess, and carrying out experiments with a dilution series of the ligand at a set of known concentrations.

In the assay taught herein, the protein encoded by the essential insect gene is identified, and the chemical ligand is unknown. Therefore the protein may be purified using an affinity system and immobilized. The chemical ligands will be labeled, incubated with the immobilized protein, washed, and the amount of retained label assessed.

Proteins may conveniently be immobilized using an epitope or other affinity tags provided by the expression vector (see above), on a support material to which the appropriate antibody or binding agent for the tag is attached. The support material may be nitrocellulose membrane, Sephadex or other type of protein purification column support, or specialized beads such as those commercially available from Dynal or Promega. Alternatively, the protein may for example be biotinylated to a low level, and the same support materials derivatised with streptavidin (which has a very high affinity for biotin) used. Further, proteins may be modified chemically in a variety of ways, and covalently attached to support materials.

Nucleic acid or peptide ligands may conveniently be radioactively labeled by standard procedures. Organic chemical ligands may also be provided in radioactively labeled form. However, a more convenient labeling system for large scale screening by binding assays is the use of chemicals that are tagged with oligonucleotide sequence labels, or by other means. This allows many chemicals to be tested together initially, since each can be identified by the use of a PCR based detection system.

Monoclonal antibodies raised against a particular protein may be used to select chemicals that bind to particular regions of the protein - the epitope recognised by the antibody. In such an assay, chemicals are assessed for displacement or reduction in binding of the antibody. Remaining bound antibody is detected by a standard fluorescently labeled second antibody.

## 2. Binding assays for proteins with known ligands

For proteins belonging to families for which chemical or peptide ligands can be predicted, binding assays may be employed in a ligand-competition mode. This measures chemical interaction with the site on the protein at which the natural ligand binds, and is thus going to give a

higher rate of significant hits. This type of assay is also more quantitative.

Examples of typical known ligands which would be labeled (typically radioactively) and used in displacement assays are: pharmacological agonists and antagonists, activators and inhibitors, neurotransmitters, growth factors and cytokines, cAMP, cGMP, enzyme cofactors such as NAD and FAD, regulatory polypeptides (e.g. calmodulin) and other subunits of multicomponent proteins.

A typical assay relies on the generation of purified protein as discussed above. In general, binding assays rely on labeled ligand, usually radiolabeled, to enable competition for the binding site to be detected. A set concentration (enough to saturate the binding site) of labeled ligand is incubated with a purified sample containing the purified protein. In a parallel tube, the test chemical is also added. Bound ligand/protein complexes are washed (to remove free ligand), precipitated e.g. by TCA, collected with a cell harvester (for example) and the level of radioactivity measured. Displacement can be observed as a reduction in the amount of radioactivity detected in the assay. Enhancement of binding can also be observed in this type of assay, where radioactivity levels are increased - this indicates activity of the test chemical near to but not competing with the site of ligand interaction.

#### Examples of some possible functional assays

##### 1. Kinases

Kinases are enzymes that transfer the terminal phosphate group of ATP to their substrate molecule. These enzymes have been shown to be involved in many cell processes including signal transduction, apoptosis and regulation of the cell cycle. Protein kinases are the largest known protein family and have been characterised in mammals, plants, fungi and microorganisms.

An assay of kinase activity generally requires two distinct steps: (1) transfer of the (labeled) terminal phosphoryl group of the nucleoside triphosphate donor to the substrate and (2) separation of the phosphorylated product from unutilized nucleotide. Step 1 is generally carried out in solution, with both the enzyme and the substrate in the liquid phase. Step 2 is usually accomplished by trichloroacetic acid (TCA) precipitation, by sodium dodecyl sulphate (SDS) gel electrophoresis, or by binding the labeled product to a solid support such as phosphocellulose paper or nitrocellulose membrane. These steps are then followed by detection of the amount of labeled phosphoryl that has been transferred to the substrate.

Step 1 can also be carried out with either the enzyme or the substrate immobilized on a solid support. For example, complex protein mixtures can be fractionated by SDS gel electrophoresis, blotted onto membrane, and then tested as potential substrates by incubating the membrane with a non-specific blocking agent followed by the desired protein sample plus labeled ATP.

Another variation on this type of assay involves detection of the phosphorylated form of a protein using a monoclonal antibody directed to the phosphorylated form. The amount of phosphorylation may then be assayed in an enzyme-linked immunosorbent assay (ELISA).

#### Typical assay of kinase activity

The kinase activity of a particular sample or protein can be assayed using histone H-1 as a substrate to which the kinase transfers phosphate. For example in a reaction volume of 100 $\mu$ l containing 30 mM HEPES (pH 7.5), 5  $\mu$ M MgCl<sub>2</sub>, 40  $\mu$ g of histone, 100 $\mu$ M CaCl<sub>2</sub>, 10  $\mu$ M [ $\gamma$ -<sup>32</sup>P] ATP and 1.25 mg/ml phosphatidylserine. Assays are started by the addition of 2.5m-units (arbitrary units, dilution series) of sample, incubated at 30°C for 10 minutes and terminated either by spotting on to P81 paper (Whatman) or by the

addition of Laemmli buffer. Spotting onto Whatman paper is followed by extensive washing in 75 mM orthophosphoric acid. The papers are then washed in ethanol, dried and incorporated radioactivity determined either by autoradiography, scintillation spectroscopy or phosphoimaging. After the addition of Laemmli sample buffer the sample is resolved on a 10% SDS-PAGE gel; the gel is dried and then autoradiographed. The amount of incorporated nucleotide is then determined using either autoradiography or phosphoimaging. It may be essential to add certain co-factors that activate a particular kinase e.g. Calcium-dependant kinases would require calcium within the assay.

Such an assay is described for example in Wilkinson SE, Parker P and Nixon JS (1993) *Biochem. J.*, 294, 335-337.

## 2. Phosphatases

Protein phosphorylation provides one means of regulating cellular processes. Protein dephosphorylation by protein phosphatases plays an equally important role. Phosphatases are involved in the removal of the phosphoryl group from proteins that have been phosphorylated by kinases.

### Typical assay for phosphatase activity

Assays for phosphatase activity can be carried out in the same way as a kinase assay. This would involve the pre-phosphorylation of histone by a kinase in the presence of radioactive ATP, followed by desphorylation by the test protein. The sample is then spotted onto P81 paper and the amount of radioactive ATP still incorporated is measured as previously described.

### 3. Adenylyl cyclases - cAMP formation from ATP

#### Measurement of intracellular cAMP.

Cyclic adenosine 3',5' monophosphate (cAMP) can be measured in tissue slices, dissociated tissue, cultured cells and membrane preparations.

Two procedures are currently used for measurement of cAMP: (1) radioimmunoassay and (2) the cAMP binding protein method

Radioimmunoassay uses antibody raised to acetylated cAMP and involves competition between cAMP in the sample and  $^{125}\text{I}$ -labelled cAMP (Steiner, A.L., Wehmann, R.E., Parker, C.W. and Kipnis, D.M. (1972). *Adv. Cyc. Nucleotide Res.*, 2, 51.). Following an overnight incubation, unbound cAMP is removed using charcoal. cAMP levels are quantified by comparison with a cAMP standard curve and expressed relative to protein content of sample. This method is sensitive in the femtomolar range if the sample cAMP and the standard curve cAMP are acetylated before assay. Kits are available commercially (Amersham).

The cAMP binding protein method is based on competition between  $^3\text{H}$ -labelled cAMP and sample cAMP for binding sites on the regulatory subunit of cAMP-dependent protein kinase (Gilman, A.G. (1970). *Proc. Natl. Acad. Sci. USA*, 67, 305.). The procedure is analogous to radioimmunoassay but is more rapid because competition equilibrium is achieved in a 2 hour incubation. cAMP-dependent protein kinase preparation (Sigma) and binding protein assay kits (Amersham) are available commercially.

#### Measurement of adenylyl cyclase activity.

Adenylyl cyclase catalyses the formation of cAMP from ATP in the presence of  $\text{Mg}^{2+}$ . The main methods are: (1) the measurement of  $^{32}\text{P}$ -labelled cAMP formed from  $^{32}\text{P}$ -labelled ATP and (2) the measurement of cAMP formed in a non-labelled reaction using either the radioimmunoassay or the binding protein assay.

Assay for adenylyl cyclase using  $^{32}\text{P}$ -labelled ATP: Radioactively labelled cAMP produced from  $^{32}\text{P}$ -ATP in an *in vitro* reaction is separated from unreacted substrate and radioactive contaminants by sequential chromatography steps on Dowex and alumina columns and measured by liquid scintillation counting (Salomon, Y., Londos, C., and Rodell, M. (1974). *Anal.Biochem.*, 58, 541.). Crude or partially purified adenylyl cyclase samples may contain contaminating activities that interfere with the assay. Problems with nucleoside triphosphatase are minimised using a high substrate concentration in the adenylyl cyclase reaction and by including phosphoenol pyruvate and pyruvate kinase as an ATP regenerating system. Degradation of  $^{32}\text{P}$ -labelled cAMP can be prevented by including a high concentration of unlabelled cAMP in the reaction. The enzymatic reaction is terminated by addition of unlabelled ATP and by boiling for 2 minutes. Addition of [ $^3\text{H}$ ]cAMP as a recovery label allows correction for differences in the performance of the individual chromatography columns. To isolate cAMP from the adenylyl cyclase reactions the samples are first layered on a column of Dowex AG 50 WX 4 resin (200-400 mesh,  $\text{H}^+$  form) equilibrated in water. The cAMP has a greater affinity for the resin than ATP so the bulk of the [ $^{32}\text{P}$ ] ATP can be washed off the column with water before eluting the cAMP directly onto an alumina column equilibrated with 0.1 M imidazole HCl, pH 7.5. The remaining [ $^{32}\text{P}$ ] ATP binds to the alumina and the labelled cAMP is eluted using imidazole buffer. Samples are counted in  $^{32}\text{P}$  and  $^3\text{H}$  channels using a scintillation counter. Measurement of total [ $^{32}\text{P}$ ] ATP and [ $^3\text{H}$ ] cAMP allows calculation of pmols of cAMP present in the sample. Adenylyl cyclase enzymatic activities are expressed as pmol cAMP formed per min per mg protein in the sample. The Dowex and alumina columns must be calibrated before use to determine elution profiles of ATP and cAMP but they may be regenerated after each assay and used repeatedly. The assay is sensitive, relatively simple and may be completed



in one day. Apparatus for the double chromatography should be constructed from perspex to reduce risk from exposure to radioactivity.

*Non-labelled adenylate cyclase reactions.* Reactions contain ATP,  $Mg^{2+}$ , an ATP regenerating system and an inhibitor of cAMP phosphodiesterase such as 3-isobutyl-1-methylxanthine (IBMX). Reactions are terminated by boiling and cAMP formed is measured by radioimmunoassay or cAMP protein binding assay.

#### 4. Guanylyl cyclases - cGMP formation from GTP

##### Measurement of guanylate cyclase activity.

Guanylate cyclase catalyses the hydrolysis of guanosine triphosphate (GTP) to cyclic guanosine 3',5' monophosphate (cGMP) in a reaction analogous to that of adenylate cyclase. Methodology used in the assay of guanylate cyclase activity is essentially the same as that for adenylate cyclase. Manganese is required as a cofactor for guanylate cyclase activity. Reactions are terminated by addition of HCl and boiling for 3 minutes.

Assay for guanylate cyclase using [ $^{32}P$ ] GTP: This method depends on the separation of labelled-cGMP from unreacted substrate [ $^{32}P$ ] GTP by sequential chromatography (Karczewski, P. and Krause, E.G. (1978). *Acta Biol. Med. Ger.*, 37, 961.). Dowex 50 cation exchange columns and alumina columns are prepared and calibrated in exactly the same way as for the separation of cAMP except that the Dowex columns should be longer. cGTP is eluted from the alumina column with 0.2M ammonium formate buffer.

*Non-labelled guanylate cyclase reactions.* Reactions contain GTP,  $Mn^{2+}$ , a GTP regenerating system and IBMX. Reactions are terminated by boiling and cGMP formed is measured by radioimmunoassay using antibody against acetylated cGMP. Kits are available commercially (Amersham).

## 5. Phosphodiesterases - cAMP/cGMP hydrolysis

### Assay of cyclic nucleotide phosphodiesterase activity.

Cyclic nucleotide phosphodiesterase catalyses the hydrolysis of the 3',5'-phosphodiester bond of the cyclic nucleotides, cAMP and cGMP.

The radioactive assay uses  $^3\text{H}$ -labelled cAMP or cGMP and involves quantification of the reaction product (5'-nucleotide monophosphate) (Thompson,, W.J. and Appleman, M.M. (1971). *Biochemistry*, 10, 311.). The labelled NMP formed in the first reaction is converted to 5'-nucleotide in a second reaction by a 5'-nucleotidase present in snake venom. The labelled 5'-nucleotide is isolated by Dowex-1-chloride anion exchange chromatography and quantified by liquid scintillation counting.

## 6. ATPases - hydrolysis of ATP to ADP

Enzyme immunoassay for cAMP. The Biotrack™ assay (Amersham Pharmacia Biotech) is an enzyme immunoassay in which the sample cAMP and peroxidase-linked cAMP compete for binding to antibody raised against acylated cAMP.

### Assay for adenosine 5'-triphosphatase

Adenosine 5'-triphosphatases (ATPases) catalyse the hydrolysis of ATP to ADP and inorganic phosphate in the presence of  $\text{Mg}^{2+}$ ,  $\text{Na}^+$  and  $\text{K}^+$ . The colorimetric assay quantifies the inorganic phosphate released from ATP by measuring the  $A_{660\text{nm}}$  following treatment of the enzyme reaction with TCA and Taussky-Shorr Colour Reagent (Bonting, S.L., Simon, K.A., and Hawkins, N.M. (1961) *Arch. Biochem. Biophys.*, 95, 416-423. Tausky, HH and Shorr, E. (1953) *J. Biol. Chem.*, 202, 675-685.). Similar methods are used to assay guanosine 5'-triphosphatases (GTPases).

## 7. GTPases - hydrolysis of GTP to GDP

Assays essentially the same as for ATPases (see Sections 6 and 17). Commercial kits available.

## 8. Proteases

### General Assay for Proteolytic activity Proteases

This assay is based on the proteolytic digestion of casein and the spectrophotometric detection of released aromatic amino-acids. Briefly, casein is incubated with the suspected protease and then acid precipitated. The solution is then filtered and the absorbance of the acid soluble phase is measured at 280-290nm. See for example W. Rick in "Methoden der Enzymatischen Analyse", (H.U. Bergmeyer ed.) 3rd edition, 1046 and 1056. Verlag Chemie, Weinheim.

### Example of a specific protease assay - Assay for the serine protease Chymotrypsin.

Endpoint titration with the fluorescent molecule 4-methylumbelliferyl p-(N,N,N-triethylammonium) cinnamate. This compound is sensitive to  $10^{-11}$  moles of enzyme with a 2 min reaction time, see for example G.W. Jameson, D.V. Roberts, R.W. Adams, W.S.A Kyle and D.T. Elmore. (1973) Biochem. J., 131, 107.

## 9. Assays for secretion and import of proteins

These assays fall into three groups

- A) Reconstitution in cell-free extracts
- B) Reconstitution in semi-intact perforated cells
- C) Assays for Endocytosis

### A) Reconstitution in cell free extracts

The general principle of this type of assay is based on the detection of membrane fusion events and/or the delivery of protein contents using purified membrane compartments. The detection methods include immunodetection, fluorescence and release of chromogenic substances.

Example:- The detection of endocytic vesicle fusion in vitro using an assay based on the avidin-biotin association reaction.

The assay involves the use of two different populations of vesicles, each containing a different molecular probe conjugated to a marker protein. Upon fusion the probes bind to one another to generate a detectible signal, in this case the binding of avidin to biotin. Complexes are detected by an ELISA protocol (detecting the biotinylated protein e.g. transferrin) and fluorescent detection of avidin conjugated  $\beta$ -galactosidase, see for example William A. Braell in "Methods in Enzymology" 219, 12-21 Academic Press inc. 1992.

B) Reconstitution using Semi-intact/perforated cells

Semi-intact/perforated cells are those which have lost a part of their plasma membrane by physical perforation. These assays can be done in Yeast or mammalian cells. Though lacking many soluble cytoplasmic factors, these cells retain their internal membrane and organellar structure and can efficiently reconstitute vesicular transport between compartments. They are also accessible to exogenously added factors such as antibodies and inhibitors.

Example:- Transport of a Protein between the Endoplasmic Reticulum and Golgi compartments.

This assay is based on the expression and transport of the Vesicular stomatitis virus (VSV) G protein. This viral glycoprotein has two Asparagine linked oligosaccharide chains which undergo extensive modifications as the protein transverse the ER and Golgi compartments. Oligosaccharide processing intermediates confer different electrophoretic mobilities on the VSV polypeptide, these intermediates can therefore be detected by SDS PAGE, see for example C.J.M. Beckers, D.S. Keller and W.E. Balch. Cell. 50, 523 (1987)

### C) Assays for Endocytosis

Assays for the endocytic pathway include those for detection of the binding of proteins to cell surface receptors, formation of clathryn coated endocytic vesicles, transport to the endosome, uncoating of the vesicles, delivery of the vesicle contents and recycling to the plasma membrane.

Example:- Detection of Functional Clathryn Coated Vesicles.

This assay involves the preparation of two vesicle fractions

- i) The "donor" population containing  $^{125}\text{I}$ -labelled transferrin.
- ii) The "acceptor" vesicles, these being the clathryn coated vesicles under test. The acceptor vesicles contain internalised Anti-transferrin antibody.

The donor and acceptor populations are mixed in a solution containing cytosol and an ATP cocktail. Upon vesicle fusion a radiolabelled immunocomplex is formed. The vesicles are then solubilised and the mix passed through a *Staphylococcus aureus* column to isolate the immunocomplexes, which are then eluted from the column and the radioactivity measured, see for example P.G. Woodman and G. Warren in "Methods in Enzymology", 219, 251 (1992)

### 9. Ribo/deoxyribo-nucleases - endo/exo-nuclease activity Deoxyribonuclease

An endonuclease with preference for DNA. Pancreatic DNase I yields di- and oligo-nucleotide 5' phosphates, pancreatic DNase II yields 3' phosphates. In chromatin, the sensitivity of DNA to digestion by DNase I depends on its state of organization, transcriptionally active genes being much more sensitive than inactive genes.

### Ribonuclease

Widely distributed type of enzyme that cleaves RNA. May act as endonucleases or exonucleases depending upon the type of enzyme. Generally recognise target by tertiary structure rather than sequence. Ribonuclease E is an RNase involved in the formation of 5S ribosomal RNA from pre-rRNA. F is stimulated by interferons and cleaves viral and host RNAs and thus inhibits protein synthesis. H specifically cleaves an RNA base-paired to a complementary DNA strand. P is an endonuclease that generate t-RNAs from their precursor transcripts. T is an endonuclease that removes the terminal AMP from the 3' CCA end of a non-aminoacylated tRNA. RNase T1 cleaves RNA specifically at guanosine residues. RNase III cleaves double-stranded regions of RNA molecules.

### Endonuclease

One of a large group of enzymes that cleave nucleic acids at positions within the chain. Some act on both RNA and DNA (eg. S1 nuclease, EC.3.1.30.1, that is specific for single stranded molecules). Ribonucleases such as pancreatic, T1 etc. are specific for RNA, Deoxyribonucleases for DNA. Bacterial restriction endonucleases are crucial in recombinant DNA technology for their ability to cleave double-stranded DNA at highly specific sites.

### Nuclease

An enzyme capable of cleaving the phosphodiester bonds between nucleotide subunits of nucleic acids.

### Restriction Endonuclease

Class of bacterial enzymes that cut DNA at specific sites. In bacteria their function is to destroy foreign DNA, such as that of bacteriophages (host DNA is specifically modified at these sites). Type I restriction endonucleases occur as a complex with the methylase and a

polypeptide that binds to the recognition site on DNA. They are often not very specific and cut at a remote site. Type II restriction endonucleases are the classic experimental tools. They have very specific recognition and cutting sites. The recognition sites are short, 4-8 nucleotides, and are usually palindromic sequences. Because both strands have the same sequence running in opposite directions the enzymes make double-stranded breaks, which, if the site of cleavage is off-centre, generates fragments with short single-stranded tails; these can hybridise to the tails of other fragments and are called sticky ends. They are generally named according to the bacterium from which they were isolated (first letter of genus name and the first two letters of the specific name). The bacterial strain is identified next and multiple enzymes are given Roman numerals. For example the two enzymes isolated from the R strain of E. coli are designated Eco RI and Eco RII. The more commonly used restriction endonucleases are shown in Table R1.

Ref: Definitions taken from the Dictionary of Cell Biology (Second Edition), Academic Press.

#### General Assay

All of the above nucleases cleave DNA and/or RNA, therefore a general assay would be to incubate unknown/test protein/chemical with a known quantity and type of DNA or RNA for a given time, and separate the products using gel electrophoresis along with a known set of standards. Any nuclease activity will be readily visible on the gel. Once nuclease activity has been detected, direct comparisons can be made with the DNA cleavage patterns generated by known nucleases in order to identify the type of nuclease involved.

10. DNA metabolism - ligase, topoisomerase, etc  
DNA glycosidase

Class of enzymes involved in DNA repair. They recognise altered bases in DNA and catalyse their removal by cleaving the glycosidic bond between the base and the deoxyribose sugar. At least 20 such enzymes occur in cells.

DNA ligase

Enzyme involved in DNA replication. The DNA ligase of *E.coli* seals nicks in one strand of double-stranded DNA, a reaction required for linking precursor fragments during discontinuous synthesis on the lagging strand. Nicks are breaks in the phosphodiester linkage that leave a free 3'-OH and 5'-phosphate. The ligase from phage T4 has the additional property of joining two DNA molecules having completely base-paired ends. DNA ligases are crucial in joining DNA molecules and preparing radioactive probes (by nick translation) in recombinant DNA technology.

DNA methylation

Process by which methyl groups are added to certain nucleotides in genomic DNA. This affects gene expression, as methylated DNA is not easily transcribed. The degree of methylation is passed on to daughter strands at mitosis by maintenance DNA methylases. Accordingly, DNA methylation is thought to play an important developmental role in sequentially restricting the transcribable genes available to distinct cell lineages. In bacteria, methylation plays an important role in the restriction systems, as restriction enzymes cannot cut sequences with certain specific methylations.



DNA/RNA synthesis

DNA polymerase and RNA polymerase are enzymes involved in template-directed synthesis of DNA from deoxyribonucleotide triphosphates and RNA from ribonucleotide triphosphates.

Repair nuclease

Class of enzymes involved in DNA repair. It includes endonucleases that recognise a site of damage or an incorrect base pairing and cut it out, and exonucleases that remove neighbouring nucleotides on one strand. These are then replaced by a DNA polymerase.

Topoisomerase

An enzyme capable of altering the degree of supercoiling of double-stranded DNA molecules. Various topoisomerases can increase or relax supercoiling, convert single-stranded rings to intertwined double-stranded rings, tie and untie knots in single stranded and duplex rings, catenate and decatenate duplex rings. Topoisomerase II of *E.coli* = gyrase.

General Assay

All of the above act to modify the structure of DNA. For each enzyme involved in DNA metabolism, a corresponding assay is available commercially.

**11. Transcription factors**Transcription Factor Assays

Transcription factor activity lies in the centre of a signalling cascade that begins at the cell surface by the activation of a receptor. Intracellular signal transduction events activate or repress specific transcription factors, which in turn regulate the expression of specific genes.

The activity of a transcription factor can be assessed by linking the appropriate regulatory sequence to a reporter gene encoding among other reporters  $\beta$ -galactosidase, CAT, luciferase and GFP in an engineered plasmid vector. This vector is used to transfect a cell line and the activity of the transcription factor of interest analysed by measuring the amount of reporter activity (Brannon, M. et al (1997) Gen. Dev. 11, 2359.).

Of the many different strategies available for using genetic reporters, luciferase offers the most ideal situation because the reporter measurements are nearly instantaneous, exceptionally sensitive and there is little or no endogenous activity in the host cells to interfere with quantitation. Firefly luciferase (Ow, D et al (1986) Science 234, 856.) is by far the most commonly used of bioluminescent reporters. The enzyme catalyses a two-step oxidation reaction to yield light at 550-570nm that can be detected by the use of a luminometer. The assay can be adapted for use with single or multiple samples depending on the type of luminometer available, i.e. tube or plate.

The above is an *in vivo* transcription factor assay requiring the transfection of an appropriate cell line with the reporter vector. However, an *in vitro* method for transcription/DNA binding factor analysis also exists.

The gel shift or electrophoretic mobility shift assay provides a simple and rapid method for detecting sequence-specific binding proteins, such as transcription factors (Ausubel, F.M. et al. (1989) In: Current Protocols in Molecular Biology, Vol. 2, John Wiley and Sons, New York.). The assay is based upon the observation that complexes of protein and DNA migrate through a non-denaturing polyacrylamide gel more slowly than free DNA fragments or double stranded oligonucleotides. The gel shift assay is performed by incubating a purified protein or a complex mixture of proteins such as a nuclear extract preparation with a  $^{32}\text{P}$  labelled DNA fragment containing the putative binding site. The reaction products are then analysed on a

nondenaturing polyacrylamide gel. The specificity of the DNA-binding protein for the putative binding site is established by competition experiments using DNA fragments or oligonucleotides containing a binding site for the protein of interest.

## 12 Apoptosis

Apoptosis is the physiological process by which unwanted or useless cells are eliminated during development and other normal biological processes, e.g. tissue homeostasis, embryogenesis, induction and maintenance of immune tolerance, development of the nervous system and endocrine-dependent tissue atrophy.

The process of apoptosis involves a cascade of cytoplasmic and nuclear events that result in a series of morphological changes and eventually cause the demise of the cell. Apoptosis can be initiated by a variety of different stimuli that lead to a convergence of biochemical signalling pathways into a common collection of executioner molecules.

In the early stages of apoptosis, changes occur at the cell surface and plasma membrane. One of these plasma membrane alterations is the translocation of phosphatidylserine (PS) from the inner side of the plasma membrane to the outer layer, where PS becomes exposed at the external surface of the cell. Mitochondrial physiology is disrupted in cells undergoing apoptosis. Permeability is altered and specific protease activators are released. Specifically, the discontinuity of the outer mitochondrial membrane results in the redistribution of cytochrome C to the cytosol followed by subsequent depolarisation of the inner mitochondrial membrane. Cytochrome C release further promotes apoptosis by the activation of the caspases, cysteine proteases. Active caspases participate in a cascade of cleavage events, which disable key homeostatic and repair enzymes and bring about a systematic structural disassembly of dying cells. The biological substrates of

caspases include poly(ADP ribose) polymerase (PARP), DNA-dependent protein kinase (DNA-PK), lamins, topoisomerases, Gas2, protein kinase C (PKC), sterol regulatory element binding proteins (SREBP), U1-70kDa protein and Huntingtin protein.

The biochemical hallmark of apoptosis is the fragmentation of genomic DNA, an irreversible event that commits the cell to die and occurs before changes in plasma membrane permeability.

In concert with increased understanding of the physiological events that occur during apoptosis, a number of assay methods have been developed for its detection. These assay methods can measure one of the following apoptotic parameters:

1. Fragmentation of DNA in populations of cells or in individual cells, in which apoptotic DNA breaks into different length pieces.
2. Alterations in membrane asymmetry. PS translocates from the cytoplasmic to the extracellular side of the cell membrane.
3. Activation of apoptotic caspases.
4. Release of cytochrome C into the cytoplasm by mitochondria.

Each provides the researcher with a different level of information as each of these events occurs at a different stage in apoptosis.

The early proteolytic events of apoptosis can be monitored using an adaptation of the absorbance-based assay originally devised by Thornberry, N.A. (1994) Interleukin-1 beta converting enzyme. Meth.Enzymol. 244, 615. The colorimetric substrate (Ac-DEVD-pNA) is labelled with the chromophore p-nitroaniline(pNA). pNA is released from the substrate upon cleavage by DEVDase. Free pNA produces a yellow colour that is monitored by a photometer at 405nm. The amount of yellow colour that is produced upon cleavage is proportional to the amount of DEVDase activity present in the sample. The potent, irreversible, pan-caspase

inhibitor Z-VAD-FMK can be used as a negative control and it is suggested that apoptosis be induced by the addition of Fas or TNF agonist antibodies.

The protocol can be used to test multiple samples by performing the assay in a total volume of 100ml using cells cultured in 96 well plates. The absorbance produced by each sample is read using a plate reader.

### 13 Calcium

#### Calcium dynamics

In a multicellular organism, cell communication is essential to regulate the different activities of specialised tissues. In all animal cells, there are conserved intracellular second messenger pathways. For many of these, calcium is an important second messenger. In nerve cells, muscle and other cells, modulation of intracellular calcium activity from typical resting levels of 100 nM regulates many short and long-term processes. Measurement of calcium can thus be of great utility in following the responses of transgene products to applied pharmacological agents including insecticides.

Calcium dynamics may be detected directly or indirectly by a range of methods; including but not restricted to: a) transgenic apoaeguorin, a calcium-sensitive luminescent protein; b) other methods that monitor intracellular calcium concentration; c) other methods that monitor the operation of intracellular calcium signalling pathways; d) methods that monitor the operation of other types of signalling pathway; e) methods that monitor neuronal electrical potentials.

For example, transgenic apoaeguorin has been used to monitor calcium dynamics in the intact *Drosophila* renal system and the intact *Drosophila* brain (Rosay et al (1997) J. Cell. Sci. 110, 1683-1692; O'Donnell et al. (1998) Am. J. Physiol. 43(4), R1039-R1049.). It has also been used to provide a bioluminescent assay for agonist activity against G protein coupled receptors (Stables et al. (1997) Anal.

Biochem. 252, 115-126). Transgenic apoaeguorin can thus be used to assess the effect of an exogenous gene on intracellular calcium dynamics, the method comprising detecting a pattern of calcium dynamics in cells, tissues or organisms expressing the exogenous gene, and comparing said pattern with a pattern of calcium dynamics in cells, tissues or organisms without said exogenous gene.

Additionally, fluorescent probes (such as fura-2, indo-1, quin-2) show a spectral response upon binding calcium and it is then possible to detect changes in intracellular free calcium concentrations using fluorescence microscopy, flow cytometry and fluorescence spectroscopy. Most of these fluorescent indicators are variations of the nonfluorescent calcium chelators EGTA and BAPTA (Cobbold and Rink (1987) Biochem. J., 248, 313.).

New fluorescent indicators for calcium called "cameleons" may also be used and are genetically encoded without cofactors and are targetable to specific intracellular locations. These so-called "cameleons" consist of tandem fusions of a blue- or cyan-emitting mutant of the green fluorescent protein (GFP), calmodulin, the calmodulin-binding peptide M13, and an enhanced green- or yellow-emitting GFP. Binding of calcium makes calmodulin wrap around the M13 domain, increasing (Miyawaki et al., (1997) Nature, 388, 882-887.) or decreasing (Romoser et al., (1997) JBC, 272, 13270-13274.) the fluorescence resonance energy transfer between flanking GFPs.

Additionally, potentiometric optical probes may be used. Potentiometric optical probes measure membrane potential in organelles and in cells. In conjunction with imaging techniques, these probes can be employed to map variations in membrane potential along neurons and among cell populations with high spatial resolution and sampling frequency (Rohr and Salzberg (1994) Biophys. J., 67, 1301.).

Additionally, GFP-based reporter genes that monitor intracellular cAMP dynamics may be used, and to monitor intracellular pH changes (Miesenbock et al. (1998) Nature

394, 192-5).

#### 14 cAMP

Effects on dynamics of intracellular cAMP as reported by appropriate dyes or reporter constructs (eg. aequorin). See section 13.

#### 15 Voltage

Analysis of transmembrane potential permits study of the elements which mediate electrical behaviour of cells. This form of study may be undertaken in a number of ways, including: voltage (patch) - clamping and the use of voltage sensitive dyes.

##### Patch clamping

In brief, this involves sealing a blunt micropipette tip to a cell membrane. This is termed a gigaseal. The gigaseal electrically isolates the whole cell or a patch of the membrane allowing detection of picoampere, ionic currents while accurately controlling the voltage. This form of analysis may be utilised in the study of cultured cells, tissue slices or recombinant ion channels expressed post DNA transfection in heterologous cells. Whole cell recording measures the activity of the full complement of active channels in a cell; typically specific populations of channels are isolated using channel-blocking agents. It is also possible to isolate single ion channels, providing information on the unitary conductance and kinetic behaviour of individual channels, and allow the factors which alter these properties to be studied in exquisite detail (Crawley et al., 1997 Neurophysiology Current protocols in neuroscience Volume 1 [John Wiley and Sons, Inc.]). Patch Clamp techniques are widely used and cited throughout scientific literature (Siegel M.S and Isacoff E.Y (1997) *Neuron* 19, 735 - 741; Sensi S., Canzoniero L.M, Yu S.P, Ying H.S, Koh J.Y, Kerchner G.A, Choi D.W. (1997) *J. Neuroscience* 17, 9554 - 9564; Piller S.C, Jans P., Gage

P.W., Jans D.A (1998) Proc. Natl. Acad. Sci. USA, 95, 4595 - 4600; Maric D., Maric I., Wen X., Fritschy J.M, Sieghart W., Barker J.L, Serafini R., (1999) J. Neuroscience 19, 4921 - 4937). An example of how this kind of analysis may be used is outlined below.

*Whole cell patch clamp recording to study the effects of a viral protein on whole cell currents of cultured hippocampal neurons.*

Whole cell currents represent the integrated channel activity over the whole cell. Cultured cells on coverslips were perfused with bath solution (140 mM NaCl, 5 mM KCl, 3 mM CaCl<sub>2</sub>, 2 mM MgCl<sub>2</sub>, 10 mM glucose, 10 mM TES [pH7.3]) at room temperature (23 to 28C). Pipettes made from borosilicate glass were fire polished and filled with pipette solution normally containing 150 mM NaCl, 0.5 mM CaCl<sub>2</sub>, 2 mM MgCl<sub>2</sub>, 5 mM EGTA and 10 mM TES [pH7.3]. Reversal potentials were determined experimentally by altering the holding potential until currents reversed direction and the potential for zero current was recorded. Cells were routinely clamped at - 60 mV. Whole cell currents were recorded both before and after the addition of purified viral protein by using an Axopatch 200A. Viral protein @ 0.6 nM in bath solution was applied directly onto patched cells through gravity fed drug delivery tubing. whole-cell currents were filtered at 5 or 10 kHz, digitized at 44 kHz, and stored on videotape. For data analysis currents were replayed through the same system and digitized using an A to D converter interfaced with an IBM-compatible computer. Inward currents are depicted as downward deflections from the zero current level.

*Electrical potential may also be measured using voltage sensitive dyes. e.g. Oxonol VI / Bis-oxonol (Dall'Asta V., Gahi R., Orlandini G., Rossi P.A, Rotoli B.M, Sala R., Bussolati O., Gazzola G.C, (1997) Experimental Cell Research 231, 260 - 268; Salvador J.M, Inesi G, Rigaud J.L,*



Mata A.M, (1998) J. Biol. Chem. 273, 18230 - 18234).

In the study by Salvador et al., 1998, transmembrane electrical potential was measured by analysis of the differential absorption (625 - 603 nm) of 2  $\mu$ M oxonol using dual wavelength spectrophotometry. The medium comprised Pipes buffer, pH7.1; 0.42  $\mu$ g/ml calmodulin; 5mM MgCl<sub>2</sub> and 2  $\mu$ M Oxonol VI. The callibration was performed by several additions 130 mM KCl to the medium in the presence of 1  $\mu$ M of the K<sup>+</sup> ionophore valinomycin and in the absence of ATP. Absorption changes were standardized using the Nernst equation. Within a range 0 - 40 mV Absorption by oxonol demonstrates a linear increase with increasing membrane potential. This proportionality permits straightforward assay of changes in membrane potential.

Dall'Asta et al., 1997 visualize changes in membrane potential using Bis-oxonol. Bis-oxonol is a fluorescent dye which distributes across biological membranes according to the membrane potential and binds to hydrophobic components: since the quantum yield of the dye increases with binding, the fluorescence of the cells incubated in a medium containing the dye increases with depolarization and decreases with hyperpolarization.

## 16. Receptors/ion channels

### **Ion Channels/Receptors**

Neuronal signaling depends on rapid changes in the electrical potential difference across nerve cell membranes. These rapid changes in potential are made possible by ion channels, a class of integral membrane proteins that traverse the cell membrane. These channels have three important properties: (1) they conductions, (2) they recognise and select among specific ions, and (3) they open and close in response to specific electrical, mechanical, or chemical signals. [Principles of Neural Science, (Kandel and Schwartz), Chapter 5 Ion Channels]. Ion channels are large integral membrane glycoproteins, which have a central aqueous pore that spans the entire

width of the membrane. Many ion channels are made up of two or more subunits, which may be identical or distinct. Three major signals gate ion channels: voltage (voltage-gated channels), chemical transmitters (transmitter-gated channels), and pressure or stretch (mechanically-gated channels). Gating involves a conformational change of the channel in response to the above stimuli.

Several major classes of ion channels have now been identified. Primary sequence information has been used to suggest the structure of different channel proteins. Efforts to determine secondary structure rely on X-ray crystallography. However, additional information can be obtained by comparing the primary amino acid sequence of related channels from different species and identifying regions of sequence homology, suggesting the importance of such regions in channel structure and function. Further insight into structure-function relationships can be obtained from sequence homologies among different, but related, channels. Such homologous regions are likely to underlie a common biophysical function shared by the different channels, i.e. Voltage-gated versus transmitter-gated channels.

The flux of ions through ion channels is passive, requiring no expenditure of metabolic energy. The direction and eventual equilibrium for this flux is determined not by the channel itself, but rather by the electrochemical driving force across the membrane. Ion channels select the type of ions that they allow to cross the membrane through physio-chemical interaction between the ion and various amino acid residues that line the walls of the channel pore (on the basis of ionic charge), allowing either cations or anions to permeate. Some cation-selective channel types are relatively non-selective, passing  $\text{Na}^+$ ,  $\text{K}^+$ ,  $\text{Ca}^{2+}$ , and  $\text{Mg}^{2+}$ . However, most cation-selective channels are more selective; each one is permeable primarily to a single type of ion, either  $\text{Na}^+$ ,  $\text{K}^+$ , or  $\text{Ca}^{2+}$ . All known types of anion-selective channel are

permeable to  $\text{Cl}^-$ . Note that the  $\text{Ca}^{2+}$  influx controlled by channels can alter many metabolic processes within cells, leading to activation of various enzymes and proteins.  $\text{Ca}^{2+}$  influx also acts as a trigger for the release of neurotransmitter.

The activity of channels can be modified by cellular metabolic reactions, including protein phosphorylation, by various channel blockers, toxins, poisons, and drugs. Channels are important targets in various diseases, eg myasthenia gravis and cystic fibrosis.

**Molecular analysis:** Starting with an unknown chemical for which no information is available, and depending on the size of the starting molecule, peptide sequence can be obtained either directly or by using the chemical bound to a column to purify the target molecule in the cell (e.g., benzodiazepine affinity chromatography purification columns were used to isolate and identify the first cDNA clones encoding GABA receptor subunits in 1987 - Schofield P.R., Darlison M.G., Fujita N., Burt D.R., Stephenson F.A., Rodriguez H., Rhee L.M., Ramachandran J., Reale V., Glencorse T.A., Seeburg P. And Barnard E.A (1987) *Nature* 328, 221 - 227). From peptide sequence, best-guess oligonucleotides can be synthesized and used to screen species-specific cDNA libraries. Any cDNA clones identified can then be sub-cloned, sequenced and the primary sequence analysed for known sequence homologies with BLAST database searches. The full-length sequence, cDNA and corresponding expressed protein, can then be subjected to standard biochemical and molecular characterisation procedures.

**Functional analysis:** single-channel recording can measure the activity of a single protein molecule (electrophysiology). The patch clamp technique has made it possible to measure directly the activity of single ion channel molecules by recording the unit current flow through single open channels. Expression of cRNAs in the *Xenopus* oocyte system, cDNA in transfected cell lines or

whole tissue slice cultures can be used.

Example of cRNA expression in *Xenopus* oocyte: pure mRNA, produced by *in vitro* transcription from cDNA, is microinjected into *Xenopus* oocytes and pulses of known compounds (eg GABA, glutamate, etc) can be superfused over the oocyte while recording membrane currents under voltage-clamp conditions. Current response to applied compound can be measured.

#### Two main gene families:

- |  |   |
|--|---|
| 1. Voltage gated channels:             | Na <sup>+</sup> , K <sup>+</sup> and Ca <sup>2+</sup> |
| 2. Ligand-gated ion-channel receptors: | cation: nACh,   |
| either Integral (pore forming,         | 5HT, glutamate,                                       |
| Ion gating) or Second messenger        | anion: GABA   |
| systems (associated)                   | Glycine   |

#### **Methods**

1. cloning: sequence analysis primary and secondary
2. structure: crystallography, *in situ*, immunocyto, immunohisto, immunoEM
3. function: electrophysiology: slice culture/patch clamp transfection/patch clamp

#### Voltage-Gated Channels

In nerve cells at rest (membrane potential: -65mV), the steady Na<sup>+</sup> influx through non-gated channels is balanced by steady K<sup>+</sup> efflux, so that the membrane potential is constant. This steady state balance changes when the cell is sufficiently depolarised to trigger an action potential. A transient depolarising potential, such as excitatory synaptic potential, causes some voltage-gated Na<sup>+</sup> channels to open, and the resultant increase in membrane Na<sup>+</sup> permeability allows Na<sup>+</sup> influx to outstrip the K<sup>+</sup> efflux. Thus, a net influx of positive charge flows through the membrane, and positive charges accumulate inside the cell, causing further depolarisation. The increase in

depolarisation causes more voltage-gated  $\text{Na}^+$  channels to open, resulting in a greater influx of positive charge, which accelerates the depolarisation further.

This regenerative, positive feedback cycle develops explosively, driving the membrane potential toward the  $\text{Na}^+$  equilibrium potential of +55mV. Because  $\text{K}^+$  efflux continues through the  $\text{K}^+$  channels, the membrane potential never actually reaches the equilibrium potential of sodium. A slight diffusion of  $\text{Cl}^-$  into the cell also counteracts the depolarising tendency of the  $\text{Na}^+$  influx.

As depolarisation continues, it slowly turns off, or inactivates, the voltage-gated  $\text{Na}^+$  channels. That is, the  $\text{Na}^+$  channels have two types of gating mechanisms: activation, which rapidly opens the channel in response to depolarisation, and inactivation, which slowly closes the channel if depolarisation is maintained. The second repolarising process results from the delayed opening of voltage-gated  $\text{K}^+$  channels. The delayed increase in  $\text{K}^+$  efflux combines with a decreased  $\text{Na}^+$  influx to produce a net efflux of positive charge from the cell, which continues until the cell has repolarised to its resting membrane potential.

Intracellular recording: this technique uses two glass capillary electrodes full of an ionic conductor solution (usually 3M KCl). To measure the resting membrane potential, an intracellular electrode is inserted into the nerve cell (grown in culture or via slice culture) - the pipette acts as a salt bridge, providing electrical connection between the cytoplasm and a metal electrode that is connected to the electronic apparatus. The second extracellular electrode can be used to confirm resting potential and/or stimulate the cell. Both electrodes are connected to a voltage amplifier, which in turn is connected to an oscilloscope that displays the amplitude of the membrane potential (-65mV, at rest).

### Ligand-Gated Channels - Integral Channel

(e.g., nACh, 5HT<sub>3</sub>, glutamate, GABA<sub>A</sub>, Glycine)

A transmembrane ion channel whose permeability is increased by the binding of a specific ligand, typically a neurotransmitter at a chemical synapse. The permeability change is often drastic; such channels let through effectively no ions when shut, but allow passage at up to  $10^7$  ions  $s^{-1}$  when a ligand is bound. These receptors have been found to share considerable sequence homology, implying that there may be a family of structurally related ligand-gated ion channels.

Ion channel receptors are composed of 4 or 5 subunits, which may be the same or different, each of which contains 4 or 5 membrane-spanning  $\alpha$ -helical regions. These  $\alpha$ -helices are thought to align to form the pore of the channel, through which ions can flow. The characteristics of each channel is determined by the type of subunits that are present in each receptor subtype. Annals of the New York Academy of Sciences (1999) Volume 868) Current flow depends on the number of open channels, the concentration of the transmitter, channel conductance and membrane potential.

Receptor specific assays will have to be created for each receptor/ion channel under investigation. The best/easiest way to do this is to create permanent cell lines expressing a particular combination of receptor subunits in order to form particular receptor subtypes. There are many examples of these in the literature, and of the differences in receptor characteristics when different combinations of receptor subtypes are expressed. Initial assays established by the inventors will focus on the most clinically relevant subtype(s) of each receptor. With these permanent cell lines, functional assays can be used to investigate the effects of any chemical on the receptor characteristics e.g., electrophysiology (patch-clamp single-channel recording), binding assays (see section 1), etc.

### Ligand-Gated G-protein linked Receptors

(e.g., mACh, 5HT, GABA<sub>B</sub>, Glutamate, Dopamine, etc)

Many cell surface receptors are coupled to G-proteins (GTP-binding protein). G-protein-coupled receptors are thought to have seven membrane spanning domains, and have been divided into 2 subclasses: those in which the binding site is in the extracellular domain e.g. receptors for glycoprotein hormones, such as thyroid stimulating hormone (TSH) and follicle stimulating hormone (FSH), and those in which the ligand-binding site is likely to be in the plane of the 7 transmembrane domains e.g. rhodopsin and receptors for small neurotransmitters (nACh, 5HT, glutamate-NMDA, GABA, Glycine) and hormones. All transduce their signal by conformational change activation of an associated G-protein (see section 17).

There are two main classes of G proteins, the heterotrimeric G proteins that associate with receptors of the seven transmembrane domain superfamily and are involved in signal transduction, and the small cytoplasmic G proteins. The small G proteins are a diverse group of monomeric GTPases that include ras, rab, rac and rho and that play an important part in regulating many intracellular processes including cytoskeletal organisation and secretion. Their GTPase activity is regulated by activators (GAPs) and inhibitors (GIPs) that determine the duration of the active state. (see section 17), see for example Principles of Neural Science, (Kandel and Schwartz), Third Edition 1991.

#### 17. G-proteins (GTP binding proteins)

GTP binding proteins are a superfamily of related proteins which bind to guanosine nucleotides (Kaziro Y., Itoh H., Kozasa T., Nakafuku M. and Satoh T. Ann. Rev. Biochem. (1991). They are found in an inactive form which is bound to GDP and an active form which is bound to GTP. Other proteins such as ligand bound receptors promote the exchange of GDP with GTP, activating

the protein. G proteins are inactivated by hydrolysis of the GTP to GDP. This reaction is catalysed by the G protein itself but the rate of GTP hydrolysis can be influenced by interaction with other proteins. Activated G proteins regulates the activities of a large number of target proteins including adenylate cyclase, phospholipase C and ion-channels.

#### Heterotrimeric G proteins.

Heterotrimeric G proteins are a large family of GTPases which consist of an  $\alpha$ , a  $\beta$  and a  $\gamma$  subunit. They are involved in signal transduction from receptor proteins in the plasma membrane to second messenger systems within the cell receptors that activate. Activation of a receptor (e.g. by ligand binding) activates the G protein by promoting the exchange of bound GDP with GTP. The presence of GTP in the active site causes the dissociation of the  $\alpha$  subunit from the  $\alpha\beta\gamma$  complex. The free  $\alpha$  subunits is most active. Different  $\alpha$  subunit subtypes interact with a wide variety of different target proteins including adenylate cyclase, phospholipase C and ion-channels. The free  $\beta\gamma$  complex also has also been show to have some regulatory activity.

#### Small(p21) GTPases

These proteins consist of a single subunit similar to the  $\alpha$  subunit of heterotrimeric G proteins. These include the RAS family of proteins the abnormal activity of which can contribute to tumour formation.

#### Other GTP binding proteins

Other members of the Guanosine nucleotide binding protein superfamily include GTP binding translation elongation factors and members of the Dynamin family of proteins.



### Use of Recombinant G proteins

Expression of recombinant G proteins allows the biochemical properties of proteins identified by DNA sequencing to be studied and allows the isolation of large amounts of the proteins for structural and biochemical studies. It also allows the production of mutant proteins produced by site directed modification of cDNA sequences.

Active recombinant G proteins have been expressed in large amounts in bacterial and insect-cell/baculovirus systems. Expression of G proteins in cell free translation systems is a convenient way of producing small amounts of protein for biochemical studies. The addition of  $^{35}\text{S}$  methionine to the *in-vitro* translation reaction results in the production of specifically labelled protein.

It is also possible to express the proteins in cultured cells and look for whole cell effects such as increased cell proliferation, increased DNA synthesis or changes in the activity of various enzymes.

### The use of cell lines lacking G protein subunits.

Several cell lines have been isolated, or made using gene-disruption techniques, which lack particular G protein subunits. The most widely used of these is the *cyc<sup>-</sup>* variant of the S49 mouse lymphoma cell line lack the  $G_{\alpha}$  subunit. It is possible to add back recombinant or purified G proteins to investigate their function. Purified or *in-vitro* translated protein can be added back to membrane preparations from the cell lines or the cells can be transfected with plasmid constructs which express the protein.

### GTP binding assays

The nonhydrolyzable GTP analogue  $^{35}\text{S}\gamma\text{GTP}$  will bind to most GTP binding proteins in the absence of any activator molecule. Purified or *in-vitro* translated G protein can be incubated with  $^{35}\text{S}\gamma\text{GTP}$  and the reaction products passed through a nitrocellulose filter. Protein bound  $^{35}\text{S}\gamma\text{GTP}$  will

be retained on the filter and the activity measured (Carty D.J. and Iyengar R. (1994). Methods in Enzymology. 237: 38-45.).

#### GTPyS activation

Conformational changes in G proteins and changes in subunit interaction can be studied by incubating the G protein with GTPyS which binds to, and irreversibly activates, the protein. Conformational changes in subunits and changes in subunit interaction alter the sites available for degradation by trypsin. The tryptic fragments of radio-labelled protein can be run on a SDS PAGE gel and visualised by autoradiography. Subunit interaction can also be studied by looking at sedimentation rates during ultra centrifugation and by using chemical crosslinking agents (Audigier Y. (1994). Methods in Enzymology. 237: 239-254.

#### Activation of other proteins as a result of G protein activation

G proteins in cell extracts can be activated by incubation with GTPyS and the activities of possible downstream target proteins such as adenylate cyclase and phospholipaseC measured.

#### Receptor stimulated GTP binding and GTP hydrolysis.

Receptor stimulated binding of the radio-labelled non-hydrolyzable GTP analog  $^{35}\text{S}$ yGTP can be used to show if the addition of a receptor ligand leads to the activation of a G protein (Wieland T and Jakobs K.H (1994) Methods in Enzymology 237, 3 - 13). It is possible to study the activation of endogenous G proteins or to use a membrane preparation lacking particular G proteins and add back a purified or recombinant G protein.

$^{35}\text{S}$ yGTP is added to a reaction mix containing a membrane preparation of the cells being studied. After incubation at 37°C for an appropriate length of time the

reaction is stopped. The reaction mix is then passed through a filter which binds protein of membrane. The amount of radioactivity incorporated into the protein/membrane fraction is then measured. The amount of radioactivity incorporated in the presence and absence of candidate receptor ligand molecules can then be compared.

As an alternative to measuring the binding of  $^{35}\text{S}\gamma\text{GTP}$  it is possible to measure GTPase activity. Activation of a G protein by a ligand bound receptor results in an increase in GTP hydrolysis activity. This is more often a result of increasing the rate of exchange of GDP with GTP rather than an increasing the rate of hydrolysis of bound GTP.  $\gamma^{32}\text{P}$  GTP is added to a reaction mix containing a membrane preparation of cells and the amount of  $^{32}\text{P}$  released from the labelled GTP is measured.

The present invention will now be further described by way of non-limiting example.

#### Example 1

The construct of the P{lacW} element used below is a defective P-element. A defective P-element is one which cannot transpose itself without the provision of a transposase enzyme from another source. Thus, once inserted into a site in the genome, a defective P-element will remain in position and will not distribute copies of itself. The reporter gene in P{lacW} is an *E. Col*  $\beta$ -gal lacZ gene under the control of a weak promoter. This weak promoter, however, responds to enhancer elements in the neighbourhood of the insertion site to give a pattern of lacZ expression that is related, to a variable extent, to the pattern of expression of the gene targeted. This provides temporal and/or tissue expression patterns which may be useful in deciding whether a gene/protein could be a potentially valuable target for insecticide or therapeutic development.

In addition to the reporter gene, P{lacW} carries a mini-white eye colour gene to identify flies that contain insertions. P{lacW} also contains a bacterial origin of replication and the  $\beta$ -lactamase gene coding for ampicillin resistance at its 3' end. This feature permits easy cloning of DNA flanking the insertion site of P{lacW} and further clone relevant genes (Bire, E., H. Vaessin, S. Shepherd, K. Lee, K. McCall, S. Barbel, L. Ackermam, R. Carretto, T. Uemura, E. Grell, L.Y. Jan and Y.N. Jan, 1989 Searching for pattern and mutation in the *Drosophila* genome with a P-lacZ vector. *Genes and Development* 3: 1273 - 1287).

The mutant flies, in which P{lacW} was inserted on the second chromosome are on the *y w*; P{lacZ,w<sup>+</sup>}CyO genotype (Torok, T.G. Tick, M. Alvarado and I. Kiss, 1993 P-lacW Insertional Mutagenesis on the second chromosome of *Drosophila melanogaster*: Isolation of lethals with different overgrowth phenotypes. *Genetics* 135: 71 - 80). The mutant flies, in which P{lacW} was inserted on the third chromosome are of the *y w*; P{lacZ,w<sup>+</sup>}TM3, *sb ser* genotype (Dèak, P., M.M. Omar, R.D.C. Saunders, M. Pal, O. Komonyi, J. Szidonya, P. Maroy, Y. Zhang, M. Ashburner, P. Benos, C. Savakis, I. Siden-Kiamos, C. Louis, V.N. Bolshakov, F.C. Kafatos, E. Madueno, J. Modolell and D.M. Glover, 1998 P element insertion alleles of essential gens on the third chromosome of *Drosophila melanogaster*: Correlation of physical and cytogenetics maps in chromosomal region 86E-87F. *Genetics* 14: 1697 - 1722).

The genetic background of the *w/w*;P(lacW) mutants was equilibrated with that of the wild-type (Canton-S) strain by repeatedly backcrossing heterozygous *w/w*;P(lacW)/+ females (which carried the *w*<sup>+</sup> eye-color marker) to *w*(CS) males for more than five generations. The *w*(CS) strain was derived by backcrossing *w*<sup>1118</sup> flies to wild-type (Canton-S) flies for 10 generations; the *w*(isoCJ1) strain was derived from *w*(CS) and carries isogenic X, 2nd and 3rd chromosomes.

### Example 2 - Plasmid Rescue and cDNA Cloning

Genomic sequences flanking the P-element were cloned by plasmid rescue using standard techniques (*Drosophila*: A practical Approach, the 2nd ed. 1998). Briefly, genomic DNA was digested with *EcoRI*, followed by ligation to form a rescue plasmid, which was propagated in *E. coli*. The rescue fragment then was <sup>32</sup>P-radiolabeled by random priming and used to screen plaques from a *Drosophila* genomic bacteriophage lambda library. The lambda genomic fragment was subcloned into the plasmid vector pBluescript, radiolabeled and used to probe a *Drosophila* adult head cDNA library and a Northern blot of adult whole fly polyA<sup>+</sup> RNA, etc.

Southern blotting was carried out essentially as described by Sambrook et al. (1989). Hybridization was carried out at 64°C in 6xSSC, 5xDenhardt's reagent, 0.5% SDS, 100µg/ml denatured, fragmented salmon sperm DNA. Filters were washed in 1xSSC and 0.1%SDS for 15 min, and then in 0.1XSSC and 0.1%SDS for 30 min.

### Example 3 - DNA Sequencing

Prior to DNA sequencing, rescued plasmids were quantified by restriction digestion with *EcoRI* to linearise followed by electrophoresis on a 1% agarose gel, comparisons being made to a Bacteriophage lambda 1kb marker ladder. For DNA sequencing 500ng-2µg of rescued plasmid was used in each sequencing reaction. Sequencing was carried out using a BigDye dideoxy terminator kit (Perkin-Elmer) with the following sequencing primers:-

- 1) 3' primer 5'-CGCACTTATTGCAAGCATACG-3' sequences into the rescued chromosomal DNA immediately 3' to the point of insertion (5' end of the chromosomal DNA insert)
- 2) 5' primer 5'-GCCACCTGACGTCTAAGAAACC-3' sequences the rescued chromosomal DNA from a point in the P-element vector 5' to the *EcoRI* site, in a reverse orientation to Primer 1 (ie the 3' end of the chromosomal DNA)

NB. Sequence obtained from Primer 2 is only included in those sequences where the combined sequence runs yielded the complete insert of a particular clone.

The reactions were run on 5% polyacrylamide sequencing gels in 373A STRETCH PE Biosystems automated sequencer. Greater than 900 separate lethal/semi-lethal fly lines were identified by sequencing. The sequence obtained from these fly lines is represented in SEQ 10 Nos. 1-902.

DNA sequence analysis/storage was performed using GeneJockey II (Biosoft, Cambridge, UK). BLAST queries and Flybase queries were carried out on secure mirror servers within the Neuropa computing network.

Table 1 shows in summary the fly lines which display similarity to previously identified sequences deposited in nucleotide databases. Over 400 fly displayed no apparent sequence similarity with previous sequences.

Table 2 shows in summary details of the sequences of the fly lines which display a similarity to previously submitted mammalian sequences.

#### Example 4 - X-Gal Staining of Tissues

The procedure for X-gal staining of embryo is essentially as described by O'Kane (1998). Embryos are collected from yeasted apple/grape juice agar plates into a container with a nylon mesh screen at the bottom, dechorionated by dipping into 50% bleach for 4 minutes and washed thoroughly with water. Embryos are placed into an Eppendorf tube containing a mixture of 0.35ml fix solution (1% glutaraldehyde in PBS) and 0.7ml n-heptane and fixed for 15 minutes at room temperature on a rotating mixer. After removing heptane and fix solution from tube, embryos are washed three times for 10 min. in PBS and 0.1% Triton X-100, and resuspended in staining buffer with 0.2% X-gal for 1-2 hours at 37°C. After staining, staining solution are removed and about 400µl of mixture solution (Glycerol : staining buffer = 2:1) are replaced. Embryos can then be mounted on a slide in a coverslip chamber.

For whole-mounts, larval, pupal and adult brains were dissected in PBS, and fixed in 4% paraformaldehyde for 20 min. They were then washed three times for 20 min in PBS, and stained with staining buffer and 2% X-gal for 1-2 h at 37°C (Ashburner, *Drosophila. A Laboratory Manual*, Plainview N.Y.: CSH Lab. Press 1989). They were then washed for 20 min in PBS, cleared overnight at 4°C with PBS/12.5% hydrogen peroxide, washed for 10 min with PBS, dehydrated through graded ethanol, and mounted in glycerol gelatin (Sigma).

To obtain sections, flies were mounted in "fly collars" (modified from Heisenberg and Böhl 1979), soaked in OCT embedding medium (Miles, USA) for 10 min and then embedded in the OCT medium. 12  $\mu$ m serial sections of head or body were cut in a cryostat (Anglia Scientific) at -18°C. The sections were stained and mounted as described by Yang et al. (1995). Thereafter sections were examined and photographed on a Nomarski optical microscope.

#### Example 5 - In situ Hybridisation to Polytene Chromosome

In situ hybridisation to polytene chromosomes localises a DNA sequence (such as a gene, or an inserted P-element) on the physical DNA map of *Drosophila*, and may be related to the genetic map. For those insertion mutations which affect genes of known function, localisation of the P-element to the site where the gene mutated is known to reside is evidence that lethality does in fact result from insertion of the P-element in this gene.

Tagging the genes with a PlacW transposon allowed its immediate localization in situ to a precise cytological region using P element DNA as a probe. The procedure for in situ hybridization to third larval instar polytene chromosomes was essentially as described by Pardue (1986). pBluescript were labelled with Bio-16-dUTP by nick-translation. Hybridization was detected using DAB/H<sub>2</sub>O<sub>2</sub>. After hybridization, the slides were stained with Giemsa and mounted using DPX.

TABLE 1

SEQ ID NO.	ID Number	Class	Chr	Feature	AccNo	Name of match	
1	NPS1	GNL	2	4-133	X54648	Frizzled gene	
2	NPS2	GNL	2	68-345	D17389	Ryanodine receptor	
3	NPS3	GNL	2	1-354	M23412	Muscarinic acetylcholine receptor. Genomic AC006938 intron.	
4	NPS4	GNL	2	9-277	U91980	Tpr homologue	
5	NPS5	GNL	2	1-587	X61209	Type II topoisomerase	
6	NPS6	GNL	2	270-408	U22439	Neuron surface antigen 2	
7	NPS7	GNL	2	30-461INV	Y13272	Indora	
8	NPS8	GNL	2	1-267	L03209	GDP dissociation inhibitor homologue	
9	NPS9	GNL	2	345-583INV	L17340	germline transcription factor gene	
10	NPS10	GNL	2	1-480	AB003784	Histone H3	
11	NPS11	GNL	2	179-360	AA699128	EST matching 5' of V-ATPase C subunit	
12	NPS13	GNL	2	226-409	U94702	MtPolB	
13	NPS14	GNL	2	110-191	L13305	AND 396-472, integrin beta subunit (beta neu)	
14	NPS15	GNL	2	1-432	X57484	tra-2 gene	
15	NPS16	GNL	2	61-276	X15805	EF2 Translation factor	
16	NPS18	GNL	2	1-532	X15008	49bp upstream of TU-36B gene, cytochrome b related protein.	
17	NPS19	GNL	2	250-536	M29602	G0 protein alpha subunit homolog class II	
18	NPS20	GNL	2	81-476	L13255	Lachesin	
19	NPS21	GNL	2	119-457INV	U63556	larval serum protein 1 beta subunit	
20	NPS22	GNL	2	121-417	AF027300	418-481 intron, 481-577 exon. Positive transcription elongation factor b	
21	NPS23	GNL	2	1-577	X84681	organellar-type Ca-ATPase gene.	
22	NPS26	GNL	2	1-534	X71866	GTP-binding protein.	
23	NPS27	GNL	2	1-523	M23094	Intron of G protein alpha subunit gene	
24	NPS28	GNL	2	19-215	AF041048	AA246996 est match. EST matches CD39-like NTPase gene	
25	NPS30	GNL	2	387-473INV	AF071417	phosphatidylinositol 4-phosphate 5-kinase, skt11	
26	NPS31	GNL	2	1-319	S55886	rbp9	
27	NPS32	GNL	2	1-493	L34276	manganese superoxide dismutase (mnSOD)	
28	NPS33	GNL	2	233-377INV	D84313	rab2	
29	NPS34	GNL	2	1-63INV	AF003826	myosin V	
30	NPS35	GNL	2	325-528	U09369	ribonucleoside-diphosphate reductase large subunit gene	
31	NPS36	GNL	3	234-271	U95821	transmembrane GTPase (fzo)	
32	NPS38	GNL	3	322-450	U00669	mitochondrial single-stranded DNA-binding protein	
33	NPS39	GNL	3	14-385	X52846	RM62	
34	NPS40	GNL	3	1-422INV	AF069297	pterin-4a-carbinolamine dehydratase gene	
35	NPS41	GNL	3	329-346	Y09065	330-414 intron, 415-511 exon. cytochrome c oxidase subunit Va preprotein	
36	NPS42	GNL	3	1-283	M22428	Ubiquitin	



37	NPS43	GNL	3	1-213	M28870	heterogeneous nuclear ribonucleoprotein isoforms, exon 1A.
38	NPS44	GNL	3	1-380	M17719	Intron of Rhodopsin 4 and M17730
39	NPS45	GNL	3	1-449	U27561	TipE
40	NPS46	GNL	3	463-528	X99665	mitochondrial ATPase coupling factor 6. Match on EST AI405330
41	NPS47	GNL	3	1-246	K01294	heat shock locus 87C1: proximal gene, 3' end.
42	NPS48	GNL	3	221-318	U73160	AA440389 EST matching Dros fas gene
43	NPS49	GNL	3	15-95	M32141	AI297861 1st EST in 8 contig matches 49-kilodalton phosphoprotein gene
44	NPS50	GNL	3	231-293	M21159	Tcp-1
45	NPS51	GNL	3	1-349	V00213	Hsp70
46	NPS52	GNL	3	1-241	U59923	glutamyl-prolyl-tRNA synthetase gene,
47	NPS53	GNL	3	225-237	D16257	238-333 intron, 334-499 exon ribosomal protein S4
48	NPS54	GNL	3	1-462	X73216	Rib1
49	NPS55	GNL	3	1-164inv	U62005	Rel/NF-kappa B homolog (Relish)
50	NPS56	GNL	3	1-207inv	X07311	HSP2
51	NPS57	GNL	3	15-438	X54061	205K microtubule-associated protein (MAP)
52	NPS58	GNL	3	1-80inv	J01102	HSP68
53	NPS59	GNL	3	1-450	Y10015	anon-66Da gene
54	NPS60	GNL	3	56-187	M63792	RAD6
55	NPS61	GNL	3	391-465	U28966	Septin 2
56	NPS62	GNL	3	1-514	M98351	fructose 1,6 biphosphate aldolase gene,
57	NPS63	GNL	3	46-251inv	U01035	Bottleneck gene
58	NPS64	GNL	3	49-450	U38238	HLH106
59	NPS65	GNL	3	328-581	AB004232	DAD gene
60	NPS66	GNL	3	1-436	U22176	15bp upstream of Brother gene on AC005557
61	NPS67	GNL	3	46-176	M90755	Transcriptional repressor protein Aef-1
62	NPS68	GNL	3	224-298	Y07908	Match to EST AI292767. This then matches serine/threonine protein kinase.
63	NPS69	GNL	3	1-531	M32311	Fascin 1
64	NPS70	GNL	3	1-421inv	X03889	HSP23
65	NPS71	GNL	3	548-882inv	Y12861	bifunctional ATP sulfurylase/APS kinase.
66	NPS72	GNL	3	83-135	U12010	putative serine/threonine protein kinase (nemo)
67	NPS73	GNL	3	1-357	U20554	UDP-glucose:glycoprotein glucosyltransferase mRNA
68	NPS74	GNL	3	1-20bp	U87925	Cbl gene confirmed by match to EST AA441040
69	NPS75	GNL	3	468-539	U23485	Guanylate cyclase. Match found via EST AA392994
70	NPS76	GNL	3	1-547	Y11349	UbcD4
71	NPS77	GNL	3	1-163	U09374	SNAP
72	NPS78	GNL	3	1-104inv	U62388	chromatin assembly factor 1 p55 subunit
73	NPS79	GNL	3	374-518inv	AB007692	Elongin B

74	NPS80	GNL	3	1-231	L06861	232-401 intron, 402-590 exon matching TAF110
75	NPS81	EST	2	1-314inv	AI259618	From genomic data.40bp upstream Prob. cytochrome B5. AC005641
76	NPS82	EST	2	509-591	AA202837	hypothetical yeast/arabidopsis/prot and mouse EST
77	NPS83	EST	2	166-393	AI293734	
78	NPS84	EST	2	261-377inv	AA202757	Match to Human EST
79	NPS86	EST	2	1-247	AA696498	
80	NPS87	EST	2	100-646	AA950073	
81	NPS89	EST	2	1-50inv	AA695104	
82	NPS91	EST	2	1-427	AA942153	
83	NPS92	EST	2	42-334	AA540352	
84	NPS93	EST	2	115-162	AI238523	
85	NPS97	EST	2	1-69inv	AI260872	EST matches mouse signalling factor U29156
86	NPS98	EST	2	5-77bp	AA801728	
87	NPS99	GNL	2	228-675	AF053083	Drosophila SMT3 gene
88	NPS100	EST	2	1-210inv	AA439866	
89	NPS105	EST	2	31-590	AA820803	Poss related to human aldolase
90	NPS106	EST	2	30-478	AA803545	AA697132 match to frog/human MSS1
91	NPS108	EST	2	76-178	AA438591	
92	NPS109	EST	2	1-169	AA979551	also AA567400
93	NPS111	EST	2	138-414	AA439261	Match to Rat EST
94	NPS113	EST	2	7-354	AI107509	
95	NPS114	EST	2	1-48bp	AA540348	
96	NPS115	EST	2	1-311inv	AA735555	
97	NPS118	EST	2	1-582	AI064020	match to AC005646. 26bp 5' to EST match area. AI542218/AI25740 765bp. Def SEC61 homologue
98	NPS119	EST	2	7-170	AA263700	also AA978721
99	NPS120	EST	2	364-583	AA941785	also AA695548
100	NPS121	EST	2	1-260 and 562-645	AA802928	also AA817115
101	NPS122	EST	2	1-395	AA539001	
102	NPS123	EST	2	1-35inv	AA735863	Poss. related to human death assoc prot 3 X83544
103	NPS125	EST	2	68-195 and 475-621	AA941860	
104	NPS127	EST	2	1-210inv	AA246460	
105	NPS128	EST	2	66-593	AA141928	
106	NPS131	EST	2	1-332	AA979014	
107	NPS134	EST	2	52-475	AA817254	
108	NPS137	EST	2	1-37bp	AA536262	1209bp EST contig.AA948897. AA539274, AA392320. Poss glycogen synthase

109	NPS139	GNL	2	35-86 and 475-581	AF113612	Drosophila Aspartate ligase
110	NPS140	EST	2	368-636	AA390587	
111	NPS141	EST	2	55-110inv	AA979454	sim to human REC1L protein. Acc. X57303
112	NPS142	EST	2	31-460	AA941359	
113	NPS143	EST	2	65-299	AA201303	also AA541066
114	NPS144	EST	2	538-581inv	AA698119	Matc to Human glycerol-3-phosphate dehydrogenase
115	NPS145	EST	2	111-549	AA696174	
116	NPS146	EST	2	107-243	AI064230	Also AA263288. Match to Mouse proteasome subunit
117	NPS147	EST	2	1-212 and 276-382	AI106957	1756bp EST contig. Also AA391125, AA567307, AA735971
118	NPS149	EST	2	1-107inv	AI114218	Also AA820473. (AF034644) putative cytochrome bc-1 complex core protein [Haematobia irritans irritans]
119	NPS150	EST	2	19-102 and 115-485	AA978449	Also AA940834. 103-114 gap of unknown length
120	NPS152	EST	2	182-362	AA802905	
121	NPS154	EST	2	235-279 and 376-452	AI259166	Also AI296787. Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex precursor (human)P10515
122	NPS155	EST	2	1-238inv	AA951193	
123	NPS156	EST	2	326-482	AA696743	Also AA803977
124	NPS157	EST	2	11-512	AA990758	Also AA246427. 975bp contig
125	NPS158	EST	2	1-406	AA697797	
126	NPS159	EST	2	1-29inv	AA802206	1341contig. AA202662, AA801949, AA942041
127	NPS160	EST	2	344-592	AA978904	
128	NPS161	EST	2	101-223 and 292-551	AA202366	
129	NPS162	EST	2	103-468	AA950164	
130	NPS163	EST	2	23-98 and 102-602	AA952159	99-101 gap of unknown length. Match to mouse EST
131	NPS166	EST	2	102-512	AA392519	also AA695318 and AA441243. 758bp contig.
132	NPS168	EST	2	304-541	AI515517	also AI404462. Poss Ras related protein
133	NPS169	EST	2	191-387	AA698481	
134	NPS170	EST	2	451-606inv	AA803082	2166bp EST contig. Poss. Alt splice. AA941565, AA820668, AA978815 and AA697381
135	NPS1067	EST	2	1-570	AI405762	Seq.sim to hypothetical prots from arabidopsis and C. elegans
136	NPS173	EST	2	1-38inv	AA391495	1135bp contig. AA439145 and AA949325. Match to mouse EST
137	NPS174	EST	2	353-476	AA942305	
138	NPS178	EST	2	72-391	AA951839	also AA979603
139	NPS179	EST	2	1-112	AI386817	also AI404737
140	NPS180	EST	2	435-475	AA438658	
141	NPS181	EST	2	31-212	AI106794	also AI107315

142	NPS1068	EST	2	1-228	AI403747	
143	NPS188	EST	2	1-272	AA802791	also AA390699
144	NPS189	EST	2	1-190	AA949990	also AA246423
145	NPS190	EST	2	1-202	AA201161	also AA438658
146	NPS191	EST	2	202-472	AA978927	poss. PCF11p homolog (Homo sapiens)
147	NPS192	EST	2	84-318	AA541084	also AA538937
148	NPS195	EST	2	390-509	AA951890	RIR2_mouse ribonucleoside- diphosphate reductase m2 chain
149	NPS198	EST	2	1-140	AA439230	
150	NPS199	EST	2	3-522	AA948907	also AA942191
151	NPS200	EST	2	25-76inv	AA802379	also AA246624
152	NPS1069	EST	2	9-100 AND 179-411	AI404485	
153	NPS1070	EST	2	60-449	AI108647	
154	NPS1071	EST	2	1-49inv	AA951902	other ESTs inc AA949796
155	NPS204	GNL	2	1-489	AF143860	Drosophila RanGap gene
156	NPS205	EST	2	1-278	AA940865	Xenopus/ human chromosomal assembly protein(U1367)
157	NPS206	EST	2	117-263	AA803314	also AA941391. Human B-cell receptor associated protein.
158	NPS207	EST	2	209-405	AA201448	856bp contig.AA438721 and AA247046
159	NPS209	EST	2	37-243	AA696343	also AA696180. Match to human/ C. elegans calponin
160	NPS210	EST	2	261-580inv	AA540783	
161	NPS211	EST	2	26-267 and 336-459	AA695850	also AA698310. FK84_RABIT P59 PROTEIN
162	NPS212	EST	2	1-224	AA441346	also AA390646 and AA696470. 1677 contig
163	NPS213	EST	2	1-514	AI064375	
164	NPS216	EST	2	181-299	AA540197	also AA695503 and AA941503.732bp contig
165	NPS217	EST	2	167-212inv	AA979442	also AA392418
166	NPS218	EST	2	89-159	AA536378	also AA949458
167	NPS219	EST	2	1-570	AI515537	Genomic AC004345. Also AI062109. 50bp upstream of EST.
168	NPS220	EST	2	1-184	AA390646	1705bp contig with AA440523 and AA696470
169	NPS225	EST	2	1-104 and 310-467	AI064169	also AA816652
170	NPS226	EST	2	1-288	AA439345	802contig with AA949877 and AA439626
171	NPS227	EST	2	1-350	AA979503	181bp upstream of EST Genomic AC005452
172	NPS228	EST	2	1-93 and 170-446	AI293141	
173	NPS229	EST	2	12-244	AI107445	also AA390813
174	NPS233	EST	2	12-478	AA390942	
175	NPS235	EST	2	11-103 and 296-389	AA802688	Poss 10k HSP

176	NPS236	EST	2	1-414	AA392415	
177	NPS239	EST	2	1-22bp	AA695619	
178	NPS240	EST	2	399-542	AA142132	
179	NPS241	EST	2	366-520	AA536537	
180	NPS242	EST	2	26-303	AA264253	Poss. SNF7 homologue
181	NPS243	EST	2	186-593	AA441247	also AA820771
182	NPS244	EST	2	318-431	AA202196	1942bp contig with AI108811, AA950029, AA202725, AA440491, and AA697007. Match to mouse EST
183	NPS245	EST	2	83-319inv	AI064123	also AA263284. Match to human androgen induced prostate proliferative shutoff assoc. protein.
184	NPS247	EST	2	1-89bp	AA441173	
185	NPS250	EST	2	65-414inv	AA440852	also AA541034
186	NPS251	EST	2	2-131	AI062640	
187	NPS252	EST	2	1-77inv	AA695507	Poss. match to Rat cytochrome C
188	NPS254	EST	2	89-251	AA736186	also AA801973. Poss. match to horse Thioredoxin
189	NPS255	EST	2	1-417	AA697603	also AA801716
190	NPS256	EST	2	1-528	AA950741	
191	NPS257	EST	2	1-53bp	AI063204	887bp contig with AA697347 and AA201878
192	NPS258	EST	2	1-44bp	AA441029	
193	NPS259	EST	2	1-157	AI114266	1141bp contig with AA949325, AA735675 and AA391495. Poss.match to human GMP
194	NPS260	EST	2	1-562	AA951648	1340bp contig with AA539581, AA802940 and AA263326
195	NPS261	EST	2	26-137 and 360-422	AA391135	Match to SEC61, different area to NPS118
196	NPS262	EST	2	1-124	AA696531	C.elegans pro7, Z66519/ mouse EST
197	NPS265	EST	2	442-549	AI124332	
198	NPS266	EST	2	52-382	AA949873	
199	NPS1073	EST	2	1-167	AI133902	see also AC006562 poss phosphate transporter
200	NPS269	EST	2	1-550	AI403609	Genomic AC005129, 420bp upstream of EST
201	NPS271	EST	2	299-375	AA391470	
202	NPS272	GNL	2	37-77bp	AF085601	Drosophila inorganic pyrophosphatase NURF-38
203	NPS273	EST	2	1-76inv	AA696584	
204	NPS275	EST	2	1-319	AA439099	1132bp contig with AA949325 and AA940848 poss. GMP synthase (human)
205	NPS276	EST	2	21-377	AA695424	
206	NPS277	EST	2	152-590inv	AA440949	
207	NPS278	EST	2	132-312	AI062455	also AA440915
208	NPS279	EST	2	68-311	AA816432	
209	NPS281	EST	2	1-258	AA979191	Match to human CGI-28
210	NPS283	EST	2	2-318	AA391495	

211	NPS285	EST	2	1-89bp	AA441636	AA820540 and AA817484. Alt splice
212	NPS1075	EST	2	59-488	AI295363	
213	NPS288	EST	2	51-170	AI114059	also AA941565
214	NPS289	EST	2	3-355 and 443-479	AA801691	also AA441008
215	NPS290	EST	2	378-471	AA950084	also AA978669
216	NPS291	EST	2	20-236 and 292-439	AI062945	
217	NPS293	EST	2	1-312	AA440345	2293bp EST contig. Poss. human cleavage and polyadenylation specificity factor, 160 kd subunit. AA201536, AA539993, AA942332, AA979174, AA202096
218	NPS294	EST	2	10-501	AA696930	
219	NPS295	EST	2	8-437inv	AA440135	
220	NPS296	EST	2	75-157	AI063979	also AA802032
221	NPS297	EST	2	1-144	AA699194	
222	NPS298	EST	3	507-547	AA441233	also AA392152
223	NPS299	EST	3	1-79inv	AA438352	33% over 113 AA Plant oxygenase
224	NPS300	EST	3	480-534	AI455428	
225	NPS301	EST	3	11-190inv	AA246916	Rat Mitochondrial import receptor
226	NPS302	EST	3	233-348	AA392258	
227	NPS304	EST	3	1-41inv	AI296848	Prob. 40-kDa V-ATPase subunit (mam)
228	NPS305	EST	3	255-354	AI388389	
229	NPS306	EST	3	335-448inv	AA441471	also AA540182. 52% over 107 AA like Bov/Hum/Mouse RHO GDP-dissoc. inhibitor 1
230	NPS307	EST	3	22-242	AA439855	also AA567284.
231	NPS308	EST	3	1-141 and 397-446inv	AA941606	
232	NPS310	EST	3	209-435	AA392324	
233	NPS311	EST	3	1-393inv	AA264796	
234	NPS312	EST	3	1-152	AA540030	Poss rat calcium binding prot.
235	NPS313	EST	3	85-596	AI109898	
236	NPS314	EST	3	365-473	AI259723	
237	NPS316	EST	3	1-141	AI294469	
238	NPS317	EST	3	145-325	AA140945	
239	NPS318	EST	3	1-331	AI259816	Related to Epsin (Hum)
240	NPS322	EST	3	209-433	AA141103	
241	NPS323	EST	3	1-98inv	AA246767	also AA141059
242	NPS324	EST	3	1180239inv	AA441468	also AA142226. 42% over 128 AA like C. elegans prot. Z66496
243	NPS327	EST	3	1-82inv	AA247070	1366bp contig with AA567381, AA568013, AA540724. C. elegans prot/human EST
244	NPS328	EST	3	433-469	AA802401	Prob. Alg2, glycosyltransferase hom./ Mouse MER 5

245	NPS330	EST	3	1-96inv	Alt splice	AI135263
246	NPS331	EST	3	243-489		AA695904
247	NPS334	EST	3	1-317	also AA541060	AA246386
248	NPS335	EST	3	311-427	57% over 82AA like mouse/ human Thioredoxin	AA264961
249	NPS337	EST	3	136-293inv	Poss Ca 2 + ATPase	AA202880
250	NPS338	EST	3	74-276 and 344-438		AA263803
251	NPS339	EST	3	3-166inv	also AA202128	AA202200
252	NPS340	EST	3	1-48 inv		AA439530
253	NPS341	EST	3	28-207	Poss GPI-anchored protein(human)	AI109459
254	NPS342	EST	3	471-506inv		AI109779
255	NPS343	EST	3	147-247		AA141054
256	NPS1061	EST	3	65-118inv		AA141365
257	NPS345	EST	3	144-549		AI063643
258	NPS346	EST	3	1-148	also AA390813	AI107445
259	NPS347	EST	3	1-75bp		AI297362
260	NPS348	EST	3	96-230inv		AA392916
261	NPS349	EST	3	1-47 and 145-317inv	2631bp contig.	AA201223
262	NPS351	EST	3	537-687	AA538867/AA439491/AA390780/AA390983/AA201661/AA391700/AA202007. Human 88	AI454966
263	NPS352	EST	3	10-441	715bpcontig with AA201231 and AA392823. 31% over 129AA like Rat Nup84 and Human 88	AA202767
264	NPS353	EST	3	3-40inv	KDa nucleopore complex	AA201212
265	NPS354	EST	3	1-33inv	And AI260898. Alt splice	AI404994
266	NPS356	EST	3	1-292	1042bp contig with AA201959	AA539914
267	NPS357	EST	3	36-454		AA440953
268	NPS359	EST	3	145-253		AA264591
269	NPS360	EST	3	47-380		AA539491
270	NPS361	EST	3	202-381inv		AI403737
271	NPS362	EST	3	270-443inv		AA567141
272	NPS363	EST	3	1-478		AI134670
273	NPS364	EST	3	413-535inv		AA263763
274	NPS365	EST	3	1-99bp		AA568011
275	NPS367	EST	3	64-449		AI107456
276	NPS370	GNL	3	212-414	Drosophila Karyopherin alpha	AF074957
277	NPS371	EST	3	1-146	and AA141054. Alt splice	AI295205
278	NPS372	EST	3	8-382		AA567704

279	NPS373	EST	3	74-224 and 297-344	AA539252	
280	NPS374	EST	3	1-347inv	AI260759	
281	NPS375	EST	3	1-77inv	AI260646	
282	NPS377	EST	3	160-306	AA202424	and AA264609.
283	NPS379	EST	3	300-379	AA802555	
284	NPS380	EST	3	322-573	AA802438	1030bp contig with AI063681
285	NPS381	EST	3	34-470inv	AA438500	
286	NPS382	EST	3	14-153 and 216- 348, 419-445	AI456286	
287	NPS383	EST	3	41-56 and 223-353	AI062265	1475 contig. AA694862 and AI064128. UNC51 ser/thr kinase (C.elegans)
288	NPS384	EST	3	1-429inv	AA247020	
289	NPS385	EST	3	1-143	AA264635	
290	NPS387	EST	3	58-491	AA201749	877bp contig with AA803278/ human hypothetical gene
291	NPS388	EST	3	1-162	AA392551	
292	NPS389	EST	3	1-379	AA438539	EST contig 1200bp, ORF at 5' end. Matches Human ERF 1. AA201773, AA263752 and
293	NPS390	EST	3	297-447	AA141715	
294	NPS392	EST	3	80-161	AA695862	
295	NPS393	EST	3	2-132	AA201517	
296	NPS394	EST	3	176-239	AA202297	Vertebrate vacuolar ATPase
297	NPS395	EST	3	1-33bpinv	AA567483	
298	NPS396	EST	3	1-209 and 271-468	AA817479	
299	NPS397	EST	3	17-139	AA441327	ATG orf hits Rat (and other) sodium dependant dicarboxylate transporter AB001321 58% over 74 AA
300	NPS398	EST	3	1-391	AA698011	
301	NPS399	EST	3	67-207	AA951986	nucleolar protein p40 [Homo sapiens]
302	NPS400	EST	3	1-186	AI295731	2018contig with AI258429, AA696170, AI109519, AA391348. MouseAPG-1, hsp/osmotic shock gene
303	NPS402	EST	3	1-82bp	AA201430	
304	NPS403	GNL	3	15-54bp	AF132912	Drosophila ARP gene. Match to EST matching ARP
305	NPS404	EST	3	1-140	AA541045	May be distantly related to cystatin
306	NPS406	EST	3	392-501	AA390337	
307	NPS407	EST	3	1-202 and 273- 440inv	AA141555	Matches mouse/human ESTs
308	NPS408	EST	3	158-252	AA263730	A little like yeast hypothetical protein YOL124c
309	NPS409	EST	3	324-370 and 448-545	AI259832	and AA990765. Human Ubiquitin conjugating enzyme 12



310	NPS410	EST	3	75-483	AI514268	
311	NPS411	EST	3	1-435	AI293256	20bp 5' to EST on AC006562. Part of ORF similar to molybdenum cofactor biosynthesis protein AlHomo sapiens]
312	NPS412	EST	3	1-71 and 148-435	AA201987	Poss Asparaginase
313	NPS413	EST	3	12-408	AA540020	
314	NPS415	EST	3	1-38bp	AA201670	
315	NPS416	EST	3	15-404	AA201957	Mouse ESTs
316	NPS417	EST	3	1-353	AA695344	
317	NPS418	EST	3	1-450	AA441018	
318	NPS419	EST	3	301-334inv	AA202301	
319	NPS420	EST	3	245-393	AA735819	
320	NPS421	EST	3	1-147	AA440886	also AA695395. matches UMP kinase from C.elegans and bacteria
321	NPS422	EST	3	76-217	AA803640	859bp with AA803683 and AA803676. Human Ribosomal L28 protein
322	NPS424	EST	3	472-786 and 842-1073	AI257267	chick glycine cleavage system h protein
323	NPS425	EST	3	1-75bp	AA539327	
324	NPS426	EST	3	419-468	AI530922	
325	NPS427	EST	3	92-265	AI402854	
326	NPS428	EST	3	1-222 and 291-354	AA441362	40% like human/mouse proteasome subunit HsN3
327	NPS429	EST	3	1-219	AA202487	A little like hypothetical yeast protein YEY6
328	NPS430	EST	3	328-455	AA263590	39% over 61AA like human hRNP F
329	NPS431	EST	3	50-113	AA201496	57% over 50 AA like human oxoglutarate dehydrogenase
330	NPS432	EST	3	281-510	AA391430	
331	NPS434	EST	3	1-50 inv	AI292722	also AI534704
332	NPS435	EST	3	1-65inv	AA439393	
333	NPS436	EST	3	299-512inv	AA820797	also AA438876
334	NPS437	EST	3	1-52inv	AA697891	Homologue of Bovine gamma COP
335	NPS438	EST	3	1-31inv	AA696845	
336	NPS439	EST	3	1-384	AI259031	
337	NPS440	EST	3	1-82bp	AA803464	may match human hypothetical protein KIAA0258
338	NPS441	EST	3	169-489	AA539974	
339	NPS442	EST	3	1-46 and 432-524	AA941993	
340	NPS443	EST	3	43-431	AA803074	
341	NPS444	EST	3	1-197 and 268-534	AA695870	Dog/rat/ Yeast signal peptidase 18kd subunit
342	NPS445	EST	3	775-911	AA433251	
343	NPS446	EST	3	718-1007	AI297203	1122bp contig with AA438815 and AI455195
344	NPS448	EST	3	1-106inv	AA694869	1632bp with AA735812, AA568063 and AA695306. mammalian transketolase

345	NPS449	EST	3	1-99inv	AA392932	
346	NPS451	EST	3	1-260 and 310-510	AA391707	
347	NPS452	EST	3	45-141 AND 445-582	AI294564	Match to mouse EST
348	NPS453	GNL	3	345-460	AF152928	Drosophila karyophyllin alpha 3.
349	NPS454	EST	3	1-177	AA540743	1129bp with AI064562, AI519458 and AA568024
350	NPS456	EST	3	1-325	AA539054	Match to rat EST
351	NPS457	EST	3	1-73bp	AI062939	
352	NPS458	EST	3	927-1070	AI109224	
353	NPS459	EST	3	43-146	AA696728	Poss. isopentyl pyrophosphate isomerase
354	NPS460	EST	3	59-533	AI518328	
355	NPS461	EST	3	43-432	AA263622	
356	NPS463	EST	3	1-164	AA539661	Matches Human Proton ATPase like protein
357	NPS464	EST	3	1-152 and 214-579	AI388964	
358	NPS465	EST	3	365-462	AA438987	also AA264877. FXR1 mental retardation gene, Human
359	NPS466	EST	3	6-257	AA392117	
360	NPS468	EST	3	45-120 and 545-591	AA821194	987bp with AA736168. human 40s ribosomal protein s29
361	NPS469	EST	3	12-469	AA539752	
362	NPS473	EST	3	1-382 and 456-484	AA803203	
363	NPS476	EST	3	105-154	AA802887	also AA820871. Hypothetical C. elegans prot B0336.11
364	NPS477	EST	3	22-177	AA817394	V. similar to Dead box family of DNA helicases (initiation factors)
365	NPS479	EST	3	1-77inv	AI064638	
366	NPS480	EST	3	1-37bp	AA736157	also AA140746. Match to mouse EST
367	NPS482	EST	3	7-369	AA820427	
368	NPS483	EST	3	1-533	AA391736	1692bp with AA202259 and AA820861.
369	NPS484	EST	3	158-470	AA567184	
370	NPS486	EST	3	1-122	AA735277	1176bp with AA697907
371	NPS487	GNL	3	514-616	AF129080_1	Drosophila COP9 complex homolog subunit 1-2 DCH1-2
372	NPS489	EST	3	140-189	AA202581	Match to human EST
373	NPS490	EST	3	41-377	AA390775	
374	NPS491	EST	3	169-488	AA539898	
375	NPS492	EST	3	1-127	AA390453	
376	NPS493	EST	3	1-321inv	AA568061	1356bp with AA264532 and AA441674
377	NPS495	EST	3	102-311	AA141908	794bp with AA802528
378	NPS496	EST	3	1-100inv	AA539224	
379	NPS497	EST	3	431-622inv	AA246367	Hum ribosome S6 PK

380	NPS499	EST	3	46-319	AA817295	
381	NPS501	EST	3	35-383	AA439743	
382	NPS503	EST	3	1-264	AA441568	
383	NPS504	EST	3	337-408 and 479-568	AA247082	
384	NPS505	EST	3	1-321inv	AA201685	868bp contig with AA540405
385	NPS506	EST	3	83-218	AA540693	1450bp with AA441321, AA440080 and AA392794. Match to mouse EST
386	NPS507	EST	3	452-1044	AI295950	
387	NPS508	EST	3	2-339	AA439667	
388	NPS509	EST	3	12-394	AA539198	
389	NPS510	EST	3	83-227 and 498-518	AA696927	Match to human citrin
390	NPS512	EST	3	360-501	AA438961	Human KIAA0160 gene
391	NPS513	EST	3	53-260inv	AA735138	
392	NPS514	EST	3	1-237inv	AI064414	
393	NPS515	EST	3	1-67inv	AA540712	809bp with AA440879 and AA440431.human cyclin G assoc. Kinase.
394	NPS516	GNL	3	596-682inv	AF132145	Drosophila damage-specific DNA binding protein DDBa p127 subunit
395	NPS517	EST	3	1-513	AF007159	
396	NPS518	EST	3	13-235inv	AI511691	
397	NPS519	EST	3	1-61inv	AA264883	also AA392712. Alt splice.
398	NPS520	EST	3	30-451	AA438399	821bp contig with AA439438
399	NPS521	EST	3	600-627	AA440272	1324bp contig with AA438941
400	NPS526	EST	3	65-483	AA264865	
401	NPS527	EST	3	1-246	AA263693	
402	NPS528	EST	3	137-160 and 379-475	AA698620	
403	NPS529	EST	3	1-51inv	AA391350	
404	NPS530	EST	3	100-499	AA392183	DNA J homologue
405	NPS531	EST	3	149-348 and 412-457	AA696390	mouse/human yeast/ub fusion protein 1
406	NPS532	EST	3	1-267inv	AA802961	816bp with AA817584
407	NPS533	EST	3	1-259inv	AA699045	Poss. Slug cDNA25
408	NPS534	EST	3	1-99bp	AA952055	1205bp with AA202358, AA202625 and AA951416. Siah binding protein 1(human)
409	NPS535	EST	3	1-610inv	AA142266	
410	NPS536	EST	3	52-534	AA696974	Matches Human CGI-37 protein
411	NPS537	EST	3	503-626 and 734-1069	AI532170	1565bp with AI544333 and AI062662. Definite transcription factor, MTF-1

412	NPS538	EST	3	442-569	AA567128	Match to mouse EST
413	NPS540	EST	3	1-79bp	AA950480	
414	NPS541	EST	3	2-360	AA950161	1217bp with AA950864 and AA950181
415	NPS542	EST	3	30-194 and 291-366	AA539625	882bp with AA202440 and AA390927
416	NPS543	EST	3	1-255	AA951297	
417	NPS544	EST	3	20-95 and 479-654	AA948996	781bp with AA541068 and AA950730
418	NPS545	EST	3	1-378	AA941568	
419	NPS546	EST	3	228-522	AA801928	
420	NPS547	EST	3	14-98	AA951147	695bp with AA695598 and AA540269
421	NPS548	EST	3	1-279	AA697191	1002bp with AA392404 and AA438791
422	NPS549	EST	3	650-689	AI518422	
423	NPS1065	EST	3	27-689	AI535025	
424	NPS551	EST	3	8-563	AA950826	
425	NPS553	EST	3	48-150	AA949934	Mam. Casein kinase
426	NPS555	EST	3	411-582	AI109292	
427	NPS556	EST	3	1-279inv	AA202259	1693bp with AA391736 and AA820861
428	NPS557	EST	3	131-647	AA142065	poss. succinate semialdehyde dehydrogenase
429	NPS558	EST	3	76-559	AA536402	
784	NPS921	GENO.	2	1-537INV	AC006073	In intron of gene coding for 246AA protein at 1663-44895. No database matches
785	NPS922	GENO.	2	1-720	AC004299	In space before Drosophila Homologue of Human C-TAK 1 ser/thr kinase
786	NPS924	GENO.	2	1-599	AC004115	In space before gene coding for 372AA protein. 16297-18074. No database matches.
787	NPS925	GENO.	2	1-581	AC004716	In intron of gene coding for 355AA protein. 51777-83843bp. No database matches
788	NPS926	GENO.	2	1-628	AC005889	No good predicted exons in this area.
789	NPS927	GENO.	2	1-536	L49408	space before gene coding for 401AA protein. 75943-77148bp. Sequence similarity to Mammalian glia maturation factor.
790	NPS928	GENO.	2	1-86inv	AC004296	In space before gene coding for 878AA protein. 39765-47183bp. Sequence similarity to Mouse G-protein
791	NPS929	GENO.	2	1-573inv	AC004306	No good predicted exons in this area.
792	NPS1077	GENO.	2	1-648	AC006472	In intron of gene coding for 1876AA protein at 62506-79351. Seq similarity hypothetical proteins from human and yeast
793	NPS931	GENO.	2	1-463inv	AC006092	In space before gene represented by ESTs AA990657 and AI294791.
794	NPS932	GENO.	2	1-519	AC006073	No good predicted exons in this area.
795	NPS933	GENO.	2	1-704inv	AC007176	In gene coding for 566AA protein. 85106-110350bp(complement). Possible transcription factor
796	NPS935	GENO.	2	1-307inv	AC004423	In space before gene coding for a 702AA protein at 47585-59400bp. Sequence similarity to Xenopus DNA repair protein XPGC

797	NPS336	GENO.	2	1-412inv	AC005448	Part of gene coding for 422AA protein at 34104-35373(complement). Strong sequence similarity to Drosophila Septin 2
798	NPS937	GENO.	2	1-478	AC004313	Possibly in 3'UTR of gene coding for 355AA protein at 39720-40727. Weak sequence similarity to potassium channel gene
799	NPS938	GENO.	2	1-489	AC004641	In intron of gene coding for 402AA protein at 101233-153110bp. Strong sequence similarity to Xenopus FLAP endonuclease.
800	NPS1078	GENO.	2	1-558inv	AC004306	No good predicted exons in this area.
801	NPS940	GENO.	2	1-623	AC001646	In intron of gene coding for 724AA protein at 9930-72686 (complement). Strong sequence similarity to Mouse serine C-palmitoyltransferase
802	NPS941	GENO.	2	1-544	AC005334	ESTs matching at 74650 (AA803646, AI518976, AI108114) Sequence similarity to U5 snRNP
803	NPS942	GENO.	2	1-201	AC004154	In intron of gene coding for a 292AA protein at 12210-30840bp. Sequence similarity to human geranylgeranyltransferase
804	NPS943	GENO.	2	1-524	AC004766	In intron of gene coding for a 1442AA protein at 40620-93241(complement). Sequence similarity to hypothetical C.elegans gene ZK1128.2.
805	NPS944	GENO.	2	1-621	AC004361	No good predicted exons in this area.
806	NPS945	GENO.	2	1-569inv	AC007185	No good predicted exons in this area.
807	NPS946	GENO.	2	1-462	L49408	In space before gene coding for 401AA protein at 75943-77148bp. Sequence similarity to Mammalian glia maturation factor.
808	NPS947	GENO.	2	1-233inv	AC005750	In intron of gene coding for an 1813AA protein at 51190-77775 (complement). Sequence similarity to Rat CPG2 protein
809	NPS948	GENO.	2	1-525	AC005269	No good predicted exons in this area.
810	NPS949	GENO.	2	1-531	AC005554	In intron of gene coding for 2355AA gene at 16134-35638. Sequence similarity to Rat Fatty acid synthase.
811	NPS951	GENO.	2	1-443inv	AC004758	No good predicted exons in this area.
812	NPS952	GENO.	2	1-498inv	AC005894	In intron gene coding for 196AA protein at 57158-63906bp. Weak sequence similarity to rat metalloprotease.
813	NPS954	GENO.	2	1-320	AC004564	In intron of gene coding for a 156AA protein at 20899-39698bp. Sequence similarity to Arabidopsis Immunophilin
814	NPS956	GENO.	2	1-429	AC005716	In intron of gene coding for 732 AA protein at 63422-80946bp. Sequence similarity to Rat follistatin
815	NPS958	GENO.	2	1-71bp	AC007180	In intron of gene coding for 217AA protein at 81722-84603 (complement). No database matches
816	NPS1079	GENO.	2	1-75bp	AC004758	In intron of gene coding for a 945AA protein at 87648-113518. Strong sequence similarity to Human retinoblastoma binding protein 2
817	NPS962	GNL.	2	1-116inv	AC001661	In intron of gene coding for a 286AA protein at 49143-60866bp (complement). Is Dros Wfing blister gene
818	NPS963	GENO.	2	1-512inv	AC004758	In intron of gene coding for a 945AA protein at 87648-113518. Strong sequence similarity to Human retinoblastoma binding protein 2

819	NPS964	GENO.	2	1-54bp	AC004334	In space before gene coding for 433AA proetin at 21602-22903. No database matches.
820	NPS666	GENO.	2	1-557inv	AC005149	In intron of gene coding for 424AA protein at 70149-97938. No database matches.
821	NPS968	GENO.	2	1-202	AC005333	No good predicted exons in this area.
822	NPS970	GENO.	2	1-534inv	AC005334	In intron of gene coding for 309AA protein at 64276-77888bp. No database matches
823	NPS971	GENO.	2	1-438	AC006421	No good predicted exons in this area.
824	NPS972	GENO.	2	1-524INV	AC005443	No good predicted exons in this area.
825	NPS973	GENO.	2	1-492	AC005981	space before gene coding for 310AA protein at 39927-45298bp. Sequence similarity to mammalian Uridine phosphorylase.
826	NPS974	GENO.	2	1-535	AC005889	No good predicted exons in this area.
827	NPS975	GENO.	2	1-47bp	AC005130	In intron of gene coding for 826AA protein at 3650 -13339bp (complement) ESTs AA949050 and AA817663 come from this gene. Sequence similarity to Helix-loop-helix genes
828	NPS976	GENO.	2	1-551	AC005554	In intron of gene coding for 2355AA gene at 16134-35638. Sequence similarity to Rat Fatty acid synthase.
829	NPS977	GNL	2	1-100, 146-499	AF097364	Drosophila Drongo gene
830	NPS978	GENO.	2	1-580	AC005554	Part of gene coding for 2355AA gene at 16134-35638. Sequence similarity to Rat Fatty acid synthase.
831	NPS979	GENO.	2	1-256inv	AC004722	Space before gene coding for 834AA protein at 33470-40630. Sequence similarity to bromodomain containing proteins.
832	NPS980	GENO.	2	1-406	AC003054	In intron of gene coding for a 822AA protein at 9312-46969. No database matches.
833	NPS982	GENO.	2	1-460	AC004280	No good predicted exons in this area.
834	NPS983	GENO.	2	1-99bp	AC004722	In intron of gene coding for a 289AA protein at 43804-61450bp. No database matches
835	NPS985	GENO.	2	1-178inv	AC001661	In intron of gene coding for 300AA protein at 30647-46841. Weak sequence similarity to Mouse surfeit gene
836	NPS986	GENO.	2	1-602	AC005269	No good predicted exons in this area.
837	NPS987	GENO.	2	1-562	AC004362	No good predicted exons in this area.
838	NPS988	GENO.	2	1-521	AC004370	In intron of gene coding for 1277AA protein at 40819-69834 (complement). Sequence similarity to human nuclear transport receptor.
839	NPS989	GENO.	2	1-619	L49408	No good predicted exons in this area.
840	NPS991	GENO.	2	1-535inv	AC005447	In intron of gene coding for a 802AA protein at 28001-49228bp. No database matches.
841	NPS992	GENO.	2	1-342	AC004120	No good predicted exons in this area.
842	NPS993	GENO.	2	1-512	AC005454	In space before gene coding for a 399AA protein at 66560-68732bp. Sequence similarity to mitochondrial carrier protein genes.
843	NPS994	GENO.	2	1-515inv	AC005130	No good predicted exons in this area.
844	NPS995	GENO.	2	1-499bp	AC005439	No good predicted exons in this area.
845	NPS997	GENO.	2	1-565inv	AC005127	No good predicted exons in this area.
846	NPS998	GENO.	2	1-568	AC005889	3bp overlap with gene coding for 1365AA protein at 67351-74867bp. ESTs AI106939 and AI296430 come from this gene

847	NPS999	GENO.	2	1-503	AC005558	In intron of gene coding for 1277AA protein at 40819-69834bp (complement). Sequence similarity to human nuclear transport receptor.
848	NPS1000	GENO.	2	1-620	AC004351	In gene coding for 676AA protein at 34511-37955bp. Sequence similarity to mouse LUN gene.
849	NPS1001	GENO.	2	1-519inv	AC004766	In intron of gene coding for 1467AA protein at 867-18363bp. Sequence similarity to Drosophila Lipase 3.
850	NPS1002	GENO.	2	1-80inv	AC006247	In gene coding for 805AA protein at 160506-163420bp. Sequence similarity to Mammalian Valyl tRNA synthetase.
851	NPS1003	GENO.	2	1-370inv	AC005129	In intron of gene coding for a 1208AA protein at 56208-83122bp (complement). No database matches.
852	NPS1004	GENO.	2	1-748inv	AC005894	No good predicted exons in this area.
853	NPS1005	GENO.	2	1-535inv	AC005447	Part of gene coding for 239AA protein at 507-13551bp (complement). Sequence similarity to C. elegans gene acc. no. AF002196
854	NPS1006	GENO.	2	1-581inv	AC005643	In intron of gene coding for 242AA protein at 33006-40459bp (complement, incomplete sequence). No database matches.
855	NPS1007	GENO.	2	1-342	AC005554	Part of gene coding for 2355AA gene at 16134-35638. Sequence similarity to Rat Fatty acid synthase.
856	NPS1009	GENO.	2	1-77inv	AC004532	In intron of gene coding for 1145AA protein at 5993-19843. Sequence similarity to C.elegans AF067608.
857	NPS1010	GENO.	2	1-496inv	AC007186	Space before gene coding for 351AA protein at 110375-111625bp. Sequence similarity to Human YL gene.
858	NPS1011	GENO.	2	1-582	AC007176	In intron of gene coding for 568AA protein at 84105-109350 (complement). Sequence similarity to zinc finger transcription factors.
859	NPS1012	GENO.	2	1-483	AC004423	In intron of gene coding for 604AA protein at 3052-8810bp. Sequence similarity to C.elegans AL021481 gene.
860	NPS1013	GENO.	2	1-560	AC005811	No good predicted exons in this area.
861	NPS1016	GENO.	2	1-596	AC005653	In intron of gene coding for 528AA at 40963-70180bp. Sequence similarity to C.elegans
862	NPS1017	GENO.	2	1-539	AC004516	Part of gene coding for 1730AA protein at 50171-62324bp. Sequence similarity to C.elegans UNC89
863	NPS1019	GENO.	2	1-505inv	AC005285	In intron of gene coding for 1142AA protein at 116605-128877bp. Sequence similarity to Guanine nucleotide exchange genes.
864	NPS1021	GENO.	2	1-504inv	AC007137	No good predicted exons in this area.
865	NPS1022	GENO.	2	1-191inv	AC005643	No good predicted exons in this area.
866	NPS1023	GENO.	2	1-468	AC004642	In intron of gene coding for 1296AA protein at 1037-28442(complement). Sequence similarity to putative lysophosphatidic acid acyltransferase [Mus musculus]
867	NPS1024	GENO.	2	1-578inv	AC005749	In intron of gene coding for 1481AA protein at 159-11694bp. Sequence similarity to KIAA0596 protein [Homo sapiens]
868	NPS1025	GENO.	2	1-598	AC007185	No good predicted exons in this area.

869	NPS1027	GENO.	2	1-634	AC004340	In space before gene coding for 864AA protein at 20219-29453 (complement). Good sequence similarity to Human sec24 homologue
870	NPS1028	GENO.	2	1-415	AC005456	Space before gene coding for 450AA protein at 45629-48055bp (complement). Sequence similarity to Human GMP synthase.
871	NPS1029	GENO.	2	1-198	AC004375	No good predicted exons in this area.
872	NPS1030	GENO.	2	1-316	AC005472	Space before gene coding for 626AA protein at 20859-27089bp. Sequence similarity to human NAT1/death assoc. prot
873	NPS1031	GENO.	2	1-495inv	AC004154	Space before gene coding for 292AA protein at 12210-30840bp. Sequence similarity to human rab geranylgeranyl transferase
874	NPS1032	GENO.	2	1-116	AC004328	In intron of gene coding for 1063AA protein at 63470-78557 (complement). Has been predicted from Dros genomic AL035311 and has similarity to mouse BOP1
875	NPS1033	GENO.	2	1-581inv	AC005112	In intron of gene coding for 407AA protein at 3680-49217 (complement). No database matches
876	NPS1034	GENO.	2	1-506inv	AC004367	Space before gene coding for 387AA protein at 3496-35348bp. No database matches
877	NPS1036	GENO.	2	1-411	AC005472	1st exon of gene coding for 626AA protein at 20859-27089bp. Sequence similarity to human NAT1/death assoc. prot
878	NPS1080	GENO.	2	1-492	AC007121	gene coding for 365AA protein at 22511-55594 (complement). No database matches
879	NPS1038	GENO.	3	1-291	L49405	In intron of gene coding for 665AA protein at 632-41487 (complement). Sequence similarity to human hypothetical SBB103 protein
880	NPS1039	GENO.	3	1-454	AC004658	In intron of gene coding for 394AA protein (complement). No database matches
881	NPS1062	GENO.	3	1-376	AC007757	Also matches Dros. EST AA951801. Poss. Transcription factor.
882	NPS1044	GENO.	3	1-597	AC006091	In intron of gene coding for 564AA protein at 74249-97818bp. Sequence similarity to Yli3_Yeast hypothetical protein.
883	NPS1045	GENO.	3	1-498	AC005720	No good predicted exons in this area.
884	NPS1046	GENO.	3	1-375	AC005814	Space before gene coding for 562AA protein at 60626-68675. Sequence similarity to Rat NAB1.
885	NPS1049	GENO.	3	1-486	AC004713	In intron of gene coding for 575AA protein at 10435-29297. Weak sequence similarity to CD36 genes.
886	NPS1050	GENO.	3	1-544	AC005813	No good predicted exons in this area.
887	NPS1051	GENO.	3	1-549	AC006936	No good predicted exons in this area.
888	NPS1052	GENO.	3	1-306inv	AC005425	No good predicted exons in this area.
889	NPS1053	GENO.	3	1-579inv	AC005720	In intron of gene coding for 394AA protein at 61401-93968. No database matches
890	NPS1056	GENO.	3	1-191inv	AC004266	In intron of gene coding for 931AA at 52045-70222bp (complement). Sequencw similarity to C. elegans Zinc finger protein. Drosophila EST A1259457 comes from this gene
891	NPS1059	GENO.	3	1-264	AC006936	No good predicted exons in this area.
892	NPS1063	GNL	3	488-536	A1062190	EST comes from Dros ferrochelatase
893	NPS1064	OG	3		AF104256	Sequence similarity to Human transcriptional co-activator CRSP150
894	NPS1076	EST	2	101-597	A1388606	1249bp contig with A1258281 and A1258326
895	NPS1081	GENO.	2	1-491	L49408	No good predicted exons in this area.



896	NPS1082	GENO.	2	1-475inv	AC005714	space before 390AA orf at 162294-163466. Hom to hum. death assoc prot 3
897	NPS1083	GENO.	2	1-461	AC004375	No good predicted exons in this area.
898	NPS1084	OG	2	12-419	AF000177	translational sequence similarity to human CaSm protein

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<221> misc\_feature

<222> (1)..(354)

<223> Area matching Intron of Drosophila Muscarinic

acetylcholine receptor, Acc. No. M23412. See

genomic sequence AC006938.

<400> 3

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tccgggactg aagctgaaaa ttctggccaa ggtatataac ggtacagagc cgaggagcgg 60
agagagccag agccgagcag cagccgagag agagcgtaag ggagagagtg ggcgacgcga 120
gttctttatg atggaatttg tgttttttgg gcagcatggc gagcaccctt ttaccaacac 180
cctcgacaaa aggacatacg gaaaaacggg ctggcgctgt gtgtgtgcag ccgaaaatgt 240
gctggcagcg gaacttaatg gatgaatatg aatgaaacgc cgcaacagtc caattgggct 300
agggctgggg ggagggggcag ggcgattttt gtgcaagggt gctgggggga attc 354
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<210> 4

<211> 607

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (9)..(277)

<223> Area matching *Drosophila* Tpr homologue gene, Acc.

No. U91980

<400> 4

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ccctaaagcg actttgtgca caattcgcaa aaaattaaga ctaaagtaaa gtaaaaagta 60
agaaagtaaa cttcgcaccg ctccatataa atttaaccgc tgcttgacaa ggatcaactg 120
cgaacatgga tctcagtggc ccacaaactc tgaacaacat acttcagccc gacgagttga 180
aactcgtgcc ggaagacgtc cagaagaaat tgcgggagta catcaacaat ttctcagatg 240
agtactgcaa gaaccgtgcg gccgccaatc gggtgggtaa gtttttatat ttgtatatat 300
actaaaatgc gccatatttt gcaaataacc ctttatattgc atgcgtatgc ttttacctcc 360
aactttgcgg cgtttaccgg ctcagatacc gcttcttgta ataagcaatc cgcgactgta 420
tggtttctag cgtggtaaac actcttgccg catttacata tttttgtata gaaattaaat 480
ataaaattcc gggttggtgc aattaaaaac aatggctgct gcagcaacat tattttcctt 540
ataatttcac ctaccggtgt ggtacactgg ccggcatttt ccaccaaca gtgattagtc 600
cgagttt
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607

<210> 5

<211> 585

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(585)

<223> Area matching *Drosophila* Type II topoisomerase

gene, Acc. No. X61209

<400> 5

atattgtgcgc cttgccagct ctaaaaccag caatacttct catttggtgt cggttgtgaa 60  
aagttgttaa atgtgctgtg cgtattttta tagttagttg agaactgtac aagtttttagc 120  
taaaggcagc agacgcgtgg ggcacgtaca agtcgaaaat tgtagtgac cgcctcgtgt 180  
atcgccctgca acatagagtt ttgccgcact tcggttgctg gcggcagcaa gaaaaggcca 240  
caaatacttg gcaatttttt aaccaggtaa gcagaaagtg ctgaatcata atcgtagaat 300  
tggtgtgacc gtagaaccta agagccctgt ctaattaatc ctttaatatg atggatatag 360  
caatttttcg gtggcgtcgc ttgcaaatta aaaatggcga taccggtat agacatttag 420  
ctaatttttg gcctttaaaa accatagttt tttgattttt tagcgcgag cgccgtatgt 480  
aggcctgaat ttgtttacta taaagtgaag cccctcgaag aaccttaata ggaaataata 540  
aatagccggt gactaccggc aacgccatt aacacgcaca cttac 585

<210> 6

<211> 408

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (270)..(408)

<223> Area matching *Drosophila* Neuron surface antigen 2  
gene, Acc. No. U22439.

<400> 6

gcttagatga tgattcagtg gagaagctcg gcgtcggatt gtcgtctact ccgaacttga 60  
gaagcggcgg agcttggggg ttgaccccat ttgtttatac ggccctctcg agccggcgtc 120  
gttggtcaatt atcggtttaa cccatgtcga ccgcgggggc cagtggcaat taattaattc 180  
aatcgcttca attgactgcg tategctgtt aggaacggct ttaatcgctg taattcaata 240  
aacatttcct gctctctctt cccatcgcag ccaaaatcgg aatcttctat gtggccttct 300  
acggagtcct agccgccctc gttgccatct gcatgtgggc cttcttccaa actctcgatc 360  
ctcgcatcc caagtggacc ctggaccggt ccctgatagg tacaaatc 408

<210> 7

<211> 540

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (30)..(461)

<223> Area matching *Drosophila* Indora gene, Acc. No.  
Y13272.

<400> 7

cgacgggacc accttatggt attatatgag ctgaaccata cttttttcga taaccgaatt 60  
atcccaaact tatcgggtgc agcttataag agttgcacac cgtccgata cttagctcac 120  
catactnnnt ttacattggt atgaccagc tgactgcaag ccactaccg attattcatc 180  
gagactttat cgccaactgc ttcagtcgcc tctacaaaac cccccgtac actcagacta 240  
gggtactcat agacacccta ggctgagacc gactgaaggc accttactgc cgaatgtcct 300  
tggcatgata ggttcccaca actcgtcctt ggaggtcttc cggcgcgtaa tacgcgttgc 360  
cgatcttctt cgaagtcgc gattttatga acgtcgggcc aaacttggcg ttataaccag 420  
tttgaaagca gcttggttg aaattccggc gataaacttc ttggccttcg acaaacgata 480  
ccatacgaga acngatatta tatctcttct cgntctcgnt gggcttactt ctcactcgac 540

<210> 8

<211> 267

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(267)

<223> Area matching *Drosophila* GDP dissociation  
inhibitor homologue gene, Acc. No. L03209

<400> 8

gtctgtacga caagttcgga ttggacaaga acacgcagga cttcaccggc cagccctgg 60  
cccttttccg cgacgatgag tatctgaacg agccggccgt gaacaccatc cggcggatta 120  
agctctactc cgattcgctg gcgcgttacg gcaagtcgcc ctacctttat cccatgtacg 180

gcctgggtga gctgccccag ggattcgac gtctgtcggc catctacggc ggcacctaca 240  
tgcttgacaa gcccatcgac gagattg 267

<210> 9

<211> 583

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (345)..(583)

<223> Area matching *Drosophila* Germline transcription  
factor gene, Acc. No. L17340

<400> 9

cgatactctt tggcgctacc acgagatagc agggctgccg aaacatcgat tgctgcatta 60  
tcgattgtgc ttcgcaacat catcgatttg tttcaggcca aaaacgttat tatgttataa 120  
tatatttata ataattaatt aagtataaat taaagactta aattaatttt taaattgtaa 180  
acgtattttt cacaaatgta aatgtacgat agtacaaatt agtttaaatt atagagcatg 240  
gagtgaccat cactgatcgc gttaccaaca atttttttta aataaatttg agcttgacat 300  
attcgcgctc ttgatcetta tacagttaaa gcaaacaatt gatcaattaa aaaatcatca 360  
tctcaattct ttcgtagtat tattcataca gacaattatt gtattaccaa tttttccott 420  
tttagtttac acctacgcca ctcaagtgtta taataaaagg tttgcaattc agcacatatt 480  
ttattggtaa tatatatattt cagcagtata aacagtgccg gccatgccgg ccattcatga 540  
agaatttaac caaaactact tacaaatggg aaatttgatg gca 583

<210> 10

<211> 480

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(480)

<223> Area matching *Drosophila* Histone H3 gene, Acc. No.

&lt;400&gt; 10

gtttattgtg ttttcaaacg tgaagtagtg aacgtgaact ttagtgaaac ccaaatacga 60  
 gatggctcgt accaagcaaa ctgctcgcaa atcgactggg ggaaaggcgc cacgcaaaca 120  
 actggctact aaggccgctc gcaagagtgc tccagccacc ggaggtgtga agaagccaca 180  
 ccgctatcgc cctggaaccg tggccttgcg tgaaattcgt cgctaccaa agagcaccga 240  
 gcttctaata cgcaagctgc ctttccagcg tctggtgcgt gaaatcgctc aggacttta 300  
 gacggacttg cgattccaga gctcggcggt tatggctctg caggaagcta gcgaagccta 360  
 cctggttggt ctcttcgaag ataccaactt gtgtgccatt catgccaagc gtgtcaccat 420  
 aatgcccaca gacatccagt tagcgcgacg cattcttagg ccacgtgct taagctgaca 480

&lt;210&gt; 11

&lt;211&gt; 542

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (179)..(360)

<223> Area matching *Drosophila* EST AA699128, this EST  
 matches the 5' of *drosophila* V-ATP ase gene  
 AF006655 gene.

&lt;400&gt; 11

ggccatggcg cctttttcct ttctgcctt cgtgcccctt cgtgcggctt cgtcatcaca 60  
 accggacgga ttcgtgttcg gctgacgaac cggatcgag atacttcggc cgttggtttt 120  
 ttcgacttcc atggcatctg gtcgttaggc cagccgttca ttcggcaacg aacccccgac 180  
 atagaagcac gtcagcatgt ggcacaaccg gagaaagtag gaaaaacaaa cggagtagag 240  
 gaaaagccca acaaaaaaaaa aaaacgaacg acggccaggg aaaaatgcc aaaaacctgg 300  
 tggaaaaagt tcctaaccat tctattgaga cgcaaggagt gcttaggatc aagtgttttg 360  
 tgtaagcaac gaggcctgta ccagtgtcac catgtgcata tataccatcg aaacatagac 420  
 aaactggcct ggactgttgc gccagagatt tgggtggtgtg aatgggtcat tcggggaaat 480  
 gggtcctttg ctgaaaaaaaa ggccttttca ggcttcgaca tttttacgta atggacgatt 540  
 ac



<210> 12

<211> 409

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (226)..(409)

<223> Area matching *Drosophila* mitochondrial PolB gene

Acc. No. U94702

<400> 12

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gattgttggt ctcgtttcgg atttatagct agatttttaa caataagggc tggatatatt 60
aaattgaaca aatgtgatgg agacatgtta attaaactag atcacaataa caagaaaatt 120
gcttttaaatt aagatagaat aaacacataa atcaacattt ttgcaaggac aatacttttc 180
agataacatt tagctgattg ttccgaaact cagttccacc tctgattttg tgctggtgag 240
aatgtttgct ctgttcagca gcccgttttt actgcaaaat tgcaacaaaa tcgaatgaaa 300
aggccctaaa ttggacttca agcagctaac gcatccaccc aaggtgccac agacacccag 360
tggactccga agttttccgac accagcgcct tcgaaatcca gatcgacac 409
```

<210> 13

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (110)..(191)

<223> Area matching *Drosophila* Integrin beta subunit  
gene, Acc. No. L13305.

<220>

<221> intron

<222> (192)..(395)

<223> Probable Intron in *Drosophila integrin* gene

<220>

<221> misc\_feature

<222> (396)..(472)

<223> Area matching *Drosophila integrin* gene

<400> 13

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gtagtgggga agaattggaa ggggtgacaca catgaaaaag tgttggtagc cacatgataa 60
atcaaatttg ataagataag aaaagctaaa taaaacaatt atccannnga ccaacttaag 120
gtatgcccgc tggggtgtga cttggacagc ctgatcactg gtttcgtagt cctttagggg 180
cttatactga aggctctagg accggctggg tctcgatat atccgtttca ctgcagttgt 240
agttaagtag ttgccggcga gagagacaac gatatccac ctggtattcc tgatatgcaa 300
ccaaatagga aaatgattga cttcgcaagg atgacagcag cagtaggaac aggaaccgtt 360
tatgttttct tgccatctcc ctcgactca ccttggtccg tgcaccaagc cgcattccag 420
atgagcggat aaacatcttt cgcagctgct gcgtgcctgc actgatcatc tgcgtaaaag 480
aatggcgat aacaaatccg ttatgtc                                     507
```

<210> 14

<211> 432

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(432)

<223> Area matching *Drosophila* Tra-2 gene. Acc. No.

X57484

<400> 14

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atcgggagcc actcagtagc gggcgtctcc attgcagcgc cagatataaa cacaagcgat 60
cggcgtcatc atcgtcagcg gggacaactt catccggaca caaggaccgc aggtaaatgt 120
gtacacacat atgtgagacg accctaaacg atacctcttt tgacatgaag catcgagtag 180
ttttgactgg cagtttgga aaaaggttca actgtcatag ggccctttca tttggatttg 240
ccccctcagc cgattcagct ggtgctcttg ccaagaaagt taaaaccaa aatcattcaa 300
```

gccgatttca tttcattgga agaaaccaac caaccaacca accaaccaac gaacatcact 360  
atgtaagaac ccaccgaagc aatcattttc attctacgtc cactaccaa gaatttggcc 420  
gaaagaggtc ga 432

<210> 15

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (61)..(276)

<223> Area matching *Drosophila* EF2 gene. Acc. No.

X15805

<400> 15

gtatagatcg agtggaaact cgttataata tgtacataac gatgccttat ttattttaca 60  
ggtcaacttc accgtcgacg agatccgtgg cctcatggnn nacatccgca acatgtctgt 120  
gattgccccg tagaccacgg caagtccact ctgaccgatt cccttgtgtc gaaggctggg 180  
tattggcagg agccaaggct ggtgagactc gtttactga caccgcaag gacgagcagg 240  
agcgctgcat taccatcaag tcgacgtaag accagtcatg ttccagcacc cacggctttt 300  
ttaataagct ttcttttttg cgtggctttc ctgttatttg aggtggagga aaaggatctt 360  
ggtgttgatt taccaccggg ttagcgcgag aaggagtgc aagggtttcc tgatcacttt 420  
gatcgattgc ccggttcac 439

<210> 16

<211> 532

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(532)

<223> Area matching *Drosophila* genomic sequence

AC005121. *Drosophila* TU-36B gene matches this

sequence 49bp 3' to NPS0018.

<400> 16

atcgagcgag tgcgatacga aaacaaaagc cgagcgccgc tccaataaaa gttcagttgg 60  
cgctacgtaa acaaactttg cggttagtct gcatctgggg tgtccagaac gaccggttct 120  
ttcgttaggc actaagatga acttggggaat caaacggcta gttatcagca acgattaagc 180  
actagcgttc aaggtacttc tgggggttaa ataaactcca tttatcagtg tacatcgatt 240  
aacaacagt gcacaaaatg acgccaatg ttaaggacga tggtgactgg agagtatccg 300  
gaatatccag aaattaccg agctatcgcc agcatcgacc gattaccagt gaaaggtttg 360  
catcgaatat acccataaat ttcaaattaa ttaaataaaa ctacatattt acattttctc 420  
ttgctcagct ggctggaggg gaaaaatgta gatgacgaag ccgaaggtct ttggcgaatt 480  
aacgatcgct ctacgactta agcgactttg ccggtcgctc cgggtgggtc at 532

<210> 17

<211> 536

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (250)..(536)

<223> Area matching *Drosophila* GO protein alpha subunit  
homolog class II gene, Acc. No. M29602

<400> 17

atcggtgcaa taaaaacagc gagtcgcaa aaagaagcgc aaagcgaacg gaaccaataa 60  
gaacagccaa acgcaaagag agcctcctgc acacacacgc acacagcagg ctgaagcaga 120  
cccacacaca cgcatacact agtgcggtgt gtatacgact ggaaaactag gcggtggtaa 180  
atgtgaagct gaaaaaagct gaaaaaaagg aaaaggaaaa ctcgtggggg ggtgggtggc 240  
ggcccagtg ggggggggtg tggcagtgtg cagcgcgtga gagtgccgta gtgcgtgccg 300  
tgtgagtgag tgagtgtgtg cgcgcgtgtg agtgaaacag cgacaaacta aatgaaaatt 360  
tatacatccg aaatgggttaa cagtttgcac aaaaacggca ttactttttg catatgttaa 420  
tgtgcttagg caaacgctcg aaaaagaaaa cttcacacc caccggcttt tttttcacca 480  
accggcgct tttttagcgc ctacgcccac gcttaataca taccctgca taaaaa 536

<210> 18

<211> 476

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (81)..(476)

<223> Area matching *Drosophila Lachesin* gene, Acc. No.

L13255

<400> 18

ggcacattca aggtgcccac ctccaggcaa gttgcgctct tgatggcgca cttttcaaag 60  
ccagagattc attcgtttcg cgactttcga actgtgaagt tgtctctccg gcgcgttatc 120  
tccgtcttgg ccaaaactcg tgactgatcg agagaagaag tctgaaacca gctctgagcg 180  
agaagacaag tgtggagact gcagttcagc atccgcgttt gctgtgctca agaaagaaac 240  
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gaagatttgg agatcttgga gcgcagctct tgagaaacac tacatatatt aaatcgcgcg 360  
cttgcaagggt ggtggtgcta aaagtcaatt ttaaagatgt ggcgggccgag tatctcgaat 420  
tggcggtgtg agcacctgct ctggccattt tttgtgcaca aacgctagca cagcga 476

<210> 19

<211> 457

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (119)..(457)

<223> Area matching *Drosophila larval serum protein 1*

beta subunit gene (inverted), Acc. No. U63556

<400> 19

ctcgtgcgtg taatttttgg tagccgggaa tggcgttcgc gccgtcccga catctgcaat 60  
aaattttaaa agtatcatta ttttcatata tgtagcctgc cttgcaacta cattgataga 120

atcaaatgac ccccgaaagt gtattactac cgatgaggaa cgaacgcctt ttcaaattgt 180  
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 tagacttttt gcacacctta ctagctaggt atcagacact ctaaaaacat ccgcgctcat 300  
 tcagtagatc gttccgtgga tcgttttccg gatttcgcaa tcgaagccgc acacacaacg 360  
 acgacgctca gacttgaaga cttggtgtag taatcgtgaa gaaaggtgta gtccgagtgg 420  
 cccgtagttg gagtacctct tgtacttgga gtaggct 457

<210> 20

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (121)..(417)

<223> Area matching *Drosophila* Positive transcription  
 elongation factor b, Acc. No. AF027300

<220>

<221> intron

<222> (418)..(480)

<223> Probable intron

<220>

<221> misc\_feature

<222> (482)..(577)

<223> Area matching *Drosophila* Positive transcription  
 elongation factor b, Acc. No. AF027300

<400> 20

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 ctgtttgacc catcgatttc ttatcgatag gccttgacag tgtgtgcaca ccggtatttc 120  
 tttagtcaac agctgtagaa acaccaattg ttgccgattt ctttcttttc gactgtcggc 180  
 ttctcgcgaa actgtgattg tgaaaattgt acaaataagag gcaaatttaa ccatggcgca 240  
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atcgcgacg atgtccctga tggagaaaca aaagtacatc gaggactacg actttcccta 360  
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 agtctccaaa ttggtgaaaa ctaactttaa actaaaacat acgaccctt tgattacaga 480  
 agaggttttt aaggctcgcg agaaaaaggg cacaagaagt ttgtggcgtg aagaagggtgc 540  
 tgatggacaa cgaaaggagg ccgtgcgtga aagcaca 577

<210> 21

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(577)

<223> Area matching *Drosophila* organellar-type

Ca-ATPase gene, Acc. No. X84681

<400> 21

agctgagcta aaaggtggga taataaccta ataattgcca ggactgaaaa ttcttaaaag 60  
 ttggagaaag aggcagctct gcacaaataa cgtaactcgg acgatatacg ttttcagtca 120  
 gccctgtctt gtgcgaataa tgtcgtgtca tagtgaggca gaacggcgat aggcagtaaa 180  
 tcggcgcttg gtacttagtg caatagttat cagcacacat attcagaaaa aagcgccatg 240  
 gggttatatta tatagagagt cagtggaaaa aagtacttaa cacacgcagt gcgtcgttta 300  
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 gaaactgaga atagaaaaac gaaaattgcg tctgttggtgc cgaagtgaca cgtgtgtgaa 420  
 tctcataagc ggagcgattt ggccagggtg acaaccctca tagtaatgca atattccagc 480  
 atattcttcg accccgatcc gacaattccg atcctaagtt ggccgccgata ctgcgcgact 540  
 ttatgggcaa tccgggcccg tcagaatgcc tgaatcg 577

<210> 22

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(534)

<223> Area matching Drosophila GTP-binding protein,  
Acc. No. X71866

<400> 22

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gtccacgcga gagttttata tattttatatt ttacatgcat atttggtgat aactgggggtt 60
ttctgtgaac cgcgttaact ctcagccagc catgagcaca atattggaga aaatctcggc 120
catcgagtcg gaggtgagtg gaacttggag tacctgccga tcttacagaa actaacctgt 180
ctcgcatcca tttacccgcg ggattccccc ctggattcta tctaaatcac cggggttggtg 240
gaccaccttc ttaactgaat cctagatggc ccgaacccaa aagaacaagg ccacctcggc 300
ccatttgggg ctactgaagg cgaagctggc taagctgcga cgcgaaactga tttcccccaa 360
aggaggcggc ggcggaaccg gcgaaggtgg gctcttgggt atacaattaa ggcaatcact 420
aaacattatg tatttccagc tggcttcgag gtggccaaga ctggagatgc ccgggtggga 480
ttcgtaggat ttccttctgt gggtaaatec aactgctct tcaacttggc ttgg      534
```

<210> 23

<211> 523

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(523)

<223> Area matching Drosophila genomic sequence

AC004351. Drosophila G protein alpha subunit gene  
matches in ssame area indicating that NPS0027 lies  
in an intron.

<400> 23

```
gctgtagaca gcaagaggag gagaatcgta agaaagtgtt tgcgccatga gtaatcaagt 60
taaatggcgc ctggcctcag ttatcgaagt gggaaatgtg ttaatcagcg gggagtgtga 120
aattgagcgg acccaccgaa aaagtaaaca attaaatcag atgaaatgcg gccccaaaac 180
ggaagcccc cacctagtag tgactttcac gcagatctct cgattatcat gaaatttcct 240
atatgtgatg tacatacata tgtacatcaa ttatttaacc acatatagta tattgacgta 300
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catatgtata aggtcgctcg cttggcgata attttgataa gcccaatgat acttttcagtt 360  
 taaatgtggtt ggtaagcgag ttcttaaata attgtagatt attaagttgc tgtgtgttga 420  
 cagtctgagt gcccgatttt gatattggtg ccccgacgagc atgacactat tttggttata 480  
 tattattttc ttccattttt ttcatatattc tttttttttt ttt 523

<210> 24

<211> 305

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (19)..(215)

<223> Area matching *Drosophila* EST AA246996. This EST  
 matches *Drosophila* CD39-like NTPase gene, Acc. No.  
 AF041048

<400> 24

gttgattcca agacgccatt ccgtgcgcgt tggcttctctg atcagagttt atcattcggc 60  
 gggcgcgggcc tcattagatt agatcgacat tagtgcggtc cgctcggcga tcggcagcaa 120  
 tcgatccgaa ataaacaaac gctcgcgtat ttacataatt taagtgaaaa gtaacgacga 180  
 cagaatgacg aacaccgatg tgcgaaagag aaaagtaagg aaaagggtcaa aagggcaatc 240  
 cacagcaciaa atttaatgcc aatttcattg cgctctctca cacacacacg cacacatgcg 300  
 aattc 305

<210> 25

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (387)..(473)

<223> Area matching *Drosophila* phosphatidylinositol  
 4-phosphate 5 kinase gene (inverted) , Acc. No.

AF071417

<400> 25

gtcggcggca tctcctatat atctttcctc gtgtctgttt tccttttttt tttaatat 60  
atcgcacgca tgacacgtag aatagaacaa aaacaacaat aattgtacgt taacaacgga 120  
aagttttgcc aaattcagtg aatgaaacta aactaactga aatgtgcgag gctagttgct 180  
ttattagcaa taacgttgga tcttatttaa atggaagaag tccctctaaa gttaataact 240  
tgccacttga cctcgttttt tgtgggtcgtt gttgttgtgt tgctgttgct gtggctgctt 300  
ttgccttggg accatttggt gtgaattatg agcttgcaat tatagcgttt tgccgggtttt 360  
atttgtaatt taattagcgt acttacacag aaatgctcga gggaatagtt tgctagaggt 420  
caaaaaaacc gaaagatatc cagcgaaaag agataattat ttgccctcgg ctg 473

<210> 26

<211> 319

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(319)

<223> Area matching *Drosophila* rbp9 gene, Acc. No.

S55886

<400> 26

cgtctttggg tttaaagccc ctctggcacc ttcccttcag tcagctgccg ttgttggtgt 60  
tgcttaagtg tttgtttggg tgccgtgctg gctctctcag ctccaacaac agcaatgcgg 120  
ccggcttacg agccccgggt ctcttcgcct cttttggagc tcgctctttg ccgaacggag 180  
aacctaccgc aattcgtttc gtgttcacgg ctgcatttcc ttgtttatgt tttgcgaagc 240  
caaagtgttag ggtacatcgg tttaagtgcc gagccaggaa gaaaggagag agcgagcgaa 300  
ccgagtaccg tttatgttg 319

<210> 27

<211> 493

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(493)

<223> Area matching *Drosophila* manganese superoxide  
dismutase gene, Acc. No. L34276

<400> 27

```
atttgaacaa tttactgcta gagatgagca gatgagaaaa tatcgaaaga cccaatcag 60
tcagtgatgt gagatcaact tatatatatt gaagttaaag agtaaaacta aaagaaatta 120
aaaactatct ttgaaggcca ctgaaacata ttcaaatcat attgaggatt tcttaaata 180
ttcttatgtt taaatactac tttagtgaact attagcatat tttagctgca tacgtatcga 240
ctgcatccat tcgattgata cttgaattaa tcgattttgg cctctgtatg atgtcatggc 300
gctaaattgg aaataaacta tgaaattaac gtcataagtt taaaaatccg actggaacac 360
agcacacaac atgtctacat ttcaaatacc ttcccgaatc aaaatcgata taacaaataa 420
acgggcacag aacattcttc acaaatatct acatttaccg taagttgctt aaataagcta 480
aagattttat gat 493
```

<210> 28

<211> 571

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (233)..(377)

<223> Area matching *Drosophila* rab2 gene (inverted),  
Acc. No. D84313.

<400> 28

```
cttcggccca ccgactccag gaatatcttc ctgcgaagca attttgatct cacggtatca 60
acttttcact tgagaccacc tgaaaccccc attttttgat ttccgggtac gaccctacg 120
cctgcgatgc cctttgtttt gttgtgttgt ttgcaattac agattgtttc cctgacaatg 180
gccaaacttt cactggccat tccgtttcaa aggaagtgc agcttgcaact cacctgtgtc 240
tccgataatg atgtatttga acaagtacgc gtaggacatg ttttaagctg acgggggtta 300
```

cggtaagcta gtttttagaa agtacgatct cgtaatgcca cagataatac gcaattcttg 360  
 tacgttttcc aatctgttcg tatttatgat gactggctag cgacagtgtg gcactttgtg 420  
 gccagggctg gcggaataac cgaaataccc gcaaggctgc aatgcctat cgatacga 480  
 cgactggcg tggccaatcg atagtatatg tatgtatgta gaattgcaga aatttctcgc 540  
 acaagcaaag tgtttgggag gataaacgcc a 571

<210> 29

<211> 550

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(63)

<223> Area matching *Drosophila myosin V* gene (inverted),  
 Acc. No. AF003826

<400> 29

gttccactgg ctctctctcc tactccaggt tccgcttcgc gctccttctt tctctctctt 60  
 ccttcttctt actcgctgg gagtgagttg ggtgcataaa tcccgtagg tttaatttcc 120  
 ttggtggtac gtttttttcc tggtcttgac agcctcttta aattaccatt ttcgtggtct 180  
 ttttttgggt ttatgtaaat gtactgtcct aaattactta aaattagcca ggaataattt 240  
 ataaaaacat tgataatttt tagatcgcaa cgccaaagtg tgagaaaaac aaacaaactt 300  
 ccgtccctgt caccgctga ctgactgact tatgttttgt tgttgcaaa agggcagggt 360  
 tgccaaaggg cgtgcagttt gggccaaatt agaaatgtgt ggttctaacc atggattaaa 420  
 tttgaacaaa gtaaaatata ttgcaaaaag atttgtataa tgccacagta actgaatttt 480  
 ttcttgcaaa acaccccaga aagcaccaat tatttggcgc gcaatgcctt gcagttagat 540  
 ttcagcactg 550

<210> 30

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (325)..(528)

<223> Area matching Drosophila

ribonucleoside-diphosphate reductase large subunit  
gene, Acc.NoU09369.

<400> 30

```
agctggatta acatgcaatc atcccgacta cgccatcctg gctgctcgca ttgcagtgtc 60
caatttgcac aaggaaacca agaaggcttt ttctggtaag ttcatagctt gtattctgag 120
ttcttcgggt aatccaatca tgattcttat tagacgtctt cgaggatctg tataatcatg 180
tgaacaagga gacgaatcaa aaagtgcctt tggtatccga gtttcactac aatgtgggta 240
agaagaacgc cacacggctg aactcatcca taatctatgg atcgtgactt tggctataac 300
tattttggct tcaagaccct ggagcggttc tatctgctca aaagaaacgg gaaagatcgc 360
agagcgaccg cagcatatgc tgatgccgcg tgggcgatcg gaatccatgg agaggatatc 420
gatgccgggc cgtggaaact tataatcttc tatcggagcg ctacttcacg catgcatcgc 480
cacactgggt gccgctgcac aaccggccgc agttgtcgtc ggggttcct 528
```

<210> 31

<211> 271

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (234)..(271)

<223> Area matching Drosophila Fzo gene, Ac. No. U95821

<400> 31

```
atatggacgc tttgtttaag cccgatgtct tctacaataa aacaaaaaaaa aagccaaaac 60
tggttctctt gttcttattc ccagcatgtg catgttccac agccagaaac tgtgtgtgtg 120
tgtgtgtgtg agccattagg aggaaggaaa aacaatctaa tcaagcaatt taaacagtca 180
acagcaataa aaactgctta aatttgcatg gcttagattc tcgtggtacg aagtaacttt 240
aaagtagtga aagaccaacc gtttaattatt t 271
```

<210> 32

<211> 450

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (322)..(450)

<223> Area matching *Drosophila* mitochondrial  
single-stranded DNA binding protein, Acc. no.  
U00669

<400> 32

```
aatctggaat gggccttgaa atcacatctc ataggaggga aataaaaaag ctacataaat 60
gtagacaatt aagttagttc ttagccttaa cctccaagaa aatatcacgt tgagctgcta 120
attcagattt atgtaatgag ttattagaac atttgctgta tgtaattacc taatgataac 180
ggcaatagtg tacatttcct tgttcaatta acttcagtga tcaatttctt cttaggatcc 240
atgaaatgcc ggatttcata aagaaaatag ctaccatttc atttaaaaag cattcatgaa 300
gtcttaaata tttcccaca gatatgagaa cggcgactgg gcccacgca ccgactggca 360
tcgtgtagtg gtgttcaagc ccaatctgcg tgacaccgtg ctggaatact tgaagaaggg 420
acagcgaacc atggtgcagg gaaagatcac                                     450
```

<210> 33

<211> 385

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (14)..(385)

<223> Area matching *Drosophila* RM62 gene. Acc. No.  
X52846

<400> 33

```
ccgtgctgcg tatgataaat ccgtcattag cataaccgca ttgaagctaa gtcttcggga 60
aaatgcttaa gcttgtgcaa tacatagccc cccgggtggg cggcgccacg ccccgaccga 120
```

ctgcctgcgg ctggggcaac ttgctattga tttccccgag aagtggcgcg agctccgaga 180  
aatgtataac gcaacgtcgc ctttttcttt tctctccgc cagcagcagc ggcactttcg 240  
cttcttcttc ttgcgtctgc accgaacaac gacaacagtt ccacgggagt cgcaggaatc 300  
gtgagacaat actggttcca agcacatata gtagtctcca agctcagtcg cagcgtgcgt 360  
ttcgagacag ctcgaaacca gattc 385

<210> 34

<211> 442

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (422)

<223> Area matching *Drosophila* pterin-4a-carbinolamine  
dehydratase gene, Acc. No. AF069297

<400> 34

gctgctggag aatacataac tgagatttgc gacaggctgc gcgaaaaata aagctcagat 60  
ttaagtttgg tatttttggc cctccctctc cctccgcaca ttccacctt tgaatacctt 120  
cgtactcggt gctgttggtg cagttgtggg gaataaacca gctctgcggt tgctggcaag 180  
caaattggcc actttctggc agttcggctt aatcacattc tgagcgcatt taattgttaa 240  
caacattttc gatccaaaac tcgtttggtc ttagctgctg tttttgttgc tgtttctgtc 300  
ggcgcggaac agctgacttt tgctgatgt tagctaaca tgagttaaca tggagctggg 360  
aaaaactgcc aacttgtttt tgacaacgtc tgctagcaac ataactgtta taaagtctaa 420  
tgccgcgtaa tttgaattta aa 442

<210> 35

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (329) .. (346)

<223> Area matching *Drosophila* cytochrome c oxidase  
subunit Va preprotein gene, Acc. No. Y09065

<220>

<221> intron

<222> (347)..(414)

<223> Probable intron

<220>

<221> misc\_feature

<222> (415)..(510)

<223> Area matching *Drosophila* cytochrome c oxidase  
subunit Va preprotein gene

<400> 35

```
gcacgcgtca agttgaagat gcagtgtgac cgcaattaaa tcatcaaaaa ataccgcctg 60
gcagtagcca gcatcaatgt ggaccgttga aaaagaaaca aggtttgatt ttgatttttt 120
ttttgctttt tttgggcaag atagaagaaa ttaaataataa ggaaaatgat aaactaactg 180
tgatcttacc cgaatttgaa atatactgaa gcagaaacat tttaaataatc tcaactgttcc 240
gtgacagcga cagttataaaa cgtgtccatc cctggaaaag ccagtgtttg ccaaccatca 300
ctcagatctg tcatacccggt gttgaaaagt agcaagaaca agaaaagtga gttcaagctg 360
tttctttaac caaatTTTTG caattaacaa gcattttact gttttttaacg gcagcatgtt 420
gagcatcacg gcccgtaacc tggcaagcgc cctccgcagc agcctcgtcg gcacatcgtc 480
gcgcgtggcc gccgtgcgct gtctgcacgg                                     510
```

<210> 36

<211> 401

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(283)

<223> Area matching *Drosophila* Ubiquitin gene, Acc. No.  
M22428



<400> 36

atcagtactg tccaaaatcg aaaatcgccg aaccgtagtg tgaccgtgcg gggctctgcg 60  
aaaataaact ttttttaggta tatggccaca cacgggggaa agcacagtgg attatatgta 120  
ttaatatatt atgcagggtt tcattactta tccagatgta agcccactta aagcgattta 180  
acaattatth gccgaaagag tataaacaaa tttcacataa aaatggatta agaaaagctt 240  
gtgtaagatt atgcgcagcg ttgccagata gctccattta aaacacttca aaaacaataa 300  
gttttagaaaa tatatacata aatagcagtc gttgccgcaa cgctcaacac atcacacttt 360  
taaaacacccc tttacctaca cagaaatact tttttaattt c 401

<210> 37

<211> 445

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(213)

<223> Area matching *Drosophila* hnRNP gene Acc. No.

M28870

<400> 37

gtctgtctac ggcttttctt tccacaggaa aatatattht cagtttttagg gaaggggtgc 60  
tacagtgage gtctttcggt cccagtgtcg ttatttctat agtattgctg agatatatat 120  
cagagcagta aagatattht aatataagtt cttecgaaatg ggtgggtcacg acaactggaa 180  
caatgggtcaa aatgaggagc aagatgtaag tagcacacaa aaccgcgact gcacagggaa 240  
aaaactcagt tcggccataa tcccaatata tatatattht ggtgatcaac gcgctttttac 300  
ccatgcggca actaaagttt gatgttgcta aagcatttcc gttgcgggtt tgttacttaa 360  
gactaagact aacagtagtt gtttcttaat aattgctagg gaattacaaa gcctgtcgggt 420  
attggtttct cttttaactt tttag 445

<210> 38

<211> 380

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(380)

<223> Area matching Drosophila genomic sequence

AC006933. Drosophila Rhodopsin 4 gene(Acc. No.

M17719) also matches in this area indicating that

NPS0044 lies in an intron.

<400> 38

gttactggtg acagcgatat tattgtaact ttaccacccat tcctttccaa aggtactttt 60  
tctgggttcac agttttacatg catattggat cacttttgtc attggcaacg catgtaaatc 120  
tgcttataat tgatgaacaa attcggaggc aatatgttgt attacacttt tcacgctttt 180  
tcctattttct caaaccaatg agctgcgagt taatagcact gaacataagt ttcacatcatca 240  
acatctatgc ctgcattcta tcaactcataa tggtgggata tcagatacca gcattgtatc 300  
tgaataccac attctatacg ccaaaggatt atagatacaa tcaagggcta ctgggcaact 360  
tcatggcctt catgggaaaa 380

<210> 39

<211> 449

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(449)

<223> Area matching Drosophila TipE gene, Acc. No.

U27561

<400> 39

gaatagccaa ccaaagcaaa aaagtgaaaa agacaaacaa aactgtccgt ccagcattcg 60  
tttttctaca cacatttcga aagaatgtaa atgtaaagtg aagaaaaaca gagagtaaga 120  
gagagacctc aaaactggcc attggcaggc caaacacata cacaggcaca ccaagcatac 180  
aggacacaca ggccacacac gacacacacg cacgaacatc cagtgtcttg ccgcagtcac 240  
aaaataatca agaagcagct aaatcaggca aaagcaagac gactgcaacg tgctgatgtt 300

gacgaaacat ctccattggg acgaataaag caattagcaa aggttcacga ttgttgccac 360  
ccacactgcc aggaggcgga agaagctgga agggattaag aatgcgggat acgttgggac 420  
tcccactcgg actccgtgga gtttttagc 449

<210> 40

<211> 572

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (463)..(528)

<223> Area matching *Drosophila* EST AI405330. This EST  
matches *Drosophila* mitochondrial ATPase coupling  
factor 6 gene, Acc. No. X99665.

<400> 40

gatgagatag aataatttca aagtttttag ttcattattca tattcttcat attcatatta 60  
gagtaataca agaatttatt attcatattc aatttagatc cgattttggc ttgtgtggga 120  
ttttagatac agtttaggtg ttgttttggt atgaacgttt atggagcagt tttgatttaa 180  
gttggacata tatagtaaga tacataaaca gacacagtgt ataaattagc ttttcataat 240  
ttgtaatatatt tttattatag gcagtatttc gatagaggca actaatttaa gcggattggt 300  
gattaaaatt cttgttcgca acgaatataa tttatatgat acagctaaca aatacaggat 360  
taagccaaaa atcggcttag gaaataacct tactatttaa aaagcttaca tacgatagta 420  
tcccatacac ccatcacgcy cacatcacta acaccaact gccattgtga actgacaatt 480  
gtaacttttc cgcacgaaag ttagcatttg caaaggaaaa taagatgaaa acaagattta 540  
aaatccttaa aatttattgg gggagttcca at 572

<210> 41

<211> 246

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (246)

<223> Area matching Drosophila heat shock gene at  
87c, proximal end, Acc. No. K01294.

<400> 41

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ctaaagccaa atagaaaatt attcagttcc tggcttaagt ttttaaaagt gatattat 60
atttggttgt aaccaaccaa aagaatgtaa ataactaata cataattatg ttagttttta 120
gttagcaaca aattgatttt agctatatta gctacttggt taataaatag aatatattta 180
tttaaagata attgcgtttt tattgtcagg gagtgagttt gcttaaaaac tcgttttagat 240
ccccgg                                           246
```

<210> 42

<211> 407

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (221) .. (318)

<223> Area matching Drosophila EST AA440389. This EST  
matches Drosophila Fas gene, Acc. No. U73160

<400> 42

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gtctagacat atcaaacta accctgacct cagcaatggg caaataaaac cgcccatttg 60
gccaacatct accacatcta atctgctaata gagaatacac gcacatacca cacatatgta 120
tgtataggcg cgcgcacgca cacacctgca aaagctttta ctaatctaaa gctcacgagc 180
gagcttttgc tgaaatgctg cagggtcttc gtcgtcggca atttttgcac atcagtttta 240
aaaccaagtg taaccgaaac ggcttggtta tttctagctg cggcggtata aaacaccttt 300
ttttttggtg taatccaggt taaaacaata aacagtgggt ctcaaataaa aattccatcg 360
aactttgcgg ctgttcactt ttgctgaaca gtttgcaatt cttgttt                                           407
```

<210> 43

<211> 537

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (15)..(95)

<223> Area matching Drosophila EST AI297861. This EST  
forms a contig with ESTs AA697916 and AI063366  
which overlap 5'end of Drosophila 49KDa  
phosphoprotein gene, Acc. No. M32141.

<400> 43

gtttgcagat ttacctgtta gaagagcggc tctcgagaac attttccagg cagttgcgac 60  
gaatttatgc tactaaattc acccgaaatt gtcagttcac aatagtgaca ggttaagaga 120  
gcgttgccag atcaaccgct tgtcagaccg gttttacaac actggcaaag tgagccctat 180  
atttgaactt ttcaaaataa aaatttggtt attgaaattg tatgtttata acttttattt 240  
gtattttcaa cttcttttaa acttattttt atgatattaa ttttatattt aatcgagtgt 300  
ttggcagtat taaaccattt acgcaaactg tttacatatt taaaattcga agttggaata 360  
taaaaagctt tagtagaata aattaataat taaacagcca aattgtatag ccattttaca 420  
atgcttaaga ttaaaacgga aaaagatact cgtcataact ttacaagttt ttattttaaa 480  
aaatattaca atttgctaga taaattgtgc cttaaagttat cagatttagc tgcgaaac 537

<210> 44

<211> 292

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (231)..(292)

<223> Area matching Drosophila Tcp-1 gene, Acc. No.  
M21159

<400> 44

atccccggggt tttgtcaaca tctgcggtgc gtctgcgggc ggagcacgtt tcttactcat 60  
cgcggggtcac gctctccacg aagaatgttc cggaaccaac ccggggggagg gcgatcttat 120  
tttaattgga ttaacaaaaa aactcattga atccaaggag ctacaagatc ctgtggacaa 180

gcctatgcga agtgaggtta tgactacaac tcggctttta tatgctttca gttatggccg 240  
ctctgtccat atcgaacatc gtgaaaagct ccttgggacc cgtgggtctg ga 292

<210> 45

<211> 349

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(349)

<223> Area matching *Drosophila* HSP70 gene Acc.No. V00213

<400> 45

cagtaaacgg cgcaactgttc tcgttgcttc gagagagcgc gcctcgaatg ttcgcgaaaa 60  
gagcgccgga gtataaatag aggagcttcg tcgacggaga gtcaattcta ttcaaacaag 120  
caaagtgaac acatcgctaa gcgaaagcta agcaaacaaa caagcgcagc tgaacaagct 180  
aaacaatctg caataaagtg caagttaaag tgaatcaatt aaaagtaacc aacaaccaag 240  
taattaaact aaaaactgca actactgaaa tcaaccaaga agtaattatt gaagacaaga 300  
agagaactct gaatactttc aacaagtcgt taccgaggaa agaaagaac 349

<210> 46

<211> 241

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(241)

<223> Area matching *Drosophila* glutamyl-prolyl-tRNA  
synthetase gene, Acc. No. U59923

<400> 46

cgtagcagc tggccgtact cgtgccgttt aaaagccgaa atttcatcag tttgatttca 60  
attgcaaaca aacaacctgc gaacatgtca ataaagctca aagcgaacct taacaatccg 120

cccataagtg agtatcaaac ggatgccggc tgctgtgacc tccagtcccc ggaggatctg 180  
 cacttagtga ggttatatcc gcatcggggg ctatttatgt acacaatata tccggcaatc 240  
 c 241

<210> 47

<211> 499

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (225)..(237)

<223> Area matching Drosophila ribosomal S4 protein  
 gene, Acc No. D16257.

<220>

<221> intron

<222> (238)..(333)

<223> Probable intron

<220>

<221> misc\_feature

<222> (334)..(499)

<223> Area matching Drosophila ribosomal protein S4 gene

<400> 47

cgctggccac accgcccga aatctgcctt ttccttttcc tggtgtattg cccgacggac 60  
 ggtatgtgta ttttttgcag ctagccacgt gctaagtttt gtcaatggaa ggcccggcat 120  
 tggggatttg ctggccacgg atgcggcact ggcagtggcg agcgaatgct ggcacaaaac 180  
 taacgtttga ttgttctatt tgcagtgatc gcccgttcaa tatagtgaat caaacatggt 240  
 gagtatctgt tgggtggtgaa gatatgggtca cgattgtttg tctttgcctt tggaataacct 300  
 gactaacggc taaaaccac tcacactttg caggctcgtg gcccgaagaa gcatttgaag 360  
 cgtttagccg cccccaaggc atggatgttg ggacaagctg ggaagcgtct tccgccccgc 420  
 gtccccctga cgggtccaca caagctccgt gagttcctgc ccctgctgat cttccttgag 480  
 aaaccgcttg aagtacccc 499

<210> 48

<211> 462

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(462)

<223> Area matching *Drosophila* Rl1 gene, Acc. No.  
X73216

<400> 48

```
ggctgtacgt agctgtgagg atactagagc tggcaccaag ccgatggcac tatcgatagc 60
gatggctgca ttctggccgg caccatcgat ggacttgcaa tagcgattgc tatatgaaaa 120
ctaatactaaa gaggtggatg cacttcagtc gactttctat aatttgctta aactaataaa 180
tgatttgatc aatacagctt tctgtaaaaa ctggcagacg ctttctgctt ttaataattg 240
ttaatttaag ttcaacgggc tggcatcacc gtttcttagc acggactcaa gcctgagtct 300
attattttcaa ccaccactgt aacgaaaaca gcatggacag attgaaattc aataatttgg 360
taaataaacg attttattta aaattataga gttctaatta aaaagaactt ttacaggtga 420
tatccaacaa gaaggtcatt caaaaggcac gcgccagac ca 462
```

<210> 49

<211> 164

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(164)

<223> Area matching *Drosophila* relish gene(inverted),  
Acc No. U62005

<400> 49

```
atcgaaacga gtcgccgca tggctgacca ttcgttttag gtacttcccc gatgttcggc 60
```



ggatgggaaa ttatctgcgg cggccacgtc gagatgactc acgggttttt caggcgcacc 120  
actcagtgtg atttttttga tcggctatac tataagcatg tacg 164

<210> 50

<211> 207

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(207)

<223> Area matching *Drosophila* HSP2 gene(inverted), Acc.

No. X07211.

<400> 50

ccaggagcct ttgtagatca ccacactaaa atgagcatac atatgtatat gtatccgata 60  
taaagtattg caactataat aaacttttaa agtcacttg ctgtatccct gacttttggc 120  
aattttctct gcttccaaga ctcgatttcc cgaccggcag gtgaatatga ttggcgactg 180  
cttctccggt ttcgatatcc cgtactt 207

<210> 51

<211> 438

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (15)..(438)

<223> Area matching *Drosophila* MAP gene Acc. No. X54061

<400> 51

gggtgggtgt gcgcaaaaat tagtcggcaa gcaattcaaa agtaagagca accggagcga 60  
acaaaaaagg gaataactta ctaaaatctc tgaaagaaaa ataaaaagac taacgggctc 120  
ggcaagctgt gtttatttcg acaagtaatt atatacttgg agtgcaagca aaggcgaagg 180  
aagtgaagg acaagcaacg aaatcgtgct cttatccggt cctgtactgt gtctctcttt 240

cgctgggaga gtgtgtgtat tgggtgtgagt gtagaaatct gcaagaacag caacgccaat 300  
 aaaagtggaa tcgagaaaaa aaacgcagtg gcgcgtgaat cacgagcaat ctgaatcatc 360  
 tctctacaaa aatacctggt tctgttggcg catcatttat acccaattaa atcctaaagg 420  
 atgggaacac cacgaagg 438

<210> 52

<211> 554

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(80)

<223> Area matching *Drosophila* HSP68 gene (inverted),  
 Acc. No. J01102

<400> 52

gtcagaacat tccagtcagt tcgtgtgtgt gcgagcgagt caactagtgt gcacttcgca 60  
 ggggaaattg tcagttgaag gactgaaaag ttcaggaaat ttcgagaaat atattttttt 120  
 tattgacata ggatcatcatt ccaagtgggc attaaactaa attcgtatgc aagctatttt 180  
 tggctgattt gcggattgat acgttaagcc attcatattt ttagattctg tttttggttt 240  
 atatctcttt tattatatgt gcaatacata tgtgtgtatt tttcttctga ttggaatatt 300  
 tcctctgcag aatatgacat acaattacca taaaagtttg aacacacttt tcaaaaactta 360  
 attattccaa ttaattattt ccaaaaattt aaagaatccg tactgctcta tatccaggat 420  
 acataaatat atagatacct atagtaggaag tttcatagat aagatgtttt atagaatact 480  
 tccgtagatc gggtagaatc tttaatgttt tttataaata ggggaatttta agaagccaga 540  
 accaatgccc aaaa 554

<210> 53

<211> 450

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(450)

<223> Area matching *Drosophila* anon-66Da gene, Acc. No.

Y10015

<400> 53

```
gctcgggtggt agcatggcgt tagtgttgct aaacacagag ttgcatgtgg tctagtgttg 60
tgcagaaata ttagtgacag taaatcatat acatcttatg tggatatttt cgctatcaac 120
tgttacagtc aactaagcc aattcgatag atttcgatag taaaaataaa cattttggaa 180
taacataatt actttttagt aagttacttt ttacgggggtt aatttcaagc agacattttc 240
ccaacatggt ttacatacac ttccccaaca atttaaccga agaggagcaa atgctgcagg 300
ccaagtatca gaaactcaag aaaaagggtgg gaaaactcat gccacaaatg ttgattattt 360
atattaacaa gtttttaacc cgtagaaaaa ggcactgcaa gcgcacaagg cgccaagcc 420
ggaaccggag agctccttga ccttgaacgt 450
```

<210> 54

<211> 470

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (56)..(187)

<223> Area matching *Drosophila* RAD6 gene, Acc. No.

M63792

<400> 54

```
ctctatacca ctgctgcccg agtttgccct caattaataaa taaattacaa aattcatcgt 60
taccgttcgc taaacgcaac gcattgccca ggcgtccgag ttccaaatcc aacacaacac 120
gagtggtagt atcgctgtga aaaatgtcaa caccgcacg cagacgtctt atgagagatt 180
ttaaaagggtg agaagaaact aaggaatcga atgcgaatag aaaagaatac taactaaacg 240
aaagctaagg aaaacaggaa ggcaaggagc gaatggcaaa gttacacaca accgttggat 300
tttacgtttt acgtgtttct cgttccgaaa aaatgctggg gaaaagaaac ctgggggctg 360
ccaatacat ataagccaac acacggacac ccgttttata tgactgtgct ccacgtctgt 420
atgtagtgga aaagtttgcg ccagccaaaa tatttcgttg tgcattgtgc 470
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<210> 55

<211> 465

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (391)..(465)

<223> Area matching *Drosophila* Septin 2 gene, Acc. No.  
U28966

<400> 55

```
agctgtagac acatcagcaa tgcggacctg ccggatcgct tctgtgtgcg accagagatg 60
ccgaggcgga aacagttaag acatttaatt ttttaatcta attactttta attaataact 120
tatgcataat tatcaatgaa tgggacattt tattattagt tattaataaac tgaaacgcta 180
aatgatatgt actgaaatct taatccatga agtgcatttc actggatgat taacaatttc 240
gtttcactat ttgccattat ggcacatgta attcattaat taattgtttt ttaattcatt 300
gttaagctat aattttcttg ttcattcata tccacatact tctttgagcc gctggtattt 360
tggcctccgc cgttatctgg ccacactttg cagattccct ggcgacgcct ttgatccaaa 420
ctctgcgccc ggaatattgg attattttga cttgactatt ggaaa 465
```

<210> 56

<211> 564

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(514)

<223> Area matching *Drosophila* Fructose 1,6 biphosphare  
aldolase gene, Acc. No. M98351

<400> 56

```
ggacaaacct agaaaaaaaa aaatgtgaga gagagagagc gaagagctgc agatatagag 60
aaaagcacgt tttccgtgca tgcgccttta atctcattca atcacccgct ctttgcacatc 120
```

gaatcagctg tgaaatacac taccatgcaa agcattttatt atcttcaatg gaaaaatatt 180  
 tttaaattgg aaaaaacacc agtgacattg acctgacact gaaaacaaaa ttatataata 240  
 ccgcatcatt aaacaacagc atatgactca atggctctaa tcggttaact cagagttcca 300  
 ctttaaataa cttgaccttt acaaatattc tttttatttt atggaaataa taattaggtc 360  
 agttcagtaa aataatccaa cacttgattg atagctatct ctgtagcccg ttgttatctt 420  
 tttcagtagg aacatatgta acttttgagt tacctggatt ttgggtgtgc agactgtgcc 480  
 ggatcgtata ccgaaattta gtccaaattt ttaagtttat tttttacctc ggaaatattc 540  
 aaaatttggg gcttacgcat ggggt 564

<210> 57

<211> 251

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (46)..(251)

<223> Area matching *Drosophila* Bottleneck gene  
 (inverted), Acc.No. U01035.

<400> 57

ccccaggttg aggcattaaa aagctaacgg tttcttgttt tccgcttcgg caaacaaaac 60  
 aggtgcgttg tggcatagtg aatatacgca tatgtatgca cacgaatata ggtgtggaca 120  
 cggcggacag cgggagcacg gagtcttgcg tgattcagtt tacaacctgt ggtagtgtgt 180  
 ggatttagca attctgtttt atcagtcccc tagaactgat atattggcta ttcggaattg 240  
 ggaatttttg c 251

<210> 58

<211> 450

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (49)..(450)

<223> Area matching Drosophila HLH106 gene, Acc. No.  
U38238

<400> 58

ggcccgccag tatttaatta cgaaccgttt ttgtctcttt catcagcagc attcgcaatg 60  
gacacgacac tgatgaactt aatagacgct ccgctggacg agtccatgga tttgttcaaa 120  
gcgaggagatg tcttcgaacc gttcgacgcc gacctgcact cggacatgct ggacatcatc 180  
ctcaacgata tggacctggc gccgacgcag atgtacaaca tgctgctgga cgagcctcga 240  
acgcataccc agcagacgca gtccgtggat cagcagccgc aatccgtcga gcaacagccg 300  
cacgtgaaaa gcgagcactc ttgccagtgc cacatcaagg aggaactgca tcagcagcaa 360  
caacaatcgc cgcttctcgc tacaacccag atccccctcat agccacaagc tacaattgtc 420  
ccacaacagc cgacgggcct ttgaaggccg 450

<210> 59

<211> 581

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (328)..(581)

<223> Area matching Drosophila DAD gene, Acc. No.

AB004232.

<400> 59

accacgccat agtagccatc caacggatgc tctccactct cagatgtctt ggattctttg 60  
gtttagcact tgtagtagga atgggaatgt gaaaaatatg acgatatttt aacaagtctt 120  
ttctaattaa taataaaact gaagttctta tacattgtta gaacgggaac tttatgtatg 180  
attctaattt tacaatttct tgggtctctta attttctct ctctctctaa acctccctct 240  
cccaggcgct ctctcaggcg tttctcccac gtttattccc cacagctcca aagactatca 300  
atccgcacag ttagcgcttc gctcattgcc ccaacaattt tcaaccgcgt cgcttgtgtg 360  
ttcttttgcc gttcgagaaa tccaaatccg aaagatatca acgaaaagat gggatacttt 420  
gacgtattgc cagagaaaat tttccgaata acgttatttg tgttcgagac tgctaaatga 480  
ttttggggta attaaaatga caaaaaacgc agttctaaat atcggttttt tcgcctttcc 540  
cgatcttttt tcgcacatta acgggttttg ttttgggtgg g 581

<210> 60

<211> 436

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(436)

<223> Area matching *Drosophila* genomic sequence

AC005557. *Drosophila* Brother gene matches this  
sequence 15bp 3' to NPS0066.

<400> 60

```
agttaaacaa tacaatacac aaactacagc tgtttaatgt gcccgactc tagagttgtc 60
acctgcttgg gctgccatgg ttggcaactc cctttgctta agtgctgtgc taatcaacac 120
tgttaaaatt accgctaaaa cgtaatttcg aatttaaact taaaattata aagtgcgttc 180
aatcgtttcg ttttatttat gatagcattg tacctgcaat ccacaaagta taatattcgg 240
agctgtaaaa accctacgga ttataagaca aacctcaaat aggataccta taagtgttat 300
acctgatcct tattgtgtcc agatgggttc catccttgat taccagacga caattagggg 360
attcgttagg tagcccaatc gcaaccgat tacctggtct acaactcttt ttttttggt 420
taaataaggc gggcaa                                     436
```

<210> 61

<211> 645

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (46)..(176)

<223> Area matching *Drosophila* Aef-1 gene, Acc. No.  
M90755

<400> 61

aaccagccac agataatgct gtgaggaccc gattctgata ggcgagagca atacgcgaac 60  
accctccgaa aggcccatat ccccaaaaaa ccgaatcgag tgcgaaaaaa tgatgtaaaa 120  
cgggggaaat ctaaacctga aaggccccac acagcacagc cacaaaatgg aaaggtaggt 180  
caatgtgtgg gcgcccgaag agagttcaag tgtgtcactc agtataccca attccgtctg 240  
gaatcatttg gcaaaaatag cgtttataga cgtgtgaaaa acaatggaca tttgagctcc 300  
aaaattaaaa gtatcctaac ctcaaaagag cttttacaca gtacgtgtcc gtgtgtgcgc 360  
tagtgatgtc catabgtgtg tgcgactgaa agtggttgtg acttttagct gaagaaggga 420  
gcgcgagggg cgatctagag gcaacgtgtt agtggaaaaa ctgcttttga aaaaagggga 480  
aaatatcccc caaaaagccc gcccaaaaaa ggtcagttcg gaatcctgtc gatctgcct 540  
cgttgagatg tatccaattg gtaaagttat cactaagttc ttaagttgcc agaaaaacac 600  
atgtaatttg gcgagaaagt aacacgtgt caattcaaca caaaa 645

<210> 62

<211> 445

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (224)..(298)

<223> Area matching *Drosophila* EST AI292767, this EST  
matches *Drosophila* serine/threonine protein kinase  
gene, Acc. No. Y07908

<400> 62

gtctgcccc gacctaacc gtaagtgtgt gcgtgcgaga gtcgtttcat ttgcattctt 60  
gttttagcgca ctccctctct ctcttcgtgc gtttttcatt cataagcaca tttttactat 120  
ttggaactgc aattttttac actaagcttg aggacagaca agaatactgt gaaaatccaa 180  
tgtagatgaa agcaggccgt gctttttcca tcaaagtaat cgcaaaaagt cgagattaac 240  
acaagttcaa aattattcgt taaatttttag aacagaattt tgaaatgaac ataattcagg 300  
tactgtgtca tccacatata aagaactttt attctaaaaa caaataatcg tccgatcggt 360  
gtgggtctgtc caataaaaat tcacggcaaa ggcgttggct aaaaatacat agacaaacga 420  
gtcgggtaaa aaacaaatac atgat 445

<210> 63



<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(531)

<223> Area matching *Drosophila* Fascilin 1 gene, Acc. No.  
M32311.

<400> 63

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gtccgtggac attgcataat ttctgcggcg gccgttaatg ttaattcctg cagcccgagt 60
ttccgagaat tacgcagaat aaagaccaga gagaaaacta taaaatcgaa aacagaaaaa 120
agtgccgcag cagcgaaatg caaaggcgca taataattaa acacacagcg acggaatgaa 180
gaaaaaataa tacacaataa gcgcagcttt gtttctagtt aaattgcgtt tgtgttgtgc 240
ttgccgtttc ctcggtgggc cgtttttcgc ttgttgttct atgtgacata acggaactct 300
gggcaaaagc gaacaggaag cagcgataac cttgcaaaaa caaagaaaat accaaggagg 360
acaaaaagc atgccaagca tatatctgtg aaataatatt ttcttttccg aggaaatgct 420
gtttgtcgtc ggctaactgt tgtttgcctt tgaattgcag atcttaatcg tagagcagca 480
ctcacaccag cacacgcccc ccgcaaaaaca gcacacacag cacactcaca a 531
```

<210> 64

<211> 421

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(421)

<223> Area matching *Drosophila* HSP23 (inverted), Acc.  
No. X03889

<400> 64

```
cacgaaactt ctccgggctga aaatatcgca gagttctcga atttgccgca attacgcatt 60
atctgccatt gaaagtgaga gtatcgctat ggaaaatgag caatctccta ggggagtgagg 120
```

aatgaaaagg cctggtggag tgataagtcg catcagcacc ggcaaatatt atgtgtatgt 180  
atagatgtac gtatgtaagc acgtatgtat gtacatacat agcagatagg aaggttggag 240  
tatattccac gaaggatgga agtaaattcg cgaaaacttc gagactgcag aacaagtctt 300  
ctttttatgg cctggcattt aagctattaa ctttaattaa tatccaagaa tggggctctg 360  
gtagtgggga aatctaatta aaatcataag tggttaatgc ccgggtaggt aataaccctg 420  
g 421

<210> 65

<211> 882

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (548)..(882)

<223> Area matching *Drosophila* ATP sulfurylase gene  
(inverted), Acc. No. Y12861

<400> 65

cccgaacta aaacgcgtta agcgaccgca tgttccaaga acttggaataa tttccaagat 60  
atgcagctga taaaacagct gatagcgctg ccaacttatt gcagtgggag atcttgcgat 120  
caacgggtgcg atcgggtgtg agttgcgacc gtttggcgcg aaattcaaat ttaaattttt 180  
tatttaattt gttactatta ataataataa attaatacaa tacgtgacga tgacgatggt 240  
gatgatcgtg cccaacggca gcagacccaa ttgtaaaaag ttgtaatggc agaagcataa 300  
gtctaagtag agggctccac ctagcactgt ttgcacttc tggggccccc tgatatttaa 360  
aaaaatttta ctttattaac tcgatatttt tatgcattta attatcagga aagcatatta 420  
acacgttctt ggatcagttt aattatttca ccgcacgcac tgatctttct tggatatactg 480  
ggtcgtattg ttcatagaaa caatagctgt atgggaaatc ctcataaccg caaaaaatac 540  
aatcagttca ataagtaatt ttctatttta ttatttatat atgtattaaa aaccgtccac 600  
aaaatagctg cacgatattt tgcttaagat aaaaagaatt gggtgactta agtgtagata 660  
caagtagatt gtacgatagc aacatttagt taggaggagc acaacattca cacacgggga 720  
cagccacgga tttcggctta gaacaatgga aaaaagatgt ggtaagtggg aagcgccttt 780  
agcttgaaat atttatgtat aataagcaca cgagctataa ctaggaggaa ttgcacgttg 840  
cggatcgagt gtgagcagcg gggtacgact gcggcaggtt ct 882

<210> 66

<211> 569

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (83)..(135)

<223> Area matching *Drosophila Nemo* gene, Acc. No.

U12010

<400> 66

```
ccccggcgcg ttttacttcc atctcgctcc cacaaaggcg gaagagttaa acacaaaaaa 60
aaaagaaaaa tagaaaagaa attataaacg aaaaactgcc accgccgctg ctcaataatt 120
tgtgcatttt ttaaggtaat ttaaagtga atggaatgtc ttgtttgcat aggttaggtt 180
taattagtcc ggaaagctaa gcgaaaccct gggaaatatt acatatcccc gggcgaattt 240
cttttgcccc gttacttttc gattttcatg cgagcgtttt ttgattgcgt tcattttctg 300
gcgacttggg ggtgctcgcc attgtttggg ttttgaaca tttgtaaatt tgcataaaaa 360
gtcggatttt aagtgatttt ggtgtctttt gagcggcttt ttgcgcagggc agcgcagtcc 420
gaaaatcact cagaatcgca ctcacatgcy cacacactta caattgtaat acacggacgc 480
gccccgggtc ggcacagcta accggcactt tttcatgtcc tctcgcgcgc tctctctcac 540
tgctctcttc tcttcttttc ttttgatcc 569
```

<210> 67

<211> 500

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(357)

<223> Area matching *Drosophila UDP-glucose:glycoprotein*  
glucosyl transferase gene, Acc. No. U20554

<400> 67

aacagggcca aaaccagctg aaaactggtg aaaagtaaaa catttggaaggaggaaagcct 60  
 taagttcctc tctacgcttc gtacacgtaa tgtgcgtggt ttaatctacg ttaaaacaag 120  
 tggaaacccat gttacgtgcc gtggctttgt gtgtgtcagt ggtgctcata gcactatata 180  
 cgccaacttc tggggaatcc agtcagagct atcccattac cacgctaate aacgcgaaat 240  
 ggacgcagac gcccctatat ctggaaatcg ccgagtatct ggccgatgag caggcggggcc 300  
 tcttctggga ttacgtttcg ggggtgacaa agttggacac ggttctcaac gaatatgggt 360  
 tgtgtttata agtcatggga gaacccgcat taaagagctt ttatattctc ctcaatgtga 420  
 atcgaatcca tataaaatca agtaatgggt cggaatataa aatccctatt cccaaagccc 480  
 tataacgggg acctttccca 500

<210> 68

<211> 469

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(20)

<223> Area matching *Drosophila* Cbl gene, Acc. No.

U87925. This association is confirmed by overlap  
 with *Drosophila* EST AA441040.

<400> 68

acccacacaa ttttttcgac tttttcaatg aaatctcggt atgaccgcgg ccgcaacgcc 60  
 agtaaatacc aaacgagctc gcacggctgg tcacactgat cgaagggttg catttcgctg 120  
 tgacgtcatc gttgacccat gtaaaatgcc gttacaaaat ggcgagcttt tgaaaaaatt 180  
 cgttacaaat ttattaaatt aaataaacta atttttaaaa taatttgaat attcattttg 240  
 ggaatatggt tagaaataat agacttacag aatataatct attggtaacg attttctttt 300  
 tcacagtttt cctcctcgaa agggaagtat tttaaattgt tattacacat gggggaagtt 360  
 gctgcttggt taatgaaatt gtgttaaata tatataggga aatgctttta atctactttt 420  
 tgtaggaaac ctttcatgaa aatatgtgga atctcacgtt ttattaaat 469

<210> 69

<211> 539

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (468)..(539)

<223> Area matching Drosophila EST AA392994. This EST  
matches Drosophila Guanylate cyclase gene, Acc.  
No. U23485

<400> 69

ggcagcgtca attactgttc tcatatcatc tccgagagca cggaaatcag tgatggcaag 60  
tgagaggagc aaatcttttg cgtagtagcaa aaaccgctaa gtgtgtggca gtcaacgcta 120  
cttttcttag tatagtactt agttatacct tttatcgtgc aattttttaa tgaggactat 180  
gtttttccaa aatggatctg ctcaatataa tttgactatt tatcttttaa tccatttaaa 240  
cctagtttta aaaattttta aaaagtgttg ataatgtatc ttgatggata tctttcggat 300  
atcctacact gagcgaaact aaaattgttt gataaagcgt cctcatatgc ctaccttaac 360  
acagtgaaaa aagccaaagt gccatctctg ggagcatgcc ggtgtcgtc gcccgatttt 420  
cgtttggggc tttcagtatt attctattcg cctgcgcccc aagttgtttt tttcggatcg 480  
gcaaagcccc cgtgcgcccc atcgactct cgcacacaca catacgcact ccagaaaac 539

<210> 70

<211> 547

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(547)

<223> Area matching Drosophila UbcD4 gene, Acc. No.  
Y11349.

<400> 70

gacgtgctga gcgctgtaaa aagtcagatt cgtgttgaaa ttggaataat aagtttttta 60  
ttttccgtgc gctggtcgag ctggttgctt cgacaattcg aaaagcgatc gaaaggagca 120  
acctttagg ccaacagcca ggcgtaattt acgcaacgca caacactcac aaaatccaaa 180

attgcacggg ggggcaacaa taaaaacaga ggcagaacag aacacagcaa gaagagcgtg 240  
 gtgaagagga gcgggcggaga aaggagaacg gtgaacaggg aacagggaga gagcagaaag 300  
 gagagtccga gaaacggagg aaacatcatg gcgaacatgg caagtgtcgc ggatcaagcg 360  
 gggagttcaa gggaggtgat gcgcagcgag ggaggggtgag tcccagcac caaggcccg 420  
 aggacactca aacggcacct cggcaatgcc agcttgacc accggccctg gtcattgggc 480  
 agggggcggg ggaaggggtg ccgcgaacgt tgggtggcgt ttttggcgcg cttatggctt 540  
 ccgtttc 547

<210> 71

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(163)

<223> Area matching *Drosophila* SNAP gene, Acc. No.

U09374

<400> 71

cacccgctga aaagccgaac aagtcttaaa cttagatgca attagtgccg aggcggacat 60  
 aaatcctcga catgggtgac aacgaacaga aggcgctcca actgatggcc gaggcggaga 120  
 agaagttgac ccagcagaag ggctttctgg gatcgctgtt cgggtgcgta tcaaatcaaa 180  
 gaagtttcgc aatttctgtg ggagtgggga aatggaagct gtgtctggtc tagcctagca 240  
 tctccacaac cccacaaggt actgagccct attccaagta gcacttggat gccaatcac 300  
 tatgcttact actttgtttt tatgtatata cccactcacc ataatacgta tacgcagttg 360  
 tggactctac gcctccaccc agaaaggaga agaaaatagc gcaaaaagtg cgacttacag 420  
 aggataagtt tcagatatga agaacacaaa gtgtgcaaaa tgctgttaaa aaatatcccg 480  
 tagtacataa tatatgtaca ctatgccatt cgtaccaggt ttcgatgaat catagtgcc 540  
 aaaagtcaat cgtgtaaaat aaa 563

<210> 72

<211> 594

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(104)

<223> Area matching Drosophila Caf-1 (inverted), Acc.

No. U62388

<400> 72

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gattgagtcg aatcctggcc gggaacttac actttaaacg gcgtaacgtc agggcaaaat 60
agaaattggc taatttcctt cgtttttttg caagcgcgtc gtcgatgata gagatgcaat 120
gctaaagatt gtcgagacga ctgccatatt cgattacgat aacgataaca gagttatgga 180
gatgacactg cgcggtattt ttataacttg ttagttcctg cgtcatgatt ttagtatttt 240
gtggtttaca tcgatatatt tgggggttta aaaggtatat tttaacgggt gcagttgcgg 300
gcacactaaa gtgcataaac aaagtttact acttaattcg ttatcagtgc gaatgattcg 360
aaaccagttt acgcgccaat gaccggcttt ccattcttat ttgacgagcc taacgtgcc 420
gttgagttta agttcccca cgcgaacgac ggtgggcagc cgtgattcat cctcaacgct 480
ttttttccaa ttgtgtatgc aaaatgtttt tgcacgtaac gagctgaact attgagtttg 540
ctaaatagtt taacaagcaa taatttggcc gacatgcagg ttgatgggtg acca 594
```

<210> 73

<211> 583

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (374)..(518)

<223> Area matching Drosophila Elongin B gene  
(inverted), Acc. No. AB007692

<400> 73

```
ggttagggta aaattaaagc cgaatattat caatccatt ccaaagttca atttgtgtc 60
ggaaccatag taaattaatt gttccttgct attaacaacg aaaaatgcat atttagctat 120
tgcagttgag acggcagcta ttgcttcttc accacgctgg gaagttgaga atcgcagaca 180
aataaatctt cctcctcctt cgtccgggtc gaccatcaac ttcgatttca atttcataca 240
```

ttctgtttgc gtgggacaag cgagcgacag cagtctctgg agttagcgga tttattttgt 300  
 ctcgatttgc tgctgctggt gattttgatg atgtgtttgc tgctgtttgt tgttctcgta 360  
 ggggtgattg actgactgac tgctgtggct gcaccccttat gccacctgct cctgggccgt 420  
 tcgaggcctc ttgggttttt catgacttcg ggtaagtctg ggtgggtgccg agtaggggtg 480  
 tcattgtcca gtgtctcaaa gtgcgccacc tcgttcctta aagacagata gctatgttgt 540  
 actactacgc tgaactgtaa gcttgtaagc ggaacacgtg ccg 583

<210> 74

<211> 589

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(231)

<223> Area matching *Drosophila* TAF110 gene, Acc. No.  
 L06861

<220>

<221> intron

<222> (232)..(401)

<223> Probable intron.

<220>

<221> misc\_feature

<222> (402)..(589)

<223> Area matching *Drosophila* TAF110 gene

<400> 74

gtccgtgcga gcacgcgcga gtgtgtgtgt gcgcaggaaa acccgccgat cgggaaaagt 60  
 gtagaaaggc ttagcgggcg aaacaaaagg cagcgaatta gcgagataac acacacgcga 120  
 caacgactgc aacggatgcg ccaggagaaa ggccgacgac agtgacggca aaggcgagtg 180  
 cgagtgaacc agcgcgacac caattcagcg gagcaccgcg ttttttggcc aaggtgaatg 240  
 cgattacctg tgcgcggcat ccagggtgtac gcagcatctg gtttatggcg cacggccgcc 300  
 aggtagccgg cggtcaggta gcacctccac cgctacctg tttctccacc gccttgagcc 360



gaatcttgta taaataactaa aagcgccctcc ccttgatttg cagttcgctt ctggagcgca 420  
caagcatgca acaactccgc caacaccaac acagggatgt gcgcaactag tttgatcgga 480  
acaaggatcg cttgcccaca ccaacacaca gaaagtcagt ggaataggag aaacacactc 540  
gccaataaca taaacaccac acagcacgat gaacaccacc agacagctt 589

<210> 75

<211> 314

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(314)

<223> Area matching *Drosophila* genomic sequence

AC005641. *Drosophila* EST AI259618 matches this  
genomic sequence 40bp 3' to NPS0081

<400> 75

gtccagcctc gcactcttcc tccagggcgc acggtctcac agaactggtg gccggcggtc 60  
acactggcgc gcagcaagat ggcttggtta caccaacgcc tatcgatata gaatagtgc 120  
cgtttagact agccagattg tttgtggtat gagcacatat tttattataa tacataatag 180  
cttataactt atttatctag cttataattt gtttacagca cccaatacac aatatatcgg 240  
at ttggagcg gtgggttatgc gatgcgattg tatagtggat cacggctatt ttaccatcga 300  
catgtaaaga attc 314

<210> 76

<211> 591

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (509)..(591)

<223> Area matching *Drosophila* EST AA202837 . This EST  
has sequence similarity to hypothetical genes from

yeast and arabidopsis.

<400> 76

athtagggcc tcgagaagga cgcacgcctt gcacggctgc tgtgaggaaa cgaagccaca 60  
tcgggtgcat gtgccacgct cgggcttctt tacctgtgcc ttgaagcgaa gctgttcgcc 120  
agagtagatg atgtccatta taaccgatgg tcgcactttc tccaaatcct tgagaaacgc 180  
tcgagcgtgg ccgcgatacg cattgggggc gaatacgcac tccgttgaga agtagaccag 240  
ctttttgtag tgggcgtaca tcacgatttc tttctcgtag ctgtacttga ggggcttcac 300  
tcggggaatg gtatcctcgc cccgcgcggt gcggatgctc gtgcagcgtc gcaggcgcgc 360  
cgtgtcccca cggagcacgt tcatcaagac agtctccgca atgtcatctg cattgtggcc 420  
tgtggctatg ctatcaacgc ccaacagctt ggccctctta tccaaggcct gtccggcgaa 480  
gacccgcaaa atgtgcagtt gttagacggg ccgatctggg caacaatgcg gtccatggtc 540  
cagccgtaaa cttcttgtag gacaaggatc tttagtggca ttgggtaatc g 591

<210> 77

<211> 617

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (166)..(393)

<223> Area matching *Drosophila* EST AI293734

<400> 77

gcttagatta cgatctcaga actgagaacg tgggagagag agcgtgatag aggtaggatg 60  
agggagtgga gcccgagag agactctctt ctcttgccca ccgatatcta atcaaaacaa 120  
ataatgcttc agtccacggc ggctttactt gattcatata tttagttcta tactgcgagg 180  
catgcagtac gcttgccgtg tgctgcgttt aaaaagtaat aagtaaattgt tctggataaa 240  
aatttaataa aaagacaaat aagtgaaga acaagaaact caaaagatat aagcaacata 300  
actcgaaatt cagtacgcct gagttggaaa acaccgaaac cgaaactcaa atcgaatcta 360  
catataaccg ataccataat gaagcacaaa cttctgttgt tggtagtaa atatttcagc 420  
catctaaaac agtatcccta tcttatcgca catactttgg gctcagatag tggggatcag 480  
agagtgtttt ccgttaagct cttttctgaa tgtgcccaag tggggagacc tttttatgaa 540  
gccatcgatg accttcttcc ggacgggcag ttggcccaaa aaaaaaccac caaattagga 600

&lt;210&gt; 78

&lt;211&gt; 396

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (261)..(377)

<223> Area matching *Drosophila* EST AA202757 (inverted)

&lt;400&gt; 78

gtacagaact acttcatgcg ctgggattaa cagcactcat tgcgcataac agcacgctgt 60  
tagttttaac aggcgacaga ggtgcccaaa caaactcaac atttttgcat gcgcatacac 120  
acaagcatgc atgtatgtat gtatgcgttt gtttgtatgt atgcctttct ctgcgccatgt 180  
tacaaaaagc aagaagtttt tggcaacgac aatgaatgaa aaattgaaat ggcgaattgc 240  
aaatgcgaat tgcgcttacc tgcgtcgctg cctggccttc ctttcgcgac agtggcgagc 300  
gaaatgcccc cgtcgcgcgc actcgtagca cttatcgtcc ccacgaccac cgcgcactcg 360  
gaccgcgtcc tccgagttct ttcaccacca accgcc 396

&lt;210&gt; 79

&lt;211&gt; 586

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(247)

<223> Area matching *Drosophila* EST AA696498

&lt;400&gt; 79

agcgggcctt tctgcctctc tgtgtgcttt tgaaaaaagt ttgcttgaaa aatgtgtaaa 60  
gaaagcggcg ccgccagtga gtgcgtgtgt gtgtttttat gtgtttgcaa atacaaaggt 120  
aaaacagccc caaaggcaac aacaaagtgg cggcgttggc ggctatagcg cagtagcagc 180

gacgcagcgg agcagcagca ggcagctcca gtgcattttg gtgcaaacta attgttggtg 240  
 tgagaggtac gctatactcg tatgtgtatg tgtgcgagtg ggtgttagtt gcaggtgtgc 300  
 gtgcgatttg atttgcattt atgttggggg tttgttttca tcttttcac aagtaatata 360  
 aactaaataa atgaactatg tgtggaaatc atttaataa tatataaata aaattagaaa 420  
 gtataatatg aacatgaaag ttaaagttaa aatccgtagg aaatcaacaa aattggtgaa 480  
 tattaaaatt aaacaaattt tccgaaaaac cgccacacaa ttccagcaaa agccaaagta 540  
 aaacttaaaa atcatattta ataaacagca ttaggggact ggttgg 586

<210> 80

<211> 646

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (100)..(646)

<223> Area matching *Drosophila* EST AA950073

<400> 80

gtacaggtgt ttttcgaata gccggcactt tgatccaagc tgttattgcc atctccttca 60  
 aagttgccta tcgatagggt tctcaactag tccacgtctt ctacttgccg tttttctttt 120  
 tgtaaaataa gaatgacgt ttaatgttgt gttaaacaatg caattaccta gagcgacta 180  
 actagtatag catcagttag gtcaattgtt acctgtaggt gtaaagttca agccgcctga 240  
 tgtggataac cggtcagttt gttttttttt tgctggtggc acttggtgcc gcaaaatcga 300  
 aaacctcggc ggtgcaggat gacatcgccg agtataagga cttcaagaag ctgctgcgca 360  
 ccaagaacaa tgtcctcgcg ctctacgtga ccagtgcgaa atccgctgct gctgagctaa 420  
 agatattccg tgaggcggcg gaggcgatac ggggaaccgg gacaatgttg ctgctagatt 480  
 gcggacagca ggatcgcaag aaactgtgca agaagttgaa ggtatcgccg gaccctacg 540  
 ccattaaaca ctacaaggat ggcgacttcc acaaggacta cgaccggcag ctgagcgtcg 600  
 ctcattgaca ctttcatgcc gtgacctcc ggcgaattgc ctggga 646

<210> 81

<211> 655

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(50)

<223> Area matching Drosophila EST AA695104 (inverted)

<400> 81

gttcggtgct ttcaacattt tccgcaatcc gttgaaaccg gcaaaggcaa actgattaca 60  
tgaaatcata tgtttctgcc ggaatatcga taacggactc tgtcttttgg cgccgcaggt 120  
tatcggagtt taaattgtga taaggatgca aagaaagttg gttcttagat gttacaatca 180  
atttcacaac ccaatctttg cattgttgag ttaggatcat cctctagcct tacatctttt 240  
gccatttagt tacatcatgc aattgttcat atcttcaacc aaatccatat agaacagatc 300  
ccctgtttat atattttttt atacgtacag agttgtaact aaatcctctg agattctgtg 360  
gaatggctta ttgctagcgc taaatataaa caggaaaatg gggtcattca ccagaattt 420  
ccatcgaaat tgaggctgag acccattctc ccttccccac cagaatttgt ttaggaaccc 480  
ccgtgcatcc actattacgt cgctttattt gtagacaact tttgaaatca agagtgttaa 540  
gtacattagg cgggctgaag tggttatccg taatggatac ggctactact attggttaca 600  
gcgatctaaa aactacaggc acgccctaaa tagcgaacgt atgggtcaatg aattc 655

<210> 82

<211> 601

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(427)

<223> Area matching Drosophila EST AA942153

<400> 82

ttttgaaaca tattcagtca ttggcaatgg agttggtgaa acgcgggttc ctgctgctg 60  
gcaagaacca cagctacctc agcttcgagc tgatcgatga tatcctggcc ccgctatgtg 120  
ccaaccacaa gactacaaag cccggcgaca aggaggcgat tagggcactg gtggcggaga 180  
ttaatgacac catcagcgac ttgggccagt tgctggtctt catcaagtat ccggtcaagg 240  
ccgaggagta cctggtttac gccaaagcgg acgctacgcc ggacagcgtg gccaacaccg 300

ggctcactgc cgaggagtgt cagtactttt cgaaactgct ggacaagatc gcctccgagg 360  
 aggactgcca catcgcttgg aatgacgcct acaatgatat cgtcctacag gccagctcga 420  
 agccgttgaa gaagagccgc atgcaggagc tgctccagaa gtggatccaa atgggctact 480  
 tcatggaggt gaccgacaga atctacctag gtccacgtag cctcgtcgag ctcagtttct 540  
 atttgagctt gaaccacgcc gatacataaa aaatgcacgc ttgtgcaagt gcctgggtgtt 600  
 g 601

<210> 83

<211> 543

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (42)..(334)

<223> Area matching *Drosophila* EST AA540352

<400> 83

ggtcgggtct tcaatgtcac caatcactat cagttaaacc gtcgagtgga tcacttcaac 60  
 atgcccagtt tcaaggataa agttataatc gtgaccggag ccagttcggg aattggagcg 120  
 ggtacttcgg tgctcttggc taaactggga ggctgtctca ccatcgtggg caggaatttg 180  
 gataagctca acgagaccgc ggagcagata gtggcagctg gaggagcgcc agcactccag 240  
 gtggcggcgg acataaacag cgagtcggac gtccagggca tcgtatccgc cacattggcc 300  
 aagcacggtc gcatccgacg tgctggtgaa caacgccgga atcttgagc taggcagcat 360  
 cgaggacacc agtctggagc agtttgacct gcgttatgaa cacccaacgt ccggtcgtct 420  
 taccagctga cccacctggt cacaccggag ctaatcaaga ccaagggcaa cattgtaaac 480  
 gtgtcttagt gtgaacggca ttccgttctt ttcccgggag tttacatac aatgggttcag 540  
 tgc 543

<210> 84

<211> 162

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (115)..(162)

<223> Area matching Drosophila EST AI238523

<400> 84

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tatccgcccc aatgaagaga agctactctg tatttttgtg ctctttgtgc ccgcctcttc 60
aagtcgcttc acgtcgagge aagtcagcag ttcagtcaca tttagacatc cgcgcggtaa 120
accgcgtttc ggcggtataa cgagattttt tatttcgaat tc 162
```

<210> 85

<211> 526

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(69)

<223> Area matching Drosophila EST AI260872 (inverted).

This EST has sequence similarity to mouse  
signalling factor U29156.

<400> 85

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gcttggcgca ttgcggcccc taatttagct actctcgaat tttaaaaagc ctaaatttgc 60
ttttttgtc ggtggatagt gtgaccgttc ggataacgat taaaatacc gtacggctga 120
tgattaagta taccactagg taaatgcgt taaaataccg cataaattaa taccgttaa 180
ttaacgaaca ttattatttt tttaaagtat aattttttta aattcatttg tctatattta 240
ttcctttaac actaaacgtg aagaaaattg tgtactttga aacggacggt gcagaacagc 300
agtagcttat aaaaatgcaa tgtttccgt taccctaacg gaacagataa tgtttaaagt 360
ttaaaatttt taattctaatt tcttctttta atggagtata tttcctgtat gggatctctt 420
accttaagct aggaccttag agcagaccga aggcggcaat tggggggccc gccttgggca 480
gtacaacacc ttgcggcac cagccaact tcgtaattgg agttcc 526
```

<210> 86

<211> 568

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (5)..(77)

<223> Area matching *Drosophila* EST AA801728.

<400> 86

```
gtctgtttca tggcgcacag ccagttttcc gctctatcca tgtggcctca atggcgtaaa 60
tgtagtcggc tggtttttct ttccaccagt tttttcttgc gaccgggtat ttaaggtgta 120
tctaaatacc gttgaaggcg attgcatatt caaaagctat tacttccctt attaaaatac 180
atacgtgcat acatattatg tattaatttg ccgctcgtaa agtaaaagac gactcgctca 240
cttatcaact gttggtgcct ttatttacgt aactcagagc accaagcagt tgattcctcg 300
catgaagcgc tctccttgaa ctaaaactag ttgtcattca ttttgatagt gttggttgtt 360
ctatgtttga gtgccttaga gcttatgctt ctgatcttcc ttttgccatt ttagctattt 420
tccctgagat tttgtgatcc cctatgtcta tgtattcgtg catttacgcc aaaagtgggc 480
ataagaaaaa atttaaaatc aagctttcgt attagcaata agtgccatgt ggacgtactg 540
gacttggaac acacagtctc ttcattttt                                     568
```

<210> 87

<211> 675

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (228)..(675)

<223> Area Matching *Drosophila* gene SMT3, accession  
number AF053083

<400> 87

```
gtccagcacc agtttttttg gcgtgtagct gtagcagaag caaaaggaag ccgcttgtga 60
taaatttcaa cttccatcag caagcactga atttgaggaa atcaggtaaa tttttgcatt 120
tctacgcgat tagttgctgc cccgcgggat tgtgcttagt ttttacgtgt ggtttaccaa 180
tttccgcgta ctttaattgga cattttgcct cgtttttttt cgtacagcac gcccggcatt 240
```



cgacgctccg caaaagaaaa aaaaaacttt ttgaccact tagcagcttc aacaagcaac 300  
 caaaaaatca acatgtctga cgaaaagaag ggaggtgaga ccgagcacat caacctgaag 360  
 gtcctcggcc aggacaacgc cgtcgtccag ttcaagatca agaagcacac acccttgagg 420  
 aagctgatga acgcctactg cgaccgtgcc ggactctcat gcaggtggtg cgcttccgtt 480  
 tcgacggaca gcccatcaac gagaacgaca ctccgacctc gctggagatg gaggagggcg 540  
 acaccatcga ggttaccagc agcagactgg gtggcgctcc ataagaatac ttagttaagt 600  
 tagttacttc tcttacaact accccttaaa acgaaaagaa aaaattcccg aaaaccccaa 660  
 agcaaaacac accac 675

<210> 88

<211> 210

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(210)

<223> Area matching *Drosophila* EST AA439866 (inverted)

<400> 88

caacggcgga tccttaatac gaactaacgc gcacacgact ctacgctttt taccgctatt 60  
 tcggctacac agcggtttct gttttcgttt tgcaataata ttctattctg aaagcgcaga 120  
 tgcagcggac aaggagaatg tggatgatta ctgttaggcc agtgatctcg aacttgtctc 180  
 caaatcggat tcgaagtgct aaccgaattc 210

<210> 89

<211> 590

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (31)..(590)

<223> Area matching *Drosophila* EST AA820803. This EST  
 has some sequence similarity to to human aldolase.

<400> 89

ggctgtgcga gccaacagtt gtccgcgaag ctttcgacga gctggaacag atagagattt 60  
gatcgcgaga aaggcgtagt agcactgggt tagacttaga agcgtccaat ttgcacagcg 120  
ttaattatca gcgccagaga caagatggcc aatctggctc ccaccatccg gctgaacaac 180  
gggcgcgaga tgccaactct gggccttggc acctggaagt cgttcgagtc ggacgcctac 240  
cactcaacgc gccacgccct cgacgtgggc taccggcacc tggacaccgc cttcgtctac 300  
gagaacgagg ctgaggtggg ccaggcgatc tccgagaaga tcgccgaggg agtggtcaca 360  
cgcgaggagg ttttcgtgac caccaagcta ggcggaatcc accacgaccc tgcattgggtg 420  
gagcgcgcct gccgcctgag ccttagcaac ctgggtttgg aatacgtaga cctctacctg 480  
atgcacatgc cgggtgggcca gaagttccac aatgacagca acgtgcacgg aaccctggac 540  
tgacggacgt ggactatctg gacacctgcg cgagatggag aagctggtgg 590

<210> 90

<211> 478

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (30)..(478)

<223> Area matching *Drosophila* EST AA803545. This EST  
overlaps EST AA697132 and has sequence similarity  
to frog/human MSS1

<400> 90

gttcagtcac tctcgccgta aaacaaaagg aaaacatcgc ataaactcat tttttgcctt 60  
aaaaaccgta caattgcaat cgaataagat gccggactac ctgggcgacg accagcgcaa 120  
ggtgaagcac gatgagaagg aggacaagga gatcaagtcc ctcgacgaag gcgacattga 180  
gcttctaaag acttatgggc agagccagta tcacaaatcc atcaagagca tcgaggagga 240  
cattcaaaag gctgtgaagc aggtgaacga gctgactgga atcaaggaaa gcgacacggg 300  
tctggcgcca ccagcgctct gggatttggc cgccgacaag cagatcctgc aaaacgagca 360  
accgctgcag gttgcccgat gcaccaagat catcaacgcg gattccgacg accccaagta 420  
tatcatcaat gttaagcagt tcgccaaagt cgtggtggac ctactgactc ggggtggcc 478

<210> 91

<211> 574

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (76)..(178)

<223> Area matching *Drosophila* EST AA438591

<400> 91

```
ctctgaacag ttcttagact attgaagcca agccatcgat tgtgccccgg catatcgata 60
ctaccaacat ggccgtcgag aaaaattgaa gtgaacgcaa cgccgtgttt ttcatttgcc 120
aataaaacgt taacagctca cgaaatatcg taaagcgtgc ccgcaaacgt cgccaaatgt 180
aagcaaatta ttttagtgcc tgttttacat cgtttacata attgccagag ctgaaattcg 240
gaatttagtt gctgccgtcg ggagtatcgc caacttttgc ctcacactct ctctctgtct 300
cgctctgcat tcctctcgtg ctgacaaggc aaatatattg gtgctggtgt gagtgtatgt 360
gtgaaaaatg gaagaaattc aaaatgcata tgtgaaaaga tatacgcgca agccgattaa 420
aaatcggtc tctcgcaoga ttttgattgg gaccacaggt ccccgacccc cgcggcgtga 480
atgggttaaa tgacagccgg agcgcgtccg cgattctctc tgcgttttca ggtctctcgc 540
tctattccat tctgataact ccgctcctga attg 574
```

<210> 92

<211> 169

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(169)

<223> Area matching *Drosophila* EST AA979551.This EST  
overlaps EST AA567400

<400> 92

```
ggttgtgtcg tcgaacgtga aactacgcgt ctccgcgaat gacgcagact ggaagcttcc 60
```

actggcatga caatcgtcta aaaacattca acaatagcgg tgcacttgca aattactggt 120  
gccgcaacaa caataacaac tgcttcgcta agcagtagct gcgaccaca 169

<210> 93

<211> 414

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (138)..(414)

<223> Area matching *Drosophila* EST AA439261

<400> 93

agctgaatga taaacgaacg attttattaa accgtcacct tggttatcct caccctgaca 60  
gcgcccttgg gcgaatggca aacagctgac gccatatccg cggacgcgaa tggcacattg 120  
ctagttctgt tttcttgctt cgcgtttgct gtttatcaaa cgccttttgg ctaatgggtcc 180  
gcagtccggt ggcgttatca cgggaattgac gaggccgatg cgtcacatgt gcgtgggctg 240  
catccggaca ccatgaacta ctcgactacc gcgctgtcgc ccggcggtag cggaggattc 300  
gggtggcgttg accagcacia ccgatgttgc ggaaacaagg cctgggtgcgt caaggacatc 360  
tgcggcattg tgtgcgtgat catgacctgg ctgcttatcc tgttcgccga attc 414

<210> 94

<211> 354

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (7)..(354)

<223> Area matching *Drosophila* EST AI107509

<400> 94

gtttgtcccg tttgctcgag cacttgttcc caacgtaagt ctgaaaagac ttattttccg 60  
agataataaa tcgccgtggc tgcgcattat gtaaagtgga gtgggtccgt gccgatttcg 120

ctgcgttggg gccgttccaa acatatggaa tctaaacgca gcgtatttca ctctgcccg 180  
tgtgtgtctg tgtgtgttta tggttgtagt ggggcttccg tgtcgcaagt ggaaaacaaa 240  
tgaaattgag ttctcgcttt gagtcatatt cgagtgcaca ataaagcgcg ttatgcgttg 300  
tccatcgaat tacccttaa tttgattacc agctaatttg gtacccccca agac 354

<210> 95

<211> 48

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(48)

<223> Area matching *Drosophila* EST AA540348

<400> 95

gtccgtcgac tacttgtgcc atttgttttg aatattccga gcgaattc 48

<210> 96

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(311)

<223> Area matching *Drosophila* EST AA735555 (inverted)

<400> 96

gacacagctt ttgagtgctt ttatttcgctt tttgttgttt ctctgcgtgt acttgcagct 60  
ttagctctca attgttgctg ttgttggtgt gtgcgaggtc atcgacgcgc attagccgaa 120  
aaaatcgata tttaacactg gtcgcactag ataaaattgg ttaatggggt agcttatggt 180  
tgtcgattga caacgacaat gacaaataac tacagaaact ggagtttttc aacgcacaaa 240  
cgcatataca aattcaataa cggggccgcg aatcgaaaaa ctttccgctg acttggacgc 300  
acgttggtgc gcgagacgca atttttccaa atgggagctg caccgatgtg atttttggag 360

cccaccgaag eggcgctcgc tctcgctctc tttatctttt tcttttctcc ccttctttcg 420  
ctctgtgcgc tctctctttg cgcagactct ttatcgcttg aagtttttaa ttcggattcc 480  
tttgcatata ttatccaata gccggcttat atgccgtctt aagaggtctt ggatgatgtt 540  
tcttcggggg gaagtgtgaa tggggccgtg taacaag 577

<210> 97

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (582)

<223> Area matching *Drosophila* genomic sequence

AC005646. ESTs AI064020, AI542218 and AI25740

match this genomic sequence 26bp 3' to NPS0118 and

have sequence similarity to Human SEC61

<400> 97

ctttggtggt ggcaccgctg ccgataggct gtgacgctga ggtgacagct atcgtgcact 60  
tagacagctg gagatgacag gctaaggcaa ctcaactatc ggctgctttg gctctaaaat 120  
gaactagtaa aaaaaaacg aagaaataat atattcaagt tatgaattta atagataaca 180  
ataatagata aaatattaat tctacaaaat gaattgttta aatcaatttg aatgaatcct 240  
attaatataa ttggctatta ttaaaactcc gataataaat gctattattc ttgatttccc 300  
ttgatttaat tatataatac atacttaata actatataat tatatagaat aaaaacttaa 360  
tcacgcattt aatagatcat atagatatag aatatataga aaatcaatga aatcgatttt 420  
gatagcgata atgtgcaacc ttgcatgtaa gttattttta gatttttagct gggcaagcgc 480  
aattttcttg gcgcgcacca aacaatttgt aaataatatt ttgctcaac tggatttggt 540  
tcgactgcga atcactaaaa atattaagtg acttaagccc cg 582

<210> 98

<211> 297

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (7)..(170)

<223> Area matching Drosophila EST AA263700. This EST  
overlaps EST AA978721.

<400> 98

gtccagggtca tggcaacaca accgctgttc accgatcagt ttttattggt tttcaggaat 60  
aagtaaattg gattattgaa ggcttcactt ggcacgtatt agcttggatt tctatacgct 120  
caagctgcgc agtcttcacg ttgtgttatg agacaaaaat agatcgaagt gcggtgtgtg 180  
gttattaccc aaaggagttg tgttctttaa acttcgaacg ccaccgacat catcatgttt 240  
ttcatctcac cgaattataa atagttgtgt gtcgtttgtt ggtgccataa tgaattc 297

<210> 99

<211> 583

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (364)..(583)

<223> Area matching Drosophila EST AA941785. This EST  
overlaps EST AA695548.

<400> 99

ctggtgaata aaattcgcgt cttgtggaaa gtgaccagag tcacgaactg ggaaaacggt 60  
agaacggtaa actagttcca ttctacgatg attatgatgc gatacatcga actgctttgt 120  
tacatatcgc ttaaaatcgt gtcaatagaa aataaacggt ggatggcatt taaaaaatcg 180  
gatttgaagc aaaaaaattt aatgatttca ttogtttata tcatcaaagc cagaaaatag 240  
atgaccttac aaattaatct aatagcaata ccgatataac gtgaccaccc tcacacgtga 300  
cagctgtgaa catctgttgc acgaatcacc cactgctttc attcgtcgtc atgcgtcatt 360  
cagtcgaacc gtgctgtgac aaattacgca atgtctaaca actgatgtaa aacaagcaat 420  
ttaccaaaaca gttggccaaa ttccgtgtgt acacacactc cgatcgaccc agcgaggcac 480  
tttaaccagc tcttgaccac ttcgagatgc tgcgcaaaac ggcaacgatg ggaatcatgg 540  
cggcggttgc cgtaaagcg gctcccgagc ccagaacca gct 583

<210> 100

<211> 675

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(260)

<223> Area matching *Drosophila* ESTs AA802928 and  
AA817115.

<220>

<221> intron

<222> (261)..(561)

<223> Probable intron in gene represented by EST  
AA802928

<220>

<221> misc\_feature

<222> (562)..(645)

<223> Area matching *Drosophila* ESTs AA802928 and  
AA817115.

<400> 100

gtcacactgg caatttggtg ccgaagttg aattgccgtt ttgtgaagcg gatagttacc 60  
tgccgataat cttaaataaa aatgttttaa ctggcccgtg tgctcctgcc gcagcagcgg 120  
atcctggcca gcccgctgcg cctgcaacgc ctgatctcta ccagcgacga ggtcaacgca 180  
gagcccatca tcaagtccat ggacaccatt ggcggcctcc ccaccgaact ggtcaacgaa 240  
cagaagctga agaagactag caggtaatca atctaccggt tttcgcaact gacctttgcc 300  
ttgcctgttt gttttgttta catttcgacc ggtatgggca tgggcatggt atgcatgtat 360  
cggaggcctg ttttgggcgt gatcttcgaa aaggagtttc ggggtctttt tttcttgatt 420  
tcaagtgggg gagaaagttt gtatcgagcc gcttatgcag tcacgtagac catagatgcg 480  
tgcattgtgt tgtgtatgta tttgtgcctg cctgggtggt tcagttatgg gctctattgg 540  
tcttgacttt tggtttgtcc acagaacctt atcgacgctt caaaatcctt cggttcccat 600



tgccgttcgc gtcacggtgt cgaaagatga aagtccgact ttatggccgg ttccaggtga 660  
aaattggtta ttatg 675

<210> 101

<211> 395

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(395)

<223> Area matching *Drosophila* EST AA539001

<400> 101

ggtcaacgta aaggccggag agcacaaatc cgccgagttt ctcaagttga atgcgcagca 60  
cacgatcccc gtgctcgatg ataacggcac catcgtgagc gattcgcaca ttatctgcag 120  
ctatctggca gataagtacg caccggaggg cgatgattcc ctgtatccaa aggatccgga 180  
gaagcggcgc ctggtggatg cccgtttgta ctacgattgc ggatcatctat tcccgcgaat 240  
ccgtttcatt gtcgagccgg tgatctatctt cggagctggc cgaggtgccc agcgattcga 300  
gtggcctacc ttcagaaggc ctatgatggc ttggagcact gtctggctga aggtgattac 360  
tttgggtggg cgacaagctg accatcggcc gatct 395

<210> 102

<211> 58

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(35)

<223> Area matching *Drosophila* EST AA735863 (inverted).

This EST has sequence similarity to human death  
associated protein 3, Acc. No. X83544.

<400> 102

gggcggagac tcgcgacagg ctgccaaagc gattccggat cattttcata gagaattc 58

<210> 103

<211> 621

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (68)..(195)

<223> Area matching Drosophila EST AA941860

<220>

<221> intron

<222> (196)..(474)

<223> Probable intron in gene represented by EST  
AA941860

<220>

<221> misc\_feature

<222> (475)..(621)

<223> Area matching Drosophila EST AA941860

<400> 103

gtccgtccct accagcaacg cgaaagggtt ttgtcttget ttcttggtgc tttgtgtgat 60  
tctcgagtct ctgttctgcg tctgcgtccc gttctcgtgc caacgaactg atttcgcccc 120  
gcgttcgtgc tcaatcgtaa attcgaaata aattaaaaat gtctcgagcgt tcgtacctgt 180  
tgtgtgtgct gtttttaggt gagcgaaaga gagggagaag aaatgaagaa atcgtctcgc 240  
gatcagattt tacggatacg catctcggtt ttgcaggcgc cagctgcttg attttcagtg 300  
cgagtgcagc gcggaacaat cgaaggggtt acaaggccac ggagccgccc accaccaccc 360  
agcccccgca gacggccaag gagtatctgg acagtcgacc cggaatctcc acattcggca 420  
tcatcgccat catcttcacc gtaatcggtt tctgcctcgt cttctactac ggcataat 480  
gctaccctt actctgtcgc gatgagaaga aatatcggtt tatggaccgt atottcaacc 540  
attactgccg cacattgcgc ttcatttaat ccatagagaa ctattccgac ccgaacacca 600  
tcatacggtg gctgattcg g 621

<210> 104

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(210)

<223> Area matching *Drosophila* EST AA246460 (inverted)

<400> 104

```
ggtgtgcgct tggcgtgggt gtgcgtgtgc gccgatgtgt gtgcacgcgc cccgtgtgac 60
gatgtgcagt ttttgcaatt aaatttataa acaaaacact ctttttcctt caatataatt 120
cacagacaca gacaccactg aacaaattcc ttagtgttcg tgcttctcgt tctctgacgc 180
catcttgtgt gtgcgcaggc cagggttgtc gaggtgccgc aactgtctaa catgggcggt 240
cggaggtggc aacgctgtta gggctaacta atagtgtgac ccaatcgctt ggtattgtta 300
aattttccct caacggtcat gctttgcata acaattcaca ttttctgatt gaagaatcct 360
tattttatgc caaaacttgt attagatata taaaatatcg agatgtctct atcgccagcc 420
agtggcattg gtcgtttcta tgccaagtcg gcaaaaatca tacgtttcgt acgcctggga 480
tgcaccaatc ggccttttta tcacattgtc gtcattggagg tgccgtactt tttta      534
```

<210> 105

<211> 593

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (66)..(593)

<223> Area matching *Drosophila* EST AA141928

<400> 105

```
accatcctt aacatacaaa tattatcgag aaacttatcg actaatcgac tcgccactct 60
gcagagagcg cggcagtcag tcgctgttga accaagctaa aggacagatc aaaaataaaa 120
```

gagacacgtg aaattgtatt agaataattaa cttctgtaaa cggcgggctaa aatctcagaa 180  
 gtgggattaa taatccaaaaa tggacgataa aatcatcctg aacgactttt cgctgacaac 240  
 cctaaaagat tggctacgta ttctgggcca aaatacggag ggcacaaaaa ccgaattaat 300  
 cgcgaggctg caagacatcc caacggcagt tcggggcgat tgtccaccgg agcaccacca 360  
 gaaaaacgct ccaccaggaa acgacatttt ttcttcactg ggattttcag aattgtgaaa 420  
 ttaacaccga tcacgtaaag tgtgaatggc gatgaacaga aaagaatcaa ccgaactggg 480  
 cagtgagagg gagacaaaca tgttcgagct acagcaacta cgcgagact agcagaagcg 540  
 aaggcatgct taacggacac gatcgacttt gcagttccag aaccaccacc acc 593

<210> 106

<211> 332

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(332)

<223> Area matching *Drosophila* EST AA979014

<400> 106

attgcgtgcc tggaaatcga acgtgtgtga atttaattta cgattcgtat aattatcagc 60  
 aagagcaaac aatataagtt gcaaacgacc gttaagccct atgacactaa gatccaaagt 120  
 aagtggctac caccgaactg ttccatttgc atttgaaacc agtttccagc gattcgagtg 180  
 catgaaattg tccaaaaaag tgcaacggtc gagttcaaca aaccgatcga ttgagataac 240  
 accgcaaata tatagcagtg aaactcgcaa ataaatacct acatattctt ctgataagtt 300  
 caagaacagg ctagccattg gttaccgggt ag 332

<210> 107

<211> 475

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (52)..(475)

<223> Area matching Drosophila EST AA817254

<400> 107

ggatatagtt atacgcgact tcaactgctcg ccgcggcatc tttccacctg cccgcaacgg 60  
tcaactttgtt gttgtcaatc gtttcggtcg catcgcgctcg cggaaaatcg agatataaat 120  
acggaaaaca aagatataac tccgacgcgg cgacttccgc agcaagcaac tgcaatgcgc 180  
tcgagttgag ggcgcgccga taactatgtg cgtgtgggag cgagtgcgag tatagcacac 240  
aagtgatcac catcagcaat tagcaagtga ccaaccgacc gaccaatgag cacggggcat 300  
tggcagcagc agcagcagca cggagggagc agcagcacct gggaactgag cgcggtattgg 360  
aaggcgtgct ccctgcttgg cccgcagacc cgtcgaacgt cgataccggc aggacacgcg 420  
ctaagcagcg actcacttga acgggaagcg gcgccgcagc ccgatgtcg ccagg 475

<210> 108

<211> 36

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(36)

<223> Area matching Drosophila EST AA536262. This EST  
forms a 1209bp contig with ESTs AA948897, AA539274  
and AA392320. Sequence similarity to glycogen  
synthases.

<400> 108

cggctgccca tggattttct ttttgtttcc gaattc

36

<210> 109

<211> 614

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (475)..(581)

<223> Area matching Drosophila gene for Aspartate  
ligase, accession number AF113612.

<220>

<221> misc\_feature

<222> (35)..(86)

<223> Area matching Drosophila gene for Aspartate  
ligase, accession number AF113612.

<400> 109

gactgcaccg cgctggtggc atgtgcaata gtacacgacg ctcgtgaaat caattcgttt 60  
gtgtattaaa agggcaagat ctagctggta agtcgagtgc actcgaatgc accattgaaa 120  
taaccaatag gggaagagac aggaagtga tagaatcgg aaatgatcag ataaaagacc 180  
gcaaagttaa ggttatgtgc gagccgctag acaaggagtg tttctctgtc cccggaaata 240  
tttgtggaca tatggctatt ggaggaggag actgggtgac tgaactgcag tccggaagac 300  
aatgtcactt attcgcaaat ggggcacttc atcagccaag tgctatttat aaaaccatga 360  
cgcaacgcac acaatactcc tcctttttcg cctggtgctc gcttatcgaa actgtgtggt 420  
ctacgttctg gttttgtgac cctcttgtaa aatatacaac ccttccttct tacagccgtt 480  
tttgtgcatt ccaagatggt cgaggacaaa gagcaagtgg ccacgggaag caggtcttca 540  
agaagggacc caaaagctgg ccaaggccgt taagtgagaa tctttgtttg gggacctggc 600  
gttttgggtt tctt 614

<210> 110

<211> 636

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (368)..(636)

<223> Area matching Drosophila EST AA390587

<400> 110

caagagacca ttcacttttt tcgttttgaa gcaacaaatt tgaaaagaga aaactttatg 60

tttttccgc gggcttggtt gttttttttt tctcgctctc cgtcgaattg actctacatt 120  
 ttgatgtgat cttattatta ggtgaatcag ctgtcttcaa aagaacagtt ttaatttaaa 180  
 aaaaaatccc tcaattccaa ttcaaatttc atttagaaca caacgaagat atttctcttc 240  
 ttgtacgaac aaaatgctct cttaactcaa gttggaacgg ccgttcgggc aacatttaag 300  
 ttggcaacat tgttgcatgc tgcattgtatt tgagcacaag agtgtcattt acgattagca 360  
 actcgcgggc aacggacgtg tgtaaaaaat agccgggggag aaaaaacgaa gtgcgattgc 420  
 cgaagaaaaa cagagagatt tcaaataata aagaaatgca aatgaaacag aagaaaataa 480  
 aaataaagca aagtgccgtg agttccatct cctcagtggg gtgaaatttc cagcagagtc 540  
 taacggcgat ttgcgaatgc cgctcaagaa gtgcgaaacc aaaacggggc ccgggttaaat 600  
 attctcaagc gaaaatcatg gcttttttga tacccc 636

<210> 111

<211> 342

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (55)..(110)

<223> Area matching *Drosophila* EST AA979454 (inverted).

This EST has sequence similarity to human REC1L ,

Acc. No. X57303

<400> 111

aactcaccca tagtactcgg cgaactcctc cattgctgac atgcgaatcg attagattaa 60  
 attcaattaa taatgtaccg ctcatcaatt tgccggccgt ttccgtgctt cacataacca 120  
 ttctgccgca aaccatgtgt tttgggcata aaatcacttt tccacgcaac acaggcacat 180  
 tgccagtgca gctgccgctc tctgcattct gtcatttgcc atgaccgcag gcaaaagggg 240  
 gaagcacctc gttgaaccat tttaaataag tgttgctgca agcccaactt gaaacctcta 300  
 tttagacacc taaaaatata ttggatttta aaactttgaa aa 342

<210> 112

<211> 575

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (31) .. (460)

<223> Area matching Drosophila EST AA941359

<400> 112

```
caacgaacgt ttccacccac aatgaaaaca aaacgtgcaa ccggccaacg aaatgccgcc 60
aaagtcaagc agcaagaaaa accaggttac ttggtaccac tgcgagtcct gcggcggtcca 120
cattccctcg aaagcgagag ataaccacga gggcttatgc tccgccatca gccaggatga 180
tgttggggccc gattccgagg cggagtagct tgcagtgga gcaatctata cgagaagtct 240
tcaacagcgt aatttcgagg tggagtctct gaaggatctg cccaccaagt atgccaatat 300
gctagtcttc gtctccgagg gtgcgatgca attggcacag ctacacattg gacaacatgg 360
tggtgctgga agctccatcg acggcggagc agcgcgtggt tagggattgt atggcccaca 420
tcagagcaat tctcaccac agtatttgct agcgaagggg gtattgtgtt tcacactata 480
aaaaccgctc tcaacaataa atgatcatac ttttaaacag atttcaaact tcattgcacg 540
caacttcagg aagctactca agactctgct tgcatt 575
```

<210> 113

<211> 299

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (65) .. (299)

<223> Area matching Drosophila ESTs AA201303 and  
AA541066.

<400> 113

```
ggacagtatg tgcgagaacg aaaatttcag cacatcgcta gcgcagcagc cttgttgttg 60
ttcgtctgtc tctgtcctac aagcgtttct ttttgtttgc tgagaattaa acaaaagcga 120
tttgttcgcy ggcaatgcga atgcatttgc aaagcagggc acaaagcatc ggctgttttcg 180
actgtgattg cacaaagcca tgtagtagag gtcgagctgg cgattcgcaa ttatccacag 240
gcgacgcaac acggtgctaa aaattgcgta gccaatat ctcgaaatcc ttogaattc 299
```



<210> 114

<211> 581

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (538)..(581)

<223> Area matching *Drosophila* EST AA698119 (inverted)

<400> 114

```
atccaatggc tttctgccgc gcttttttac agctgatgcg agcttttgcg taaagctttt 60
ggccaactat cgttcaatcg gaatccgaat gtgtgttaaa tcaatactgc ggcggccaga 120
taatgataca gatatgaaac ttgggatccg gaatactgga cacaaaacag aacgtaatcc 180
gcacagctgc gtgctggacg cactatttga gtgactcaaa accgattcgt ttttcgtttt 240
gattcgatcc aatccaatcc aacccgattc gagtagaatc gtgaccatgt ttacctttgc 300
gcctcagcaa cagactgaat gcgaaacaca gaaaagccga agtcgcccga tttccgacca 360
gcgagaattg gaatgagtat gccaatggca atgcgaacgg aacgatttta gcggcggccg 420
taatggcatg tgaaaatgat tacatcagag tttgagtcac ttttccgcga cactcgccgt 480
cgttttgccg ctaccgcgat ccgcactcgg gcaaggcaaa tcggttattg agtcaccta 540
gtgctctgga tgctatctga tccgattccg aatccgaatt c 581
```

<210> 115

<211> 632

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (111)..(549)

<223> Area matching *Drosophila* EST AA696174

<400> 115

```
gccacgtctc ttctccgcca cctcggetag agttgccaac gatttggatt aatcgattca 60
```

tcattgtcgc acaatgctca ctcgataaag ttcaactatcc aggtgatttg aactaagtta 120  
 aatgttaata tgtttttacc aaacacacca tttttggtga acccgttgct ggaagccgat 180  
 atccttaaag tgaatgtatg tactttcaat gtgcacaaat acgtatttac aacaaaaact 240  
 ggcttgcaaa ttttattaac tgtaattcc tggttttgtc aagtctgctg cacttgctcc 300  
 gctgttgga tggtgtgcc ttactccaa agtcaccact tacaggggtga acactcttag 360  
 gtgttcggt gacgactttc ggaaaaagtt agaagaaaaa ctgccattc gctacggtgt 420  
 aaaatctcca aggattttact gcttgccaaa cctacccgag atgttgtgca ttgatccgct 480  
 ggactcacag ctacacaaag ctgtggccga ctccgactca aggaggtgag tggttgacac 540  
 taactgcgga gctgcactac tgcgaggcgc ccacatatac gcccccggtg tttactatgg 600  
 agtcaaact gaccgggagg aactcgcaat gt 632

<210> 116

<211> 243

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (107)..(243)

<223> Area matching *Drosophila* ESTs AI064230 and  
AA263288.

<400> 116

gggtgccgta cctgcgacag ctaacggtga agccgatagt ctgcattatt gctccaacag 60  
 aagtacggtc actctacaag taggcaacga attttggttg tcatcggcac ttgcattca 120  
 acgtttccaa ttgtttttta aggagcttta agaatggctt tagctgaaat ctgcaagata 180  
 tcgaatgctc cgtacatgcg gcccaatgcc tggatcatcg cggtatgtgga ggaagagcaa 240  
 aaa 243

<210> 117

<211> 445

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(212)

<223> Area matching Drosophila EST AI106957. This EST  
forms a 1756bp contig with ESTs AA391125, AA567307  
and AA735971.

<220>

<221> intron

<222> (213)..(275)

<223> Probable intron in gene represented by EST  
AI106957

<220>

<221> misc\_feature

<222> (276)..(382)

<223> Area matching Drosophila EST AI106957

<400> 117

gtttgtagtt tcagttcact ttctggttgg tttttagtg cttctgcgtt ctccttggtt 60  
ccttacttat gcatttttcg ttctcctttg tttccattaa acccccaccg aagtaagcga 120  
atccagcgcg atgttggtga aatcgctgat tgcgttggtg gtcattgggg ctgccgtggc 180  
ggaacaaacg cccgtctttt tgtgggggagc caacaggtgg gtgagcgctt gcaccagttg 240  
aatgtgagtg taacgagtg cttcctcctt ttttcacagt gtggcgaaac cctccctgaa 300  
gacggtgtcc caagtggagt ttgccgagca gttggcttca ttgctggaag atcacatggt 360  
cgtggccttc gaggaaaatg gcgtaagtgc ttgagcacc ctaggatag ctagggcttg 420  
tgacacatgt gtttggtccc aactc 445

<210> 118

<211> 107

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(107)

<223> Area matching Drosophila EST AI820473 and  
AA820473(inverted). Sequence similarity putative  
cytochrome bc-1 complex core protein [Haematobia  
irritans irritans].

<400> 118

ccctagtttt tcaatgcgct ccaaaatggt cacaccgagt accagctgtg acttatggta 60  
agtcacggga ttttcgaaat atcgtgatct tgaataattt gactaag 107

<210> 119

<211> 546

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (19)..(102)

<223> Area matching Drosophila EST AA978449 and  
AA940834.

<220>

<221> unsure

<222> (103)..(114)

<223> Gap of Unknown length.

<220>

<221> misc\_feature

<222> (115)..(485)

<223> Area matching Drosophila EST AA978449

<400> 119

tgctggagaa agcagtagaa tgataagttt aggccgtatt tgcacaatta ctgagtaact 60  
agtgcagccc gaacaagcgc catgtattca taagcacctg ccnnnattcg aatttaaagc 120  
ggccccggag cagaagcgac gcattttcttc gccgagcgtc cgcagagccg tcggatcgga 180  
tcggatcggg ttgattggat tgggtgactaa aacagttgga caacaacagc ggcttgatta 240

gttggcagta aacagagcta ccgaacgcac eggtcattca ctccgcaccg ttttgaccag 300  
aagcagttcc agtattggta gccataaagc cacagcaatg gggctctccg ttccagcagc 360  
tgaagaagct ctggctgctc taccttttct gctcttttcg cgttcttcat ggtagccatc 420  
agcatcaacc tggtagcgtg gccagcattc aaggcggggg acgcggagat gccgtgaagt 480  
agttggcccc gtaattaaca atgggcccc taggaccccc ggttggaatg cacaactttc 540  
ctggggg 546

<210> 120

<211> 546

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (182) .. (362)

<223> Area matching *Drosophila* EST AA802905

<400> 120

aacccccgcg agaaaaaaca tttttaccat tatgttggtg tcctcttctt tcattttatg 60  
aatgggctgt gtgaacaaga gatggatggc gcagtagtgt gacaaaaatc gtgggtaaaa 120  
agacgcagca aaatactgaa acactcatga aacggccagt cggcgaaaaa ttttcaaact 180  
gcgggggtcgt acagcggacg attttcaatc ggaacgggtc agctttggag cggagcgcgg 240  
agtttgcgat tttttgtgtt tgtagcggaa aatcggatga aaaactccaa atgtttacca 300  
aatgagcggc gacaaatacg cgaccaattg acgagatcgt gtgtgttttt ctcaattaaa 360  
cggtagtgtg gcgatagaga tggagatgta aagtatgcag tcaaattaaa gtgcggcaaa 420  
aaaatcaaag gtgaaaaagt cattaaaaaa gtaagcaaaa tagaattgct ctgtggaata 480  
taaaaatggt acatatacc atacatccat aaataaatat atatatatat atgaatatct 540  
gcaagg 546

<210> 121

<211> 572

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (235)..(279)

<223> Area matching Drosophila ESTs AI259166 and  
AI296787. Sequence similarity to Dihydropyrimidinase  
acetyltransferase component of pyruvate  
dehydrogenase (human).

<220>

<221> intron

<222> (280)..(375)

<223> Probable intron in gene represented by EST  
AI259166

<220>

<221> misc\_feature

<222> (376)..(452)

<223> Area matching Drosophila EST AI259166

<400> 121

gacagtcccg tgtccaacta tttagcatat atgtcgtatt ccccaaaaac actctcacac 60  
atacccatgc gatttgctg tggtgtgctg gctccactgc tnnccaagg tcgaatacac 120  
gctctcctat atcgcatgat gcgtgatagt gtttcggctg gctgataagc tggaaaattc 180  
cgtctaata ttaatgggtc actctttttg ggttccattg tttacatctg acgagtgggc 240  
gattgaacgc ctaaagtgtg agatagtaca ggagtgtggg tacgtaaaca acaacaaact 300  
aacagctgat cgagcgtcca taaattaacc catccaaaat gctttcatta acatgggtcat 360  
tttgtaatta taacagggtc tacaaaaatt acaccgttga gaatcagaag taaaaatagt 420  
ttccaaggat actatttact catattgcaa gtaatacacc tatactatatt atgcaatatt 480  
accaaattaa taatttatga tgaattatta agttttttta taagtggata ccaccaatg 540  
caaccactt taataaacta gttttggttg aa 572

<210> 122

<211> 492

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(238)

<223> Area matching Drosophila EST AA951193 (inverted)

<400> 122

```
ccccgaaacg gcaatggtct gcaccgaatt tattcacttt actcgccgcg cgatttactg 60
gctttttcttc gcatttggac ttgccaccgt tgttgtcagc tactttttca cacatatgtg 120
aacgacgcga ccgggttcgt tgcgagttct cggcactagc actgaatact gtatatatgt 180
gggaattttc ccacatattt attacgctcg ccaacagagt gcactgcgtg agtgtttgtt 240
tgtactcatg cctcagaatt gtcaaattgg agagtcttgg agctgctaaa acatcgctgg 300
ctgccacgat agtatcggtc gctaggtgcc agccggtgcc agcgatggac acacaactaa 360
atatcgaaac tcctttttat taaccctata atgcctgaaa ccaaatgtgt acatgtcaaa 420
agctaaatat gttggcccat cttagacaaa aaagaaacca taaataaccc tctggatagg 480
taacgtgaat tc 492
```

<210> 123

<211> 605

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (326)..(482)

<223> Area matching Drosophila ESTs AA696743 and  
AA803977.

<400> 123

```
ttcccaccta cgaagattgt ttacccttca tcttcggttt catctattac gtttcatttc 60
tctttttatt tattttttta ttttgattga aaaccttta ctgcatttgg aaacataaaa 120
aaaacttcag aagtatttta aatgaaataa tagaatatat ttataaacat aattttaatc 180
aagcctttac aataaataac aaaaacacct atttagcett ttaaggctt cgcatgcgga 240
cccagtggag acaagctata actgatttga gatagaacgg ccacacatcc accggtggcc 300
agctggattg ttactgttgc ttttgttttt gttacaaatt ttgatttttg tcttgtttaa 360
caaaaaatga taaaatcttg aacagtaaag ataatccaca caatttacta tgagcaccgc 420
```

cactgggaac agcagacgga agacggaggc gttgcagtca atatacgagg gcgacacgac 480  
ttcaaggaat agattagcgt ccatttttcag taccaagtaa gccacattgg ataaaaaaag 540  
ccacaattga taatttgtat atataatgaa atttttagtat ggcgaaaggt actaccagcg 600  
tcttg 605

<210> 124

<211> 539

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (11)..(512)

<223> Area matching *Drosophila* ESTs AA990758 and  
AA246427 (975bp contig)

<400> 124

gtcgcggttg tttgacgttt gtcgctttcc tccgttgcca atataatata ttacgtagct 60  
catttttata caaacggaat tacgagcgca acgacgacag caacactagt agcactaatc 120  
gtaagcgagc gggccaaaaa ttaaattgag tttgcggccg caaagatttg atgacgtcgc 180  
atacgccgtc ttctagggcg taaaaagcaa agcaaagcaa acaaacgcca aagcgaaacg 240  
tgtaaacggc gtagaagcga taaacgcgac tcaaatacgc agcagataaa atacaatacg 300  
cgagaagagg aaaagtcacg ggaaatattg ttcataattcc ggcgtctttc tgcgagcgta 360  
aacgtgtggt gcgtgggctt gtgctttgcc agtgcgtgtg gtgttaatgc ctgtgtggtg 420  
tgtgtgatta agaagatata aaggatataa cggtaaatgc acgccgaaaa atgtgcagct 480  
gacgccaaca catggtaaac gtacgcacag nctacaccga ctattgggaa cttcaaaaa 539

<210> 125

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(406)



<223> Area matching Drosophila EST AA697797

<400> 125

```
agctgcgctc tgtgcgtgcg tgtgtatgtg tgtgtgcgag tgagtgtgtg tgtgctggcg 60
cgtctgtgtg agtgcggtgc tttgtgtgca gaataatttt tgcaaacatt atgtaaatgc 120
gcaaattaaa gttcaatoga cgcccgtttt gagtacgaaa ccagatcgcc ttgctttaag 180
tgccacggag ctacagtttc ttttcgtacc caatttttca aagatatact ccttcagtag 240
gcaggcacgc acacaaacat acacaggatc tcaaacgac ccccgatat acctttaccg 300
ttaggaaaat tcaaatggc cagcacgcg gccgcaatgg cgcgaacgag tgtagttgtt 360
ctggatcgcg gaaacaatac aacctgcacc atcaacttgc acggtgagca gaatgtcttg 420
aaacaatgat aaacaacaaa tgaatagctg gcgaacaatt aatcataatt aagaagacac 480
caccagcact ttgccaaaat tttgttgccg ttatttttag cggatgattg gcgcttagac 540
tttccgaacc gaaccggtc gcc 563
```

<210> 126

<211> 522

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(29)

<223> Area matching Drosophila EST AA802206. This EST  
forms a 1341bp contig with ESTs AA02662, AA801949  
and AA942041

<400> 126

```
cttccaacaa accacgtttg aaaattgacg tttctctggt gacgtaaaaa aacatcgccg 60
atgcgataca tcgatacatt tcgtatagag ttgcttnnnt agctaaaaat ataataaaag 120
ttatacatct gagcttatac acgccaccga caatatacat tagatctaca tgcaagtcca 180
tcattctttt cgcttcaatt gttatatatt attttaataa acatcgagta ccaccagat 240
agttcggtaa aattgtaagc tgtgatcact gcgaataagg tattaataaac taaaaataga 300
taaattttat attattttct ttatttatgt ttcttgtaga taaaggaatc gaaggataaa 360
ctataattaa cacaggctcc tgccccggct taggattttc taaatgtaac tcttctgcaa 420
ggtcctaag gaatgtttta tataaaaata taaaagaatc tttagtgatg cgactaagac 480
```

tatgtaataa acaaaaaaaaa ccaggatgga atgctatagc cg

522

<210> 127

<211> 592

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (344)..(592)

<223> Area matching *Drosophila* EST AA978904

<400> 127

gttctgagcg cagcaatagc agcaagaaga ctaccaacaa agagcagagc gacaaatcag 60  
cggagagcag gatggccacc agcggatttg tcgagtcatn nnctgggtgcc caaggcggag 120  
acgggagtc tgaactttct gcagaagtac ccggagtacg atggacgcga cgtcaccata 180  
gccatcttca tccggcgctc atccccgggc aacgggactg gaggtgagtt ggcacttttt 240  
cgcactctct ataccggtta caaagaactt gtacagttat tcttccaata ttacaatat 300  
ttcgtcttac ctattctatt acgatttaac cttctactg tgtcacgact gcttcttact 360  
cccgtttctc attataaccg atccaatttc aatctgctcc tacgcaacag acgctgtgcg 420  
atggaaagga ccgttaaagt aatagagcgg tacgactgtt ccggatgcgg cggacgtgga 480  
catgaagaag aaggtgacgc cggacgagaa cggcaacatt aagggcctgt cggaaactcg 540  
ctcagctgaa tccggactga tggctctgac acagatccgg aaaagcgggtg cg 592

<210> 128

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (101)..(223)

<223> Area matching *Drosophila* EST AA202366

<220>

<221> intron

<222> (224)..(291)

<223> Probable intron in gene represented by EST

AA202366

<220>

<221> misc\_feature

<222> (292)..(551)

<223> Area matching Drosophila EST AA202366

<400> 128

```
ccctggagtt gcgaatttta acgtttttgt tcggttgctg aacgttttgc gcttgaaaat 60
gccagttcgc agcgccctggg cgcgagaagg tatgatgnnn atgtacctct tcaccaaggc 120
gaatctcata cgcttcctag ccggcgcgat atgcttggtg ctggtgctta actttgtggg 180
cttcgctoga cggaggtagc gccacctccc tcagcaagct caggtaacta aatctatcat 240
attgccttgg cagaggttat cttatcaatt atttttggga acggatatta gcattcggcg 300
cgtgcacaag tatgctcata tctacgggaa cgctagcagc gatggagccg gaggcagtga 360
agcatccagg ctgccgcttc cccgctcgcc ttatcaaaag acagagagcg ggaccaggag 420
ctcaatggcg gacccaactc taccataaga actgtgattg ccacggcaaa ctttactttc 480
attccacaag acttaacgcg ctttctgctg ggcacaaaga aatttttgcc cccgcgacag 540
aatccacat t 551
```

<210> 129

<211> 492

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (103)..(468)

<223> Area matching Drosophila EST AA950164

<400> 129

```
gaatattgca aacaacacca acaacaacaa gaacaacaac aaaacaaaaa gcgaaacagc 60
aaaaaataaa taaatacgag gaaccagttt accttgaggn nnacactcac actcgcactc 120
```

gcattcacac aaatgaaaca gcccgatctt actcttactg cgagtacgga cacatagtgc 180  
 acatatagtgc catatagtgc acagcacaga gcacagagta gacatagtga ccaccacata 240  
 atttcgtgat aaagccacag agaatcggag cgctccgcct tatcggcaac ccaactgccac 300  
 tgggtccggct actatgctcc agcggggatc gggacatcat cgctgggata gagacacagt 360  
 ggacaccaga actgggatgg cagttgcagc ggccccaac gcattgaaag atgatagcta 420  
 agcccaacca ggccaccacc gaaccaccat taagcttgcg ccccggaac agtgccaaac 480  
 gggtttcagc aa 492

<210> 130

<211> 602

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (23)..(98)

<223> Area matching *Drosophila* EST AA952159

<220>

<221> unsure

<222> (99)..(101)

<223> Gap of unknown length

<220>

<221> misc\_feature

<222> (102)..(602)

<223> Area matching *Drosophila* EST AA952159

<400> 130

cagcggccct ataaaaattg ctttttgtgg ggctgtcagc tcagtcagcg gctcattcat 60  
 cactttccga cgcgctctag agtagctagt agacctttnn ntattacgcy tccccccgaa 120  
 attgccccgc cgcccgaac gcaatagcat tccgcaaaaa caatacgata agcagcaaca 180  
 agtgttcaag attcccttga aacatacaca gaatctaaaa ctccattgaa attggttctc 240  
 agttgttttg tttaccagc aatcagtgcc caagaacgtg gcacatttcc aactgtgggc 300  
 gggtaaacia ttgctgcgca acaattaaga aaacttggtc gccctgtctg tgtacacgcy 360

aataaatctc gggagtacaa ttccatacca gcccggtgac gggcacggaa aagcagctct 420  
aactgtgcaa gatgattcca ggctatggac ccgtcacgca ggctctgctg ggcaccctgc 480  
ttacctgggg actgaccgcc gctggcgccg cctagtgate ttctcgggg taaccagcgg 540  
aggtctctgg acgccgctg ggattcgag ttggcgtaat gatagcagcc tcttttggca 600  
tt 602

<210> 131

<211> 558

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (102)..(512)

<223> Area matching *Drosophila* EST AA392519. This EST  
forms 758bp contig with EST AA695318 and AA441243

<400> 131

gactaacggc tctccgctct cgccagtcgg atcggtata aaagcgggac gatctcagcg 60  
agcgccgttc atttgagttt cgcggttcga ggtgtttnnn cgggtcttctg gctctggaga 120  
aaactactcg catcgaattg aattgaatct ggggaaaatc agtccgagtc ccagctacac 180  
agttagtttc acttcccagt ccaactataa aagtgcgctg cagtcccagt caaacactg 240  
cattcagata caaactattg ccaattgcat ttctatgagc taactgtctc gcatcgcgty 300  
tgaaaagtta caaacaacac aaaaacaatt gccaacgggt aatgtttaat gtccaggcaa 360  
ttataaaaag caattcgatt gtctagctta cgcaaggcca actacaatta ccaataaata 420  
cgacgaataa agcagcacag aaatcccaat ttggatttat taatagccgc tggataaaaa 480  
aatcataaaa caccaacggt gcttgtaaat accaaccaat ggtaagtatt ttttcggccc 540  
caaaggtaac ttcaaaaa 558

<210> 132

<211> 541

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (304)..(541)

<223> Area matching Drosophila ESTs AI515517 and  
AI404462. ESTs have sequence similarity to Ras  
related proteins

<400> 132

ggtggtacta agcgcgtctg ggaaatgcaa ttagtgatgg gcgatagttt tgctatcggg 60  
tggcatcttc caagcggtaa tcggggctgt gatttttcta gtagtcatat tcctgattgg 120  
aatccttgct aaccaatcaa actaacacat aaatatattt tttagaata tatttacttg 180  
tgaaacaaag ttatttcctt gcaaaattct actctgcaag accagctatc gctgccagca 240  
gcaactatcg cacctcgtgt cagccctggg aaacagctgt tcgcgcataa cataacacaa 300  
taacaacaag ctttcaaatt tattaaatct tttatcttta ctgctgactg cgcgctttta 360  
atcgcagcgc ccgctttgaa aacccccacc gactccgata aattcagttg tgcccaagaa 420  
atcagacgca gcaggccgcc aaagggccaa ttacgcgctt cccaaccact ggctctacaa 480  
gcaacaacaa caacagcagc acaccactgg accacacaca tcattctcatc cattttacaa 540  
a 541

<210> 133

<211> 494

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (191)..(387)

<223> Area matching Drosophila EST AA698481

<400> 133

gtgcatacat acaaatgcag atatgcatgg caacaagagt tacatgactt tccggtttta 60  
caggtttgct gcaaagcttt cgctctctca ttcggcgctc tctctctctc tcacacactc 120  
tggcacctgc ctaattcgat tagccgcacc gctcgaacgc tcagtcttca aagagatctc 180  
gaccgagcaa caagtgaacg gaagaatccg agcagtgaag aatcagaaag accgaggaaa 240  
cactcgagaa ctctttaata acattgtgaa ccaaaaaacc agaaacagcc actgaaaata 300  
cacggaaagc agagtgattc gcatagtttt gctagtgttt tcaagggcac ccatcatacc 360

agctgtgctg caaattttgt gccaggtagt gaatttaaata gaaaggccaa gaaaccaacga 420  
attatattga aaatttccat tatctagaga tcggtcgaga acgtacgcct gcaagacgta 480  
ttctggcaga tttt 494

<210> 134

<211> 606

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (451)..(606)

<223> Area matching *Drosophila* EST AA803082. Forms

2166bp EST contig with AA941565, AA820668,

AA978815 and AA697381

<400> 134

gctcagtggg aaaaaggata aaaacgaaga caaagtaaata cggagaaaag tagcaacgaa 60  
aaaagaacca gagcgccact aaaccgggtc gcttttcttc tcttttcctg ctgctccaac 120  
tctcttcgct gattctctcg gtctccagtt ctcgctctct ctctctctct ctctctatcg 180  
ttgcgggttaa ttaaaactcc gagaggcgtg cgacagttgt aagttgtgta ttaaaaagt 240  
gtaacaacaa caagtttagct agcgtggcca attagcattc attttccgca aagagcagcc 300  
gcggcacaca gcttttctga ttagaaattc acagtgggca ctogaagtgt gtctgttgta 360  
aacggatcct cttggatttt atacataatt cattagacct ctttgggtgct gcgttagctg 420  
tcccattctt cgatttcgg tacttacaat ttttgccaac tgcgcgggtg gtctctttct 480  
atctctctta aataggtgaa aactaactgt ggtaactgtg caattaacta gtgagagtaa 540  
tagtttaatt ggttggcact tcgcgtcttt tatttgtgta tgcaggtggt aattaaatcc 600  
cacgag 606

<210> 135

<211> 570

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(570)

<223> Area matching Drosophila EST AI405762. This EST  
has sequence similarity to hypothetical proteins  
from Arabidopsis and C. elegans.

<400> 135

```
gctgggcggtt tcacaatttt tttgggaaac acaacaaagc ttcacaaagg acacgatgct 60
cgttctggta ctcggcgacc tgcacatccc gcaccggtgc agcagcctgc cggctaaatt 120
taagaagctg ctggtgccgg gccgcataca tcacatcctg gccaccggaa acatctgcac 180
caaggagtcc tacgactacc tgaagtccct ggccaatgat gtgcacatag tgcgcggcga 240
cttcgacgag aacctgacgt atccggagca gaagggtggtc acggtaggcc agttccggat 300
cggctctgtgc cacggccacc aggtggttcc ccgcggagac ccggaggcgc tggccctcat 360
ccagcggcaa ctgggacgtg gacatcctga tcacggggca cacgtacaag ttcgaggcct 420
acgagcacgg caacaaattc tacatcaatc ccgggatcgg ccacgggtgc cttcaaccca 480
tggacaccaa tgtggtgctt tcgttcgtgc tgatggacat tcagacacca cggtggtcac 540
gttacgtgta ccaacttgat cggcgacgag 570
```

<210> 136

<211> 236

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(38)

<223> Area matching Drosophila EST AA391495 (inverted).  
This EST forms a 1135bp contig with ESTs AA439145  
and AA949325.

<400> 136

```
agccgaaaga tgacttattg acgagcggat gaccatattt cggatttggg aaaaatccag 60
ctgtgctgca aacgaaaaat accagctgtg aacgtttttg gtattaatat ttaccaaata 120
aataaattta tatttatctt gaaaacaatg aaaattcctt aataacatta cattacttct 180
ttattaggag tgcttaagta ttctttttaa taatgaatta taattaatat tataat 236
```



<210> 137

<211> 526

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (353)..(476)

<223> Area matching *Drosophila* EST AA942305

<400> 137

```
gctcaaactc ggcgctcaca ttacgcacag tggctcgagaa aatgatagat gctgcttaga 60
tggcaactaa atattttaat gggaaaaatt atgtatgcta gtgttttggt ttaaatttct 120
caaccaataa agtaatataa agaatgtaaa ttaataaaaa cattgtattg aacgaagtgg 180
ttcaataatc gtatttgaat acagaataat ttgtacgaaa atatttaagg tgtgaactac 240
tgtgcggaat caacttggtt gttccactgt gactctcttc gacgattggg tgttgccaga 300
ctgaagtcgc tacgactatc gcatcaacta acgtagagca ctgcagccct ggttgactag 360
tgccgccttg gtccgattgc cagaaaaaaa caagacaagt gaaaaagcaa gataaatcaa 420
attaaaaata ttgtaaaaaa ttggagttaa cacgcgctga gcacggtgac tgaaaatgtg 480
atgaaaccat catagagaga gacagcgaga ttggtggccc caagct 526
```

<210> 138

<211> 391

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_difference

<222> (72)..(391)

<223> Area matching *Drosophila* ESTs AA951839 and  
AA979603

<400> 138

```
ggctagtgtg tttattttta tattagcttt gtgacgttcg ctcaccaa at cagtattttt 60
```

cgtaccatcg gcgttaaaac acatgttcag cgatttagtg cgggagtgtg aactaatctg 120  
 agtaacaaca acagcatcgt cggcaaagca acaacaacgg cagcagaaaa ttttaacacg 180  
 ttgacgcttt ttctagtgtt tatagcgagc ggaaaagctt actaagcgcg taacaagcga 240  
 gaccccgaaa tcttttttca tctcggtctt ttgcctttg cgtctttgag tgtgcgtgcc 300  
 aaaattcaaa tacgtcatcg acgcgcgcag ccttaaactg aaaaggaatg aaataattga 360  
 tatacacaaa tgccagcgaa agattgaatt c 391

<210> 139

<211> 458

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (112)

<223> Area matching *Drosophila* ESTs AI386817 and  
 AI404737

<400> 139

cgtcagtgtg agcgcagctg ataacgggcg gcggagtggc gacctaaaga cgcattggacc 60  
 gcgcaggcag atggaaacag ttgcacccgg ttgcctcgag tgtgcagtag atgatccagc 120  
 ggcaggaatg gcggccacga tccagaacac cctgaagggtg gcgctgcgaa agcgcatgaa 180  
 ggatgcactg aagggcatcg acgcggaggc catcgcccgg cagtcgcagg ccgtcacggc 240  
 caaggtaaca ttggtttggc tgggccccaa ggttatcaag ttaatcccca atcctcctaa 300  
 tcggctcgat cgcacagggtg ctgcaaagcg agaccttcg gcaggcgcag cgggtaagca 360  
 ttacctgag cacagcctcg gactggacac cagcgcttg tgtcggagat gttccgctgg 420  
 agaagatggt ctttgtgccc actacgaggc acaggatg 458

<210> 140

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (435)..(475)

<223> Area matching *Drosophila* EST AA438658

<400> 140

```
gccacaatcg tgcgaaaatc acattttacat acatatatgg gttatgagta gaaaacgaag 60
agcaactcgt cgccgtatta gtcacgaaac atcgcagtcg gggaaattcg ggtagaatg 120
tgctcatcca tagttgtggg aaaaataact aaatataagt ggtatctgtc tataaaaaag 180
accaaagttt tcacatagtt gtgtgggttt tgagattaaa catatatcat atcacatcaa 240
ttgaactcgt ttttatccac tgtacagcca agtatcaaca actcatcatg cgtaacattg 300
ggcaacgcgc gatgagcaag gccaggcaat gagtagccgg ggcaaataaa atttccaaac 360
cttggacatt gtggagtttc aactccgcca acattgtttg tgtattttat ttaatatacc 420
tatctatcta tcccagcacc tcgggcagac atattccttt gtgcacacca tggcgattcg 480
aatggcgctc ggctttgtcg acaggatccg cggacgacac ggccatg 527
```

<210> 141

<211> 483

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (31)..(212)

<223> Area matching *Drosophila* ESTs AI106794 and  
AI107315

<400> 141

```
ctccagagac tggcgacact cttggttccg ccttggtga gcacagaggt gggtagagt 60
gctactgggt ggcagtgcg agcgcttcc tttgtgtgct ggcgtaggcg tgacgccatg 120
ttgtgaaaag tgtctgacag aaagtggaaa attcgcacgg aaaactgcac tcgaaagtgc 180
tggaataaaa gagcattgtt aaaacaatcc aagtgagttg tgaaaagtgc aaactttttg 240
gccagtgatt gtgtgtgtgg cgaaggaatt acgcaaatgt tgcacaggat ttccgtttc 300
cattgatttc gctgggggcg tgtgtgtata tattatatac atatatatat ttttaatgcg 360
tgaggaggac aagcggagcc aaaatatttg cgtacaattc atttgcaact cccgggattc 420
actaattgga catggactga tgaattggtt gtgggcctgt tgaacaaagt acctcgggca 480
ttt 483
```

<210> 142

<211> 430

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(228)

<223> Area matching *Drosophila* EST AI403747.

<400> 142

```
caataaacta attgtttaaa atgtgacaac agtgaaccaa atgcttgctg agtaataaac 60
caaaggatgt tttgtttttc taaaacgtgc caattgaatc ggctccacgc aaatgagagt 120
gtgggagtggt ggtctgaaaa caatggagct gccgtaaaga attgattaaa caaaatagtc 180
gagaagagag cgcaaaatgc acaaaatggt taaattatc ctcaggtaat ttcagtccca 240
acaaaaacaa catgtgccag attgctttcg tgctcttatt gctgttggtg tagttctaga 300
ctctctcttt gcgctttaat attatgaatg acgtaagcgc gcctctttgg tagcaataca 360
aaagcaataa caacaatttg gttttgttgc ttttgtaaac aaggaaaata acagaatggt 420
tttgtctgtg                                     430
```

<210> 143

<211> 272

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(272)

<223> Area matching *Drosophila* ESTs AA802791 and  
AA390699

<400> 143

```
gaacagaact agcaaagacc cacttgatcat agatgcgtac gagatcggtta accaaacaac 60
aatcacgttc gcaatcgacc agaaagacac tgaaaatcga accgaaatca ccccgagctc 120
```

ggcgagcggg tagagttgtg taacacggac ggacggggccc aaaaaaaaaa gaaacgtgaa 180  
ctagaactct gtgtctcttc cgctgggttt gttgagtttt tggcgagcag gtgaaacaaa 240  
agcatggcgc ttgaaacgga ggcgaagaat tc 272

<210> 144

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(190)

<223> Area matching *Drosophila* ESTs AA949990 and  
AA246423

<400> 144

gctccgacgg attggtgcgt cgctcgggtga aaccccgcca aaacgggtggg gcggaggggtg 60  
ggttgaatgc caacacgccg gacgacaacc aggatgcact ggacaaccta aaggaccagg 120  
aggacaatat cgacgatggc gactccaagg aaacacgact aacgctcatg gaggaggttc 180  
tgctgctggg actcaaggac aaggaggtgg gtgtgctcct tatctcatat ctgcttggga 240  
tgactaatt aattggtttc ttctgcaaca taagtgttc ttcttcacct gttaaccgga 300  
cgtctctctc tctctgtcgc tctcagcatt tctctcttgc gcaacctctt gcttggccca 360  
agtgaaccg cagtccatct tccagcaggg gccgtagtga aaattggata caggggggta 420  
acttatcact ttcagttatg gggcaaccaa tggttatctg tctacagata acatttatga 480  
actttcgat 489

<210> 145

<211> 463

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(202)

<223> Area matching *Drosophila* ESTs AA201161 and

AA438658

<400> 145

```
gtcgaaatcg aaccaatgac gtcgcgaatc tgaggcgaca aagagcagcg ggaggaaagt 60
ggtcgcccaa acgaccgtat tgtgtcagcg taatcagtat tagaagcatt agcagtccgg 120
attggacaca ccagtcaaac gaacaccccc cactgaccga cacagaaaca tgtgctagac 180
ctcctcgaaa tgggatcgcg tatcaagtga gtatgcccat gccgccagc gccagttcgc 240
agcagcagtg ggcgttgcg tccactggtc gctatcgcg cgctctcact cccgcgactc 300
atcgcccatt cctcccgcgc ctccccccag aaatggacgt gaagaagctc ttcgagttct 360
ggtgcgaggt cagcccgacg ccgggattag agaggggcac gagttccagg agcggcgggc 420
agctgttccg ccggcggtga tcgtggagag cttcccagg gat 463
```

<210> 146

<211> 506

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (202)..(472)

<223> Area matching *Drosophila* EST AA978927. This EST  
has sequence similarity to human PCF11p homologue

<400> 146

```
gtgcagccta agatttcagt gcatcacggt ttattacaaa taaaatgggc agagatgaag 60
atatcgctaa caaacatcgc aaccttaata cattattcat ccaaaatata ccgacaaaat 120
cccattaata gtgcaaactt tttcacacaa attaccttg cttttcatgt catttaatta 180
ctttgttata ttttccttg cagtcgaaac atagcaactg cgactacttc aaaccaata 240
acttgatcaa tatccggatc aagatctgga atacagagtc cacaatggag cagctatttc 300
agaattaccg cgacgatgag cgaaggatcg gcgaggagta tctgtcaagt ctccaggacc 360
tcaactgcaa cagcaagcca ttgatcaata tgctcacgat gcttgccgag gagaacatca 420
actacgcca cttcatagtt aaaggtggtg gaatattaca tcagcccagg ttaacaaaca 480
aaagcgtatt tacttaaaac caagac 506
```

<210> 147

<211> 445

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (84)..(318)

<223> Area matching *Drosophila* ESTs AA541084 and  
AA538937

<400> 147

```
ggttcaccaa aactgagctt ttctccatgg cgccgccgat caaaggcggc gagtgctaag 60
tagtogaatc tgaatcggtc ttgtgagtag gcgctttgaa accgttaacg gagactgcgt 120
atatactcaa tggtatttta tattgcacta taataaaaac cacgtgacgc ccaattcacc 180
gcaaaaatct gtttttgaag tgctgctgtc agacaccgct tatttgtcgg tgcttggtt 240
ccaaaattaa attacaaaaa ttaaataacc ataaataaat aagaaagcga aggacaatgg 300
ccaccaacct gcaaaaggta agaaaggata ttogagactg gtatcagtgg catcgcttaa 360
caatgcttca ccaaggtttt aaaagtttgt gtttcgccaa ttttgccctt tacctttcgt 420
acaatgctct gtattggtgg ggctt                                     445
```

<210> 148

<211> 509

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (390)..(509)

<223> Area matching *Drosophila* EST AA951890. This EST  
has sequence similarity to mouse RIR2 gene.

<400> 148

```
ctcaaaacta attaagtggc gtttcatcag ctgttttctg gattagtcta gggttgtctc 60
attgcatgaa atatcgatga taaaaaaatt tcaaaattta tttagtattt gaaactatta 120
atattaatat ttttcaagtg acaagctggg aagctaaaca taaaattgtg cagtaaggat 180
```

tcgatttatg gtttaagaaa agaaaactac caccaccataa ttgcattaga tttaccctaa 240  
 atttataaaa agtgaattga cgactcgcac agccctgatt ttcccatagt tttcccatca 300  
 ccaaaaatgg cggcaaactg aaacagtttg ccgcccggca taaaacccaa tgtagctgta 360  
 tttcccagat catttgccac acaactttca aactgtacac ttaatacacg tcgtgggttta 420  
 agtgaatttt accagagaat cagagaagcg cccctacctg ctaataataa tccattcaaa 480  
 acatctcaaa tggcgtccaa ggaaacatt 509

<210> 149

<211> 490

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(140)

<223> Area matching *Drosophila* EST AA439230

<400> 149

acccaaccca aaaaaaagag aaagaaaact gaacgaaaaa ctcccggaga aaacaacaac 60  
 acacaacgat aaactgcaaa agtaaacaaa ttgcgccgaa actaaacgaa tttcggaaaa 120  
 ctgcagccaa cggaaaaaag gtcagtacac agcgattgat tggccggaaa attaactaaa 180  
 ttaaagtaaa aaccctcgag tgccaaagtg gtgttgagca gcaaacacct tttaatagtc 240  
 ccccatTTga ccttcaccca tggacaccct cgcaaattgg tagcaccaaa gtcgggctag 300  
 cagttaaccc ttacccttga tcaccgttaa ttggaccccc ctctcagac tatcatggtc 360  
 atggtcagca gggttgtgaa aacgggtcat ttattggagg gtgcgttacc ctttgcatta 420  
 tataaggcac gaaactcttc aatgaaaatc taatttcaaa gggattttta cccctgtaag 480  
 aaaaaaagta 490

<210> 150

<211> 522

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature



<222> (3)..(522)

<223> Area matching Drosophila ESTs AA948907 and AA92191

<400> 150

```
cgccgaattg aacgcacgta ggggaccgga cggatatcgc atcttccgat cggaaaaatc 60
gtacagtgca gccaatcgc cgtctacaga aatctattag cgcgctgtg ttggtgccag 120
tgcggtggca aattaaaaca aaaaacatct gcgaatttga atacgcaaat ctcatgctca 180
ctaagagcgc aaaagtcata gagtgcagaa tagtgaattg aagaactttt ggacgcgcta 240
agagtcgctc tccatcccca tctctctctc tctctcttgt gtgtgcagtg ctagtgtgtg 300
cgagtgtgag tgagacgggc aaacaatttg ccgctaaata caaaaagcag ctgagaccag 360
ctgacgcattg tgtatgttcg aaatacaatt aaagttaaca ggctataaat aaattgcaaa 420
tgtttatgta gccgtcaagc agcaacagta gcagcgcaac aacaaaacca cgtggcacag 480
acattttggc cagcatagta agcaaatacc caaccgatt aa 522
```

<210> 151

<211> 590

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (25)..(76)

<223> Area matching Drosophila ESTs AA802379 and  
AA246624 (inverted)

<400> 151

```
gtctagttta gagagcatca ttaccttcga ctttaaatta tcaccaattt atattccaac 60
gaaatacgcg tccgttcaag tcgaacagct ttctgttagt cagtgtgacc gtggcggagc 120
gctcttataa cctccgattc gccaaaacaa gccctaaata tgccagcaaa agtcagcaca 180
gcaagagaac tttgataagg agcggaaactt cggtaacgcg ctttcaattg cacatttcca 240
ctagatgagc taacaccttg ttccaactga gccacattaa gcacatcttg cagataatct 300
ctaaattcct ttaaaatcgt tatattatta agttttacta cacattattg ctaagtgatt 360
tagtatatcc gatgttatcc aactagtttc tcatattatg tatgggttcg ctttaaactt 420
gtttaatatg aaattaataa ttttttatca atagacctca aaacctacta ttcaatttga 480
acctaggtac tttttgggaa atctctacca ctgcagcaac gcttttctta tcgccgctaa 540
```

attcagagct taaatctacc agacttttctg cgataggaat gccctataaa

590

<210> 152

<211> 411

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (9)..(100)

<223> Area matching *Drosophila* EST AI404485.

<220>

<221> intron

<222> (101)..(178)

<223> Probable intron in gene represented by EST  
AI404485.

<220>

<221> misc\_feature

<222> (179)..(411)

<223> Area matching *Drosophila* EST AI104485.

<400> 152

ggcaagacag tttatattaa ttgtttacct gtgcaacaat cttttgttcc gccaacaaag 60  
actatatttg caattgatcc cgccgacata atcataaaag ggtaagcaat acgctgcaag 120  
gccactggca ttgcgtcctc cgcttactaa cgtttcctac taactttctt cgctgcagct 180  
ggagtcgggc cctagacatt tcttaatggt gaaaacagca tagccttcta catatgccac 240  
cggctctcca tgagcattat caagatgagc ttgcacacac gggcgtagt gttctccacc 300  
ttctttggca gctgcctggc tattggcctc ttgctcgtca gcatgaccac taatcactgg 360  
gtgcgggcca ctccacgccg caagaactcg tcggacgccca agggatgaatt c 411

<210> 153

<211> 561

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (60)..(449)

<223> Area matching Drosophila EST AI108647.

<400> 153

```
ctgcgcgtgc taagctccga gttgctaggt ccagaacccat actttttaga tactgtatcc 60
aaactccggg caatccgctg ccgctttata aacaaacagt taaacaaacc gaccgctcga 120
acgtcgccgt gtgtgtgtgt gcctgtgtgc ttttcgccct cattgtgctc tcgtgcaaatt 180
gaaaatttca ttgagcagaa agtcgcagca gcagaagcag cagcagcagc agtagaaaag 240
tggaatatcc taaagcggcg ccagcctcag caaaaaaaga aaataaatta aaaatctcgg 300
ctagtgaatt ttcagtcag aactagacgc cgcaattaag ccaaatacag accgaaccac 360
gacgagtcaa tcgctggaaa actgccaaaa cagccacgcc aatcgattgc aggcgttccg 420
caaattgaag ttcaaccggc gcagcttgta ccgctaaatc gatcgacaaa gatgcagtgc 480
ggtctggagc agatgaacga ctgtgagcgg tcggcgaacc ggacgaacct acgggtcaac 540
ttaacgaaa agggggcgga a 561
```

<210> 154

<211> 49

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(49)

<223> Area matching Drosophila EST AA951902(inverted).

This EST matches other EST including AA949796.

<400> 154

```
gtccgtcaca caacatggac gcactctcgc cacacacacg ggcgaattc 49
```

<210> 155

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(489)

<223> Area matching *Drosophila* gene RanGAP, accession  
number AF143860.

<400> 155

```
gtctgaagcg tcatccagag tttcggaagg cgctgtggaa gaacatgttt actggtcgtc 60
tcatatcgga gattccggag gcactcaagc acctgggagc cgcgctaatt gtgcggggcg 120
ccaaactgac agtcctggat ctcagcgaca atgccttagg accgaatggc atgcgaggct 180
tagaggagtt actgcgatcc ccggtctgct actcgctgca ggagctgctg ctgtgcaatt 240
gtggccttgg tcccgagggc ggtagtatgc tgtcccgggc tctgatcgat ctgcatgcca 300
atgccaacaa ggcgggcttc ccgctccagc tgcgtgtgtt cataggttcg cgcaatcgtc 360
tcgaggatgc cgggtgctacg gaaatggcaa ccgcattcca aaccctcaag acttcgagga 420
agattgttct ggagcaaaac ttcatttaca tcgaaggcgt cagggccttg ccgaatcttc 480
aagcataat                                     489
```

<210> 156

<211> 450

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(278)

<223> Area matching *Drosophila* EST AA940865. This EST  
has sequence similarity to *Xenopus* chromosomal  
assembly protein, U1367.

<400> 156

```
attggaccca atggcagtgg caagagcaac gttatcgatt ccatgatggt tgtgtttggc 60
tgccgcgcca atcgcatccg ttgcaagcgt gtctccacct tgatccactc ctcgtctagt 120
```

tatcccaatt tacgcagctg ctcggtcgcc gtccacttca agcagatcgt agacaagggc 180  
gacggcacat gcgaggacgt gcccgactcc agcattgtta tcgaacgcac tgccatgtcg 240  
gacaactctt cctactacca gatcaacgac aaacggggcg agctcaaggg atgtggctaa 300  
gctgcttaag aagcatcatg gtgggatctg gagcacaatc gcttcctcat tctgcagggc 360  
cgaagtggga gtccattgcc atgatgaagc caaaagggca gactgaaatg aaatgggaat 420  
gttgggaatac tggaggatat tgtcggaaca 450

<210> 157

<211> 349

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (117)..(263)

<223> Area matching *Drosophila* ESTs AA803314 and  
AA941391. These ESTs have sequence similarity to  
Human B-cell receptor associated protein.

<400> 157

cgtgagagtt tcccaatttt gtacgtcgaa aaatcatacg tttattatca caaaatctat 60  
agagagtgtc ctgcgtttac cgacatttaa tatatttttt aaattcctcg tcgcagaaga 120  
caaacaagat ggcacagagc aaattgaacg atcttgccgg caagctgggc aaaggtggtc 180  
cgccgggatt gggaatcgga ctgaaggtcc tggcccgcgg tgggagcagc cgcctatgga 240  
gtcagtcagt ccctgtacac cggttaaggat aaagccgata ggataaagcc acccgatttg 300  
agggctaaaa gcataaacac gggcaatagc ggcatgtgca catacctca 349

<210> 158

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (209)..(405)

<223> Area matching Drosophila EST AA201448. This EST  
forms a 856bp contig with ESTs AA438721 and  
AA247046.

<400> 158

```
ctttgggctc tcacgccttt tctgctctct cctctctcga tttaaaactt gtaggacttg 60
tttcttgagc ttttttgca aaacataaaa accggtaa at tttttttcga aactgcaggc 120
agagaaaaga gagcgagctg tgttggtgtt cctgtattgg cattttttac cttaaccata 180
tttttcacac actttgcttt ccttacagtt ttctaaacac acacacatac agaaacgaga 240
agagccaacg aactcgcagc gacgccaag aatgaaagag agcaaggcaa catgaaaatt 300
acagcaacaa caactggctt gccgaagaag ttgtaaaaga cgcaagagca gaagaagaag 360
cagccacaac agtatttttt attagcgggg tgtttttgtt gtcatgtatg tatgcacact 420
tttttcgctc cacactctaa tataagttga tcgttggtgt gtgctggtgt aattattgtg 480
atgcttgat atattgctgg tgtgctatcg t                                     511
```

<210> 159

<211> 492

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (37)..(243)

<223> Area matching Drosophila ESTs AA696343 and  
AA696180.

<400> 159

```
ggaccgcctt tcataacgta gtaagttttc gttgcgaacg gacgtagccc aaccaacttg 60
gccttaaccc ttgcgctccc tccgatttat tccgcggcaa acacattcca gtggacagtg 120
gtgcagttca gcccaagacc aacctacatt ttagctccct gcaaaccctg ttcttcatca 180
aataactatg gcgtccaacc gtgcagcgaa gtctggtttt gccgcccagg ccagcgcaa 240
agtaagtacc aaatagcaac aacaaccgca cccccaccc aaaaaccgaa gagcgccaaa 300
caaaacaaca caataaaca attgcccaaa aaaaatcaac ttttgcacgg gtgtgtgctg 360
gagtttagag ctgcattgac tttatttggc gctgcgttgt caagatttta tcttcgcgcg 420
ccaaatgcca aaaattagcc aaaaatggtc ttgaaattgc cagcgtctaa caaggaatga 480
```

&lt;210&gt; 160

&lt;211&gt; 580

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (261)..(580)

<223> Area matching *Drosophila* EST AA540783 (inverted)

&lt;400&gt; 160

gtttggccgt ttgcagggcg ccaactacga cgggtggcata gaagttgatc tgggcttgca 60  
gttgggtgggc tcgaggaccc agttccttaa ccgccttctg ggtactttgg cagatgaagc 120  
cgaggaaggc gggattgctg gcggctctgt taataatagc agtcttggct agcggaacgc 180  
caggacgctg caacggggcg agccagtacc agtcgccatc cgatgaccgg agcctcatgg 240  
tcttaacgat ctggacaaag atcattgtct cgtgataggg cagaatcagg gccataactt 300  
cgctacgggt atactcgtga acctggaatc gtcgcagcaa ccattogaag gccatgtgtg 360  
cggggcggag cagaaggtag ggcgaaagaa ggcgcagaaa ctttgcaatg gccgcgtcca 420  
gcatcttggt aatctccggc agctccacgg aacgctccac gtcaatgtgg cctcatcgaa 480  
caacgttagc tggaactcct tgaagccgga ttaaagtcgg tcaactcctgc agtcccgtac 540  
ccgactcata aatggaccgc catccttggt ggccgctctt 580

&lt;210&gt; 161

&lt;211&gt; 494

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (26)..(267)

<223> Area matching *Drosophila* EST AA695850. This EST  
overlaps EST AA698310 and has sequence similarity  
to Rabbit FKB4 protein.

<220>

<221> intron

<222> (268)..(335)

<223> Probable intron in gene represented by EST  
AA695850.

<220>

<221> misc\_feature

<222> (336)..(459)

<223> Area matching Drosophila EST AA695850.

<400> 161

```
atacggtctt tccaacgtgc ttgagcttgg tcaactctgcc atcatcgtgc gaattaaagt 60
tcagcagcca aaaatgccgg aaggggaataa aatcgacttg tccggggacg gtggcgctcct 120
aaaggagatc ctgaaagagg gcacgggcac agagacgccg cacagcggat gtactgtgtc 180
cctgcactat acgggtcggc tggtcgatgg cacggaattc gattccagcc tcagccgcaa 240
tgagcccttc gaattttcgc tcggcaaagg tgagtgtgtc gccggcaaact tcgcgaaact 300
tctatttaat gtactcctgg ccaccggaca cctgcaggca atgtgatcaa ggccttcgac 360
atggggagtt gccaccatga agctcggcga gcgcttgctt ctaacatgtg ctccaaactt 420
acgcttacgg agctgccggc agcccgccag ccattccgcg gatgctactt gattttgagg 480
taggaatgaa attt
```

494

<210> 162

<211> 224

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(224)

<223> Area matching Drosophila EST AA441346. This EST  
forms a 1677bp contig with ESTs AA390646 and  
AA696470.



<400> 162

gctccagcga taacggtact ccaatgtgct ctctcgacg cacacagaag catccccgac 60  
acgtacacca ccaccactgc caaaaagcaa atcctgccca acagccgcac ctataaaagt 120  
gggcgtgggt agaccaagt tactgtaaca aatttgcaaa aagtgatgca tgctaattgt 180  
ttaaacaat cccagctttc ctaatcaaat acctttgcga attc 224

<210> 163

<211> 541

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(514)

<223> Area matching *Drosophila* EST AI0643375.

<400> 163

gcacagccaa aactgaagat tacatacaat ttacaatggc cgacgagagc atcacgcgaa 60  
tgaacctggc ggccatcaag aagatcgacc cgtaacgcaa ggagatcgtg gattcgtect 120  
cgcacgtcgc cttctacacg ttcaactcgt cgcagaacga gtgggaaaag accgatgtgg 180  
agggagcctt cttcatatac caccgcaacg cggagccctt tcacagcatc ttcatcaaca 240  
accgactgaa caccacgtcc ttcgtggagc ccatcaccgg cagcctggag ctgcagtcgc 300  
agccgccgtt cctgctctac cgcaacgagc gctcgcgcac ccgcggcttc tggttctaca 360  
acagcgaagg agtgcgaccg catcagcggc ttggtgaacg ggctgctcaa gtcccaagga 420  
tcagggaacg aatggccagg cccacgtcac gtcttccgcg cccagcagca aagcaggaca 480  
gcagcagccg gccagcatat tcaacatgct tgaccaaggc cagaaggact acatgcccga 540  
g 541

<210> 164

<211> 497

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (181)..(299)

<223> Area matching Drosophila EST AA540197. This EST  
forms a 723bp contig with ESTs AA695503 and  
AA941503.

<400> 164

```
atcgagttgg cataaaagaa tctgggtcttc gtgtcgtgtt attcattcct taattgcgcc 60
ttgtttaatt tgtgggtgac ggaaatcgga gctcggcgac atcgccagtt gtgcaatact 120
gactccagcg gtatctgtta atccccaacc acttcgcaaa cgtattttct ttgccttgca 180
gatttgctga ctttgtcgtt cgagtactca gcgtttaacg accacaatga atcggcaggc 240
gaaattccta atcttgtgcc tctttgtggg cctcttctcc gcgaatttgt gcgaagaagg 300
tgagtctttg atcaaattac accgaattaa aatcgaattg aagacacgcc gaacactcat 360
ttctcaatta tgcactcgga cacacacaca cacacgcttg catgtgcatg cgtaccgtgt 420
gcgcaaacc ctcgcgtgtg tgccgcctg cgggcatgtg ggtgtgtgtg tgcataaatg 480
tgcgtgtgtg tggatgt
```

497

<210> 165

<211> 523

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (167)..(212)

<223> Area matching Drosophila ESTs AA979442 and  
AA392418 (inverted).

<400> 165

```
gcccgagaa acaccacga atgactacca aatcgggatt attgggtgat taggcttaat 60
tggtggctat ctactgatg aggcgatggc cgtcagttgg gcaaggtagt aatgcaacac 120
ttttcacaca tctttggtgt tttctcgcgt ttttttgttt aattacctgc tcgaaaatga 180
aatgtatcgt attttataaa tatcgataga tatcagtggc ggtgtgcccg ttgatgggta 240
gcacaaaaac accatccggc taagagatgg cattttgcgg tataaaaata ccagataaat 300
gctctagtgc ctagttttaa aaacattgcy taaaatctta aatattatta ataagtaata 360
aattagtccc tgaaatatat gatcattcac aattacaata ataacaacaa aagggatata 420
```

taaaagggca ctgtaagaaa agtcgatgag taaagtctga aacgccactt atcgatatca 480  
ccatgactat gtggcagcac ttaattcaaa aaaagggcgg cct 523

<210> 166

<211> 414

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (89)..(159)

<223> Area matching *Drosophila* ESTs AA536378 and  
AA392418.

<400> 166

tgtggaaaca tttatcgata attttacaaa ttagagggat ataaaacaat ttggtatatt 60  
ttcatttcat acctggaggt atattgcgtt gcacaaaagc ggtcacacta attgatagac 120  
gcaaagtttt aagtaaaatt tgggttttagt taggcaaagg taattaaaaa tgataaagga 180  
gcgaaaaatg taacaaaaaa tgccgatatg ttgtattcta cgctctttta tcgatttttt 240  
aaaatgcatt tctcattgtc cattcgatga aacacgtaag cggttgtaag caaactgaca 300  
agatggcggc cacatctgct taattgaaaa tcgaaattaa atacgatata actagcctgc 360  
cgacccaaat tgcaaacggg ttgggagctg gtgtaatcat aataatttgg aagc 414

<210> 167

<211> 570

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(570)

<223> Area matching *Drosophila* genomic sequence  
AC004345. ESTs AI515537 and AI062109 match this  
genomic sequence 50bp 3' to NPS0219.

<400> 167

gtcgagtggt tgctcaaaag aaccgaaagg acgaagggtc cttcaaacag gataaacaag 60  
ccaggcaaac acgattgtca ttggcgacag gctttaaaat ctatagcgac aagcttcgct 120  
ttgctgatcc tatattcatg gcaaattcat ttaatttaat ctccttaaag aggaatgact 180  
taacatagtt aattgaaaag taaaatgggt agagtataac ttacacttaa ttatgtgtac 240  
tttcacagag ttaataaaaag tactaatttc gaaatatttg aatatttggt tattcagact 300  
gatcagtttt aaaattttta aatcgaaata ccagctagtt gtaaatttcc aatcataatt 360  
gggagatctt aaatgcagat ctgcaatagc agataaccat cgtcacttag acttcctata 420  
aacaatacct ttgcaaggat tataataata agagaggcat tcggtgagac ttcaaacgag 480  
agataacgct cttgacagtt gctcgactgc tcggttgagg cccgaatcga agccgatgcc 540  
ccggcttaag tcgatggcgg ttcgagaact 570

<210> 168

<211> 601

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(184)

<223> Area matching *Drosophila* EST AA390646. This EST  
forms a 1705bp contig with ESTs AA440523 and  
AA696470.

<400> 168

cacataccta agtagacgca cgagagctct cgtatcgca aaagcgtgtg ctttgttgtt 60  
gctcttccac tccctcgctc taagaggcgc tcccggtgtg ttttgttgtt tattgccgct 120  
gagcaaatgg cagaccctct aagcgggcgc cgctggtgat aacatgtcgt aatggccaga 180  
gaggtaagtg caaacgtgct aaaagcaaag caaagccggc aactacggct taaccgtttt 240  
agttttcccg atcaccacgg taccgcaagt tactttgcca aaatcagctg ttctcacttc 300  
atcaccatcc cccatcattc acatctgcaa ccaacggtgt tagcctctcc caacattaaa 360  
acagttaacc ctatgtcata tttttccaaa aaagttaaac ccaacactac aacttaataa 420  
taaaaatgct gcgtgtaaca aatagttatt ctctgtagga atgaattttt taattaagca 480  
gtagaaacaa aataatcaaa aataatacta ggtaatagat tttttttaat aacatgcaat 540  
ttgaccaagt aaaatttata atatattcta atatttcttt gacttggtt tgtagaaatt 600

<210> 169

<211> 467

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(104)

<223> Area matching *Drosophila* ESTs AI064169 and  
AA816652.

<220>

<221> intron

<222> (105)..(309)

<223> Probable intron in gene represented by EST  
AI064169.

<220>

<221> misc\_feature

<222> (310)..(467)

<223> Area matching *Drosophila* EST AI064169.

<400> 169

```
gttaggacga aatgagccga aagaacggaa accaggacac ctttcccaag acggagaaga 60
tgcagcgcta ctacgcggag cgcgagacca caggaccoga gttcgggtgag ttttcctcgg 120
ttcgcaatcg gtacacaatg gattcagaaa tggaatctga gtaaccgggg ctgcgagaat 180
caacccccaa agccaaagga tgtgtcttct gcgcttaggg gttgctgttt ctgcggcgaa 240
gaaacgtaga aacggaatta gaaaaccgaa acagatttta acgatttttc ccacaaatcc 300
ttgtctccag acgatcgctt gataaagctt gtgcgcgcca atccggccat ctatgatgtc 360
agccatccgc actatcgccg taatccggtg cgggtggaca tatgggatcg cattgccaac 420
gaactgggcg cctcctgtga gtatattgca tttttatcca ctgcgta 467
```

<210> 170

<211> 288

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(288)

<223> Area matching *Drosophila* EST AA439345. This EST  
forms a802bp contig with ESTs AA949877 and  
AA439626.

<400> 170

```
ttgcgaaccg aacagaacgt gggtgaaaat aatcgtagtt tttatactgt tataacggct 60
caccatgggtg cggcccaaca acaaccagct gccggagaac cttccgcagt tgcagaacct 120
catcaagcgg gatccggagt cgtatagcga tgagttccac atccagtacc aacactttct 180
cagcttgctg gaagtttttg cgctgaatcc cagcgaagaa aacaaatccc tggatgacat 240
cgtcatgttt gtcgccaggg tggctcagtg ctatccggcc gtctgcga                288
```

<210> 171

<211> 350

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(350)

<223> Area matching *Drosophila* genomic sequence  
AC005452. EST AA979503 matches this genomic  
sequence 181bp 3' to NPS0227.

<400> 171

```
ggcttgctgg tcagctgcc atggcgatac tategtcgga agtgcttggtg cagcactgga 60
cgtttgctga aacttgtttg aaatatttcc ggtcctttac gcatttaatt ctcttccgta 120
atctatattt ataatttaaa tgttcctttt tggtcctttcc cttaccattt tccctcaaatt 180
ttgtttacaa tatgtttttt ggggagccgt gcagcactgc tttctagaga tggtagtggc 240
```

gggaacgtat tggaactggt tcacctaattg ttataccttc aaaatttaca gggctagaaa 300  
tccagtagct aactattttac ataaccaat aatattatTTT taaagaattc 350

<210> 172

<211> 446

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(93)

<223> Area matching *Drosophila* EST AI293141.

<220>

<221> intron

<222> (94)..(169)

<223> Probable intron in gene represented by EST  
AI293141.

<220>

<221> misc\_feature

<222> (170)..(446)

<223> Area matching *Drosophila* EST AI293141.

<400> 172

cgccgtacag cgcacggatt gcagttgggc caacaacaag gcgcgagcat aaacagcgat 60  
accaacatgg cgggcttcgt cgcggtgcac acgggtacgt atcttggcca tggcggttcc 120  
gatccgccgg gcagacagcc agatgattga tgaccgctac ttgctctcag gggctgggaa 180  
ctgcatcgac gaaacgaagt accagcgggt gattaaggag gcctgcctgc gcgccacgga 240  
gatccttcgc aacggcggat ccgccgtcga tgcttgcgag gcggccattg tgcggttgga 300  
gaactgcggc tacacaaacg ccggctatgg ctccaatctc tgcattggac gctctgtgca 360  
gtgcgatgcg gctataatgg gatggctcaa cgcttaactt tggcgctga cgaacgttag 420  
tcggtgaaga ccccatagac ttggcg 446

<210> 173

<211> 478

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (12)..(244)

<223> Area matching *Drosophila* ESTs AI107445 and  
AA390813.

<400> 173

gtgcagacag agagagacgc gaatgtgaat taacaaacaa acaaaaatat tttgcgaaaa 60  
agacaaacac aaaaagtgaag agccaataaa gtgtattaca taaacaaacg gagctccgat 120  
atctaaataa atattatgga aatcgcacca ctgatcaata acgccgtcgc tgcgtcaca 180  
gcctctgcct ctgccgccgt ctctgcctct gctagcgtcg gcagtagcag caaggatgat 240  
aacggtaggc gggctctctag atgataagcg gtacacttcc agtgggttca taataaacta 300  
taaaaataat aaaatatatg taaatacaaa gcataaagtg tagatacgtg ctcgaaagag 360  
tcacactttc tcgttaaaga acttcacgtt ctatccatat tatatgatta ttatgtttca 420  
aaatccttta ttaatcaaaa agccgaatta gacaatcagg aatatcttcc acccagca 478

<210> 174

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (12)..(478)

<223> Area matching *Drosophila* EST AA390942.

<400> 174

gttgcgacca gcactcgatg tagacgtacg cacggatact cgatctccca gttgtatctg 60  
cgttaggggcc tcgcatagtt tttcgcgtaa tattttcggc ttcgcaattt tgttggatac 120  
ttgatgaaat aacgtcagtc ggattgtata taacccaaag cagcggcaaa tcaatgtcgt 180  
cagttgtata aataccacaa ataaacaaac acattcacia agagtttttg tgctttcatt 240



gcatagtgac caagtgtggt agtcacccat acagttttatt tatgtgctaa aatgcaaatt 300  
 caaaatcaca agaccaaaca agttgctaaa atgtggcaga ggaagccaat aagtgcgaat 360  
 aaaaataaat aaatacgcg agcgagcaa aaccaaggcg cacaaaaagg attacaccag 420  
 ataaataaca ctgaagccgg cgtaaaaata gcaaaaacgc aaaaacacat ttcattgcca 480  
 acgagcgag aaagcagcag caacaagaac taagccaaca gggccaag 528

<210> 175

<211> 539

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (11)..(103)

<223> Area matching *Drosophila* EST AA802688. This EST  
 has sequence similarity to 10Kda HSP protein  
 genes.

<220>

<221> intron

<222> (104)..(295)

<223> Probable intron in gene represented by EST  
 AA802688.

<220>

<221> misc\_feature

<222> (296)..(389)

<223> Area matching *Drosophila* EST AA802688.

<400> 175

tcccgcatct agcgagaata gttacgccgg cacgtgtagt tgagtaaaaa gttcactcat 60  
 taacttttat caaccgtcc agtttgcatt taagaattaa aatggtaagt taaaagtgca 120  
 ttgccccata tgaggtttag aagacagttt gaaatcgaag gatgatatcg gtttttcgag 180  
 aaggttccac ggctttcggt ccacatccca ttcgccgggc tgttgtgtaa tcaatgagag 240  
 aaacatgaaa cattgaaaca tgggttaatt gttgggtctt ttttaatgat cctcaggccg 300

ccgctatcaa gaagatcatc cccatgctgg accgcatcct aatccagcgt gccgaggcgc 360  
tgaccaagac gaaaggaggc attgttttgc cggagaaagc ggtgggcaaa gtacttgagg 420  
gcaccgttct ggccgtagcc ctggcaccgc taatgcccg gagtatttcg cttatcaat 480  
gcagagatgg tcatttaac actgaacatc ccattctccg cagtccatgg caaccacat 539

<210> 176

<211> 541

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(414)

<223> Area matching *Drosophila* EST AA392415.

<400> 176

cgtggtccga aagcaacgaa gcaaatacgg caagaggcga gcgaaaaagt gaaattgaaa 60  
taattccaaa tcaaaaatca aattcgaaat cgaaaatcgc aaatcacaaa gttggaagtt 120  
gagtgaagcga acgcgtgtgt ttgtgtttgt gcgtaagtgt ccctcagtgt gtgcagtgc 180  
acggtatcgt aagacgaaaa gtaacggtaa ccgagcaatt ggggtgtaag ctgtcagaat 240  
ctgtgcgcag agaaaaccga aagttttggc ttgttacctt gccgtagtaa tcaaaaatca 300  
aaaccgaata ccggattcac cgatcgccat cctggcccgc ccttcgactt tagtttaagg 360  
cgctctgccca gcggttcgcc ggaacggtaa actcccccca caccctgctg ccgctcgctg 420  
ttagcatacc gataccgata gaccaccgcc gatagcgata ctttcgaaat tcagcaatcc 480  
gtgccccatt tactaggatt ctgttcggtt ttaaccctac gaagaaggag caccgcgggc 540  
g 541

<210> 177

<211> 66

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(22)

<223> Area matching Drosophila EST AA695619. This EST  
has sequence similarity to human cysteine rich  
protein.

<400> 177

gccacgtgca ttcttccact tctttttttc gctcaaaatg gacggtcgcg ttttctgott 60  
gaattc 66

<210> 178

<211> 542

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (399)..(542)

<223> Area matching Drosophila EST AA142132.

<400> 178

ctttgtatgt atcgctgac gtatgcgcag tgtggccgaa cagggctagt gagaaatacc 60  
agccggcgagg tagatatact aaaagtgtat tatttttagt taaaacagtg cattgtcaca 120  
taaattttta tagcctcttt attaaactat atgagcggtg attgccacta tgaatatcta 180  
agcaatatat tacattacaa tatggcaatt atattggcat ttggtactgt cgaataaaat 240  
accaaacctt gcagtgtgc ccatcagcta taccaaaaaa aaacttggca gcattgcgca 300  
tcgtgttcat ttgaaatttc gaaacacaaa acattataaa taaattcaaa cgaaattagc 360  
tcgccatgga aatgcgtacg ataaaaacag ctagacttta ttaatcaata acatttatta 420  
tttacagctg aaggagtctt gattgctctt gcagaccgcg cttgaatgac aaaatgcatt 480  
agttgggttc gaaatattaa tgattggcta acaattatga tccttattat ttatacccca 540  
tt 542

<210> 179

<211> 519

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (366)..(519)

<223> Area matching Drosophila EST AA536537.

<400> 179

```
ctccagccac actaacagct gatagggctg tcatcaccgc ccaattagtg atgagcgtct 60
ttttttaaga aggtgacgca aaaacggaaa aattactaat taaaattaaa tgaaagaata 120
atattgtctt aaaaatatgt gctttttaag gatttaatta tcaactgttg ataaaaaggg 180
ctcaactttt taataagtat tatgaaatta cattttgggc caagaacgtt acctttaaaa 240
ttaaacaata tgattcaata aatttgtttc actactattg gtgttggtca actatcgaag 300
gaacctcaac tatcgattaa tgtgaccgct caccactgac caccactagc tctgcagtac 360
aagcaacatt tggcatctct actgggtatc attttcttga tccgttaaag tgatggattt 420
gagtataat agcccagtgaggaggatcaa tacttttggt tacaagcatg ataagctatt 480
cggcgaaagg ttcccctggt caaggaaatc cgcaggatg 519
```

<210> 180

<211> 480

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (26)..(303)

<223> Area matching Drosophila EST AA264253. This EST  
has sequence similarity to SNF7 genes.

<400> 180

```
ataggggacg gcaatcggta tcgggtgacg catacgaaca acagctccca gacaaccaag 60
aaacgcaata gcagaaaaaa cttacttggt cgctaaattc gggtgaaaaa acagatcagc 120
caggatgagt ttcttcggga agatgttcgg cggcaagaag gaagtggccc ccaccaccgg 180
cgaggcgata cagaagctgc gcgagacgga gaacatgctt atcaaaaagc aggagttcct 240
ggaggccaag atcgaggacg aactgaatat agcccgcaag aatgcgtcta aaaacaaaag 300
aggtatgaga ggagtgcgcc gaggtccttg gcttcctagt tggtcactca aatggggcaa 360
ggggaaatga ctcatgctt tggttttggt gcggccgcga agcctgcttc cagttaatca 420
```

agtattccca tactggccag caaatagaaa actcaataaa caatatgtat ctcttttggc 480

<210> 181

<211> 593

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (186)..(593)

<223> Area matching *Drosophila* ESTs AA441247 and  
AA820771.

<400> 181

cagtggcctt tattgtttat atatatcttg ttgcaatac atgaacaata tatgagtcac 60  
tattaaatta aaaaaattta tgggcaagcc agagcttatt taaagaccat aacaattcgc 120  
tcgatctttt aaaataccaa attgacagtc cgaatataaa cggtcactta attcacttgt 180  
ttacaaaata tttaccgcat attttcagag aaatttagtt ttaattacaa atttgaaaat 240  
ccacttagcg tggagcctta aaactatgca acgcggtaaa atttccttcg ggaaaatcaa 300  
attgaatgta aacgtgccac ccgcggagcc aaaatccaac gaaaccgagg cggaagatgc 360  
aaaggagtcc actgaagcca gcggaaatgg cggaggattc aagaaaatgg acaaggagca 420  
gatgattcgg cagatcgagg acgtggcccg aagatctgga gagccagcac ctcaggaagt 480  
gatgggcatc agtggctttg gtcgcaaggc ggccaaggtg ttcgacatca cgagcagata 540  
gaaaaggcga agagtaccgc cccggaatgg ccaaaaaagg gaggagtcca gcc 593

<210> 182

<211> 446

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (318)..(431)

<223> Area matching *Drosophila* EST AA202196. This EST  
forms a 1942bp contig with AI108811, AA950029,

AA202752, AA440491 and AA697007.

<400> 182

```
atttgaacca tcccttttca ctgttctcgg tagaggggat gtgaaaaaac cagcgactac 60
atcaacaaaa gcgtgtgtgt gaatataaca atctcgttgt tccctagttt agttgctaag 120
aagcatttta ataattgtga aatcccagta ccgaggacga caacaaatgt agattttttc 180
aaagcacaaa caactgcagc acgacgttcg tcgcccttcg ggagcgggtg tattggtggt 240
ccgtgctggt gtgtttgtgc taccaccttg ttcgatttta atgtgttggt tctgtttttc 300
acatcaaagc tccgtatttt cgtgcggaaa gtgtaaatgg ccgtgtttta aatattattt 360
cggaatggtg tctccgctat ataatcaagc tgtttgcaac gttagcgttg acgcccacat 420
ttgagcccac ttgtgtgccg gaattc 446
```

<210> 183

<211> 553

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (83)..(319)

<223> Area matching *Drosophila* ESTs AI064123 and  
AA263284 (inverted).

<400> 183

```
gccccaaattg tagcgccctt gccactgcaa tttacccaat gttttatatt aaactgcggc 60
gcagtttgga actcggaatc ttacttttca caacgggcag gaagcggcac aatttttttg 120
caattttgcg aaccctgct ttcgatgacc gcttagcgcg cgtctccttc gaatcactgc 180
actatggatg ggattgatcc tgtccagcta tttacacatg ttcggttaca agagtctttt 240
tcggtgctta tgttgtaaa aataagcaaa aaccaaggag cattttatgg tggagtgggc 300
accgccatta atccacgcat gaagcgtgc cagaggtttt ttgggaaagt gtgggccaga 360
ctcttcgcag aattagtaca tgattgcatt ttcagctgat taccttaacg tgttggttgg 420
gtgctagcga ggagagcgga agggggttgt atcacgaaat ccggatatat aatcggaatg 480
aaatcgggat ataaataact tattaaactg ggattataat ttacttaaga acacttttga 540
gatcatgggt ggt 553
```

<210> 184

<211> 89

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(89)

<223> Area matching *Drosophila* EST AA441173.

<400> 184

tgccggctga aataaattcg attgtgtgcg cgcgcgtttg tttgtgtgtc ggcattgtgcg 60  
tgtgagtgcg cagacaacaa aaggaattc 89

<210> 185

<211> 414

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (65)..(414)

<223> Area matching *Drosophila* ESTs AA440852 and  
AA541034.

<400> 185

tgacagacca atttcagacg tatgtacctt catacatatt ctatacgtat gtatatatttc 60  
gtaccttctt tcgtcttaaa tcagcggatc tctgttttgg tttctggttt tctcaatttc 120  
ttgcacacca aaatcaccga tatttgtggtt atttgttaaa ctgttaaaca ctttagcata 180  
gacactttgc aatgctaatt attaaagcgg ttacaataaa ttgtaattga atttgattat 240  
tttagcggga tttgtgttag ctggctctat tccattcatt gaacaaaaat cgcgtctggc 300  
tttgatttac ccgttgtgct gcgacgaatt tcactttcga ctgcggaacg atttgaattg 360  
gatggatttg ggtttgtgga ggggcctatg taattcaatt caaattcccc gggt 414

<210> 186

<211> 131

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (2)..(131)

<223> Area matching Drosophila EST AI062640.

<400> 186

gacgccaccg aaaatcgacc ggccggaatt ttctgcacta gtgtgcaaaa agtttcattg 60  
gccaaacgag agggaaaaaa gtaaattgtct tccggaaaat gttatatcaa ctgaagatta 120  
tgaatgaatt c 131

<210> 187

<211> 536

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(77)

<223> Area matching Drosophila EST AA695507 (inverted).

This EST has sequence similarity to cytochrome C  
genes.

<400> 187

gtcttaagtg gtgaacacca aaaattcttt cgtaattttt cacacagcta tggatcagtg 60  
tgaccgcggg aaagtaagaa aaaataccac acgctgcaga aaatatgata ttgatacttt 120  
caaagtcttg agtagaccaa ataaaaacaa acaaagtgtc ctattgttat tcgtcgtaat 180  
aattgggaaa taaactctag cttaaacaat aaagttctta aaataataat aaacatatat 240  
ttttgttagc aaccgatata ccacatttaa aaaattaatg tacaacggtc accctacagt 300  
gtgcaacaat caaccgactt aagtgttggg aaacaccggc ggaacactgg gtatcgaaac 360  
cacaagaggg cgccacttgc gttgccgggc aacaaaaatg taaaaacaaa aaattttatt 420  
aaaaaagttt attggaatct gcatgaaaaa tgtcaagcaa ggccggtaat ctgctttgat 480



actcaaaaat gaacgatttc aaatatcgga cactacaaat gatgctcgca atgaag

536

<210> 188

<211> 589

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (89)..(251)

<223> Area matching *Drosophila* ESTs AA736186 and  
AA801973. Thses ESTs have sequence similarity to  
Thioredoxin genes.

<400> 188

gtctatccat tcgaaattca ccttcaccaa acgcgacata cacatatgca aaaagagagc 60  
gtatagcaat gagaagcgtg agcatcggag taaaaaatct ataaaagcaa ctgcgacgtg 120  
ctcatttttg taaaaaattt agctgtgctg caaagagctg cccgagtggg aattaagtaa 180  
cttttgtaca tttctaccgg ttccgtctcc acatctccca tccaacatgg tgtaccaggt 240  
gaaagataag gtgagtcact tcaaccggat ctatggacgc atcacatccg tcattctattg 300  
ggtaactcga tagcgctacc ctttgacccc tcagttccag ttacacgttt attttttcgc 360  
tccggacttt gaaaatatgg cattggaagc ggcattccaa ttagcctctt actttgaatg 420  
attggattcg ctacgctttt tgccatacgc tcgcccgcga atagaaggaa ctcattgttcg 480  
gtctagacga cgagaaagcg gagagcaaac gaagaaagtt ccgaatagca gcacagcgaa 540  
atggataatg atatcattcc atggaccgca aaacgggtct taacggaac 589

<210> 189

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(417)

<223> Area matching *Drosophila* ESTs AA697603 and

AA801716.

<400> 189

```
cgctagacca cgtaacgcca cgattttcgc cggatccacc gattcgattc gattcgccgc 60
gatcgtcagt gcctatatat acagttccca acggagccga gcgataaaga taaatgtgca 120
aaaacaaagc gcacttagat aaagatagcg aagttctccc atgtggaagg cacagtgcaa 180
gtgaagtgaac acgagaacgc agttttgaat aggaaatacg aaagtactca catatataga 240
gaacccgaga cttggagtca gaatgcaaat gtggcgagca taaagtcgca aagcgtgaaa 300
atctacgata tatacgagta tagtcgattc caagtgtcag ccaagtgaaa cccagtgtgc 360
agccgaaacc aaaccgaatg actatgactt ctacggtgct ccaacggccc attcaagcca 420
agccagagaa gaaggccttc ttcaaatega ccagcttctt gagagccgtt cacgatggcc 480
tggtccaatg agaactgcgc ttctctgcat cgacaacatc ggacttaaca gct      533
```

<210> 190

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(528)

<223> Area matching *Drosophila* EST AA950741.

<400> 190

```
ctctagcagt atgctgcgca agtcaaagaa acagccacag acggtggccg agaaggtcag 60
caagctgttg cccatccgaa cagagcgaca gcgcagagga ctcggaacttc gatgtggcca 120
cggggccacg tctggtggac ttcgaggagg aggagtacga cctgccggat gcccggagca 180
ccgacttttag gaagaggaac gtcaagctgc tctcgagca gaggaccgc tacaagagaa 240
agatcagcag tcgcaaggag ttggatgacg atgaggatga ggatgatgat gaacaagagg 300
tgtcctacga agaaagcgat gaggatgatg agaacttgac agactttaag cagaagttaa 360
atgctggagg agctgaagac tccgaggagg aaacggctgc tggacattcc gaatctggtg 420
aaggaagtga agagattgag agcaatttga cagactttaa aaaaaagttt gaggctggag 480
attttaagta tgatgatgat gaagaggagg atgatgactc tgaggaag      528
```

<210> 191

<211> 52

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(52)

<223> Area matching Drosophila EST AI063204. This EST  
forms a 887bp contig with ESTs AA697347 and  
AA201878.

<400> 191

cttccaagta cttttcacat attgcaagag cgatttaata tcgtaagaat tc 52

<210> 192

<211> 531

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(44)

<223> Area matching Drosophila EST AA441029.

<400> 192

gttcagagcg tgaaaaatac gttatatgct gcaaaagttg tgaaacgaaa cgtatccgag 60  
agatacaatc ccattgggag agcgagagcc aagcaaagtg cagtttccag aagcagatac 120  
catttaaaca tatTTataac ccaaccgaaa ccaaacaat aataaaggct gaaaaattcg 180  
aatacaccca aaaaaacaaa ttttccaaca actcaacctc gacgacgacg attcgcaaca 240  
caaaactattg ttggattaac atTTTTttcg atcaaggtaa gtcggtttac atatgctgtt 300  
ttcatttttt tttttatggc catcattaac actcaaaagc attccgaagg tttaagttga 360  
ctcttggett ttatagttgg tatgtagctg tcttgcagcc caaaaaccga caaaagttgc 420  
tgtcagtttt ggatgtgact ctggctaatt gactcaagct ggtgttttca taattaagct 480  
aatgaaccg accggtagta caattgaagg ttccgtagat acatatttca a 531

<210> 193

<211> 560

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(157)

<223> Area matching *Drosophila* EST AI114266. This EST forms a 1141bp contig with ESTs AA949325, AA735675 and AA391495, and has sequence similarity to GMP synthase genes.

<400> 193

```
agtgtgtgcg tgaggaagga aaacggggga ccgcaaaca cggatcgca atttcgtctt 60
aagacaaagt cttgcgctgc ttatgcacgg tattccacgg ccttgccgac ggacttcccc 120
gttctggaaa accgcagcca ggctaaaacg agagaagggtg agagtcgcaa tatggcgaaa 180
aagatccccg atcccagcca aatcgccatg cgggtgctgct ccgcccacaa ttccgaaccc 240
cgcccgttga attcagcaaa caaatgtat atttactgat gttttagaac tttgaatatt 300
cctctataaa agttgcacat atttcacacc ccaatgcatt tcattttctct ctggtccata 360
aaacattcaa aatgtattcg cgcattcgat ctaacaaaca tttattgctt tcgaatattt 420
aaaattttatt tattttctat ttcaagaata tcatatatac atacatacca tatttgcaga 480
acatttggtt acttcccagc taatttggtt agatatccca taattgcata taattcctat 540
tcgcaacgga cttattaataa                                     560
```

<210> 194

<211> 562

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(562)

<223> Area matching *Drosophila* EST AA951648. This EST forms a 1340bp contig with ESTs AA539581, AA802940

and AA263326.

<400> 194

```
atccacgcaa ggaaagctta attcgagcga aaaaaaattt acttagctct taatattttt 60
aaaaacaacg ccctcgctgg gccagtggtc ggttaactag ttagctgtaa gatgacgcgc 120
gtaacgagaa gtgaaatctc cctggacatg gagttctggg tggaggagct gtcgccggca 180
caattggcgt actacgagaa gattactaac gagcacaacg cgggaagggt tgcactaaag 240
aacgcggtta gcgccaacga gggcaaggag ctgtttaacg gccagggtgt ccaggcctac 300
tcctttaagg gcaaagtgtc gcaggagctc aaggaggcta cgctgcccaa aaaaccaccc 360
aagccgacgg actctccctc aacacccgcc gcccaaagcg gtggcacagg gcgggggtcgt 420
ggcccgccca ccacgacaac catccaacat cgctacctg gagtctctcg atgagggaga 480
cgacgatatg ccgctggcca agcgactggc gctgtctgca ggcaaaaaag cagtggccgt 540
ggccaatgca tcttcttggc ca 562
```

<210> 195

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (26)..(137)

<223> Area matching *Drosophila* EST AA391135. This EST  
has sequence similarity to human SEC61.

<220>

<221> intron

<222> (138)..(359)

<223> Probable intron in gene represented by EST  
AA391135.

<220>

<221> misc\_feature

<222> (360)..(422)

<223> Area matching *Drosophila* EST AA391135.

<400> 195

```
gttcattcgg tttttgaaat ttgaggcggt cgctgtgcag tgaaaagtga gactttctac 60
tgttcgcgta gaaagtgata accaagccac ccactcagtg cccagactag caacacaagt 120
ccggcaaaat gggaagtaag taaccgtcat cgccagacat cttccccaaa atcgggggagt 180
gcagcggttt ttgtgtgaag tgccgccctt gcaatgccgc tcgcaccctt gtgcgtcatt 240
gcttacgtat acaaaaaaga ttccggcgtgc gccgctcggt gtgtccgaaa atcgcaatta 300
attaaaaatg gcctgagaaa cgtaactaat tcggttgcct taattcacta tttgcagtca 360
agttcctggg aagttatcaa accgttctgc agtatactgc cggaaatcgc aaaaccggac 420
gcaagggtgtg tataaaaccg taattaagat gtaatcaaag tgtagctagg tatcccaatt 480
gctgctgtac catggaatgg tcgaatttcc caacaattgc ggctttct 528
```

<210> 196

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(124)

<223> Area matching *Drosophila* EST AA696531. This EST  
has sequence similarity to *C. elegans* pro7 gene,  
Z66519.

<400> 196

```
ggccagtagc caagtaaacc gcggcgcggt ataatacatt ttagtaciaa tctcactga 60
aaaccgcgca aaatggccga ggttgaagcc gtgcagataa ttgcagagtc tttgaagcaa 120
caggtaagag gatcacctgg tcgtccagtc atttgtccga cattttggca ctgcactttt 180
ctgcacttgg gatattgccc aactactata tatctcattt gtgaacgggg gccgcggaat 240
ctgtggcgct ggcaagaaca atggagtggc ctcttatctt gaggcacctg tttgttgtgc 300
aaagttcaaa aacacttggc aactgtaagt gtggttgggt ttgttttgcg ggtgagaatg 360
tcccccgatt actccgggta ataaaagacg gagcggattt gataaagacc atgttccaaa 420
ggtttgggac caccgaccaa accaattggc gcttgcagct gcgaatatcg cgggggggca 480
gaataaaatc aataatactt taaccgggat tccgggcaaa tcacttaaga acggc 535
```

<210> 197

<211> 549

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (442)..(549)

<223> Area matching *Drosophila* EST AI124332.

<400> 197

```
gtagcgcggt tgcacttgta atccgctctc tcacgtactc tctctctccc gctgtctctt 60
tttgccgcag cgaattacat tggcgcgcgc atttttcaaa tgttttttta cggcgaaaat 120
aacgattttc gtcgctgctt gttttgtgtg ctgaaaatat acattttatg actatgtaca 180
cacgcacagg aagttgagag gggatttgga tgcccttgat caaggagatg tgtggggttg 240
agttgggcgc gtaggaccat ttcgctccgt aattctccct aatatccttt agtttgtttc 300
tcagattaat atcaaaaatg cataaataat agtgacgggc cccttatttc tgttcaataa 360
acttgcttgt aatacagtaa atcatcagcg gaacaaaaac caaaggaact ctactaactt 420
ctctcttttt tcgcttcag gccaaatccg cagaatcaaa gaaggccaag aaggccgcgg 480
ccgccgatgg agattccgat gaggaaaagc tctggaggaa atcatcgagg gcgacagtga 540
aatcgaagc
```

549

<210> 198

<211> 667

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (52)..(382)

<223> Area matching *Drosophila* EST AA949873.

<400> 198

```
gccggcagaa aaggaagaag aagaagctca taccattgcc gattgctgtc gcgttgcgct 60
ttcttcgttt ttttcggctg ccgaaactta tattttgtcg ttgtaatatt ttgcataaat 120
```

atataaatta aaacgcgtga cggaacaaca aacaaataac gaagacagca aaataaaagg 180  
 gcgaaaaatc gaaacgaaaa cgagtcgaat tactttcaag tgcaaatagt gtgcgtgggc 240  
 gtgagattgt gtgtgtgtgt tgtgtttgtg cgactgtgag tgcgtgtgtt tgtgtgcaaa 300  
 aaaaaacaga acgtgcaaca agaagcaaga agaagagcca tcagcagctg acaaaccagc 360  
 aataaaacga aatttcaata agtaagcaac atttaggcaa agctaaaatc caaaagcaaa 420  
 tcgaacaaga ggaaaaacta cctttggaag ccccgcaaag cagacgtaac aatgggcaaa 480  
 agcaacaaat ttgcggctct cagctaattg aaagcgaatg gtggtggttt agagcaatgc 540  
 actcgataaa aaatactaaa gcaatggcat aaaaatacaa attagaacgg gcagcacagc 600  
 agacgaaaac catattccac tgggaaaacg aaaagtcaaa tgagagaaaag agagagagac 660  
 cataatt 667

<210> 199

<211> 498

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(498))

<223> Area matching *Drosophila* genomic sequence AC006562  
 (1848-2353). This sequence also matches EST  
 AI133902 which has sequence similarity to  
 phosphate transporter genes.

<400> 199

gtttactcta aactcgtaac gatcccaaaa attcgacatt cggagtgcta agtgctcgga 60  
 tttttgaacc aaaacataat tgtgaaaatt gagaaacttg cttagtgtca tttttggatt 120  
 tacacattcg gatttgtact gaacacacat ttctggcgat taaaaggtaa tggttttaac 180  
 ttactgacc tatctatcca tctattctat atctatatgt taataacggc gtgcaacttc 240  
 cgttcaatat cgggcctcc tttctatttg ccacttttct atgaacacca cttgcagttc 300  
 aatggatttc cactagtaca agtattactt aattttcttg cttaatccga tttgcgtgca 360  
 ttgaactttt catctttggg tatttttccc tgttgatgtt gtagtcgctg gtattggttt 420  
 ttatctttcg tttttttttt gtgttcgact ttattttgca ccaacttctt gtggttgaat 480  
 ggtttttttt tttggttc 498



<210> 200

<211> 550

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(550)

<223> Area matching *Drosophila* Genomic sequence

AC005129. EST AI403609 matches 420bp 3' to  
NPS0269.

<400> 200

gtctgcagtt cgcgggcgctg catttttccg ggatgttttc ttttggggag gaagtataca 60  
atctgtatat ctgatatcg attaagcata taagttatcg gatgcagtag ctgccaggg 120  
gtgacatacg ttagtcaaca tatcgataac attagtagca ctttaccatt attaacaatga 180  
ggggattttt ttaaattaaa ataattttat ctttgaaata atttatgtac ctaagtatta 240  
ttttttttgg gaaataaaat atacaaaact ttgtcgccga ttttttcttc actatacaat 300  
gtttacatat attagatatc aacctatttg tcttgataaa aatctatacc ccaccaaact 360  
aaagatctat ttacaaaaca atttactcct cgtcacaaa gagtcctccc agttccaaat 420  
cttctccggc agttccggtc aactgggtgt gctctgaata ccgtaagaat tttccgctgc 480  
ttttcgaact ccagcctgct catccgactc ggcggcgatg tgcccggcgt ctgggcccgtg 540  
tgaaatgggt 550

<210> 201

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (299)..(375)

<223> Area matching *Drosophila* EST AA391470.

<400> 201

ggcaagggaa ttgttaattt tagtacattg cttagcactt catttaaacg cgcaaattgg 60  
 tgacacaaat atcgatttat taaggtttga actatttaat ttgtcgcgcc tttcagcttg 120  
 caaatagaag tatttacttt agacaatcgg atgacgcttt tgatttcgca tttgtttgcg 180  
 actgtgtgtg tgcgacgagc cttctaattc cgacaaaaag aagaagagca ccattcggtg 240  
 gcctaatttg tttcacttct ccggaatcaa gcttttccga tgcctgcttc tattaacctt 300  
 tatttaatat gactcgccgc gttcgacgat atttttgcag tagttatttt ctttttcgtg 360  
 cttgtgggag tgcacctctt ttatgccgcg gtttgaagaa gaagcacaac gtagtaagtg 420  
 tttggaatgg actgcggaat ttaagggatg ggggaatggcg taactcttgc aatcgatagc 480  
 tcgataggtc cccttttcgc gtttcgcaac acttgggccc ggatttt 527

<210> 202

<211> 77

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(77)

<223> Area matching *Drosophila* EST AI062013. This EST  
 matches *Drosophila* gene NURF-38. Accession  
 number AF085601.

<400> 202

attcagatag aacggaagcg cacgaaatca cacgagatgg ctctgtacga aaccgttgag 60  
 aagggcgcta agaattc 77

<210> 203

<211> 562

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(76)

<223> Area matching *Drosophila* EST AA696584 (inverted).

<400> 203

```
ccttggtat tagtttgcaa atttccaagt aaatacgacg aatttggcga atcagcgaat 60
cactcgcttc ccattgctgcg gcacacactc acacgctacc acccacacga acgcatacat 120
atgtttgtcg ccggcgggtcc gacaacgctg cggcaatgca actctgctg gccacttggc 180
taattttggc tatttaccag ccaactactt tatagctagc tgcttatatc ttttcttttt 240
gattgttcca gtttaataat aataatataa tacaattata tttagaaatt taaatttttc 300
ataaattggt ttaaatatgc ttacgatttt tattcttatt tatttcttaa aatattaggt 360
gactgggatt ttagcaataa aaacaagcta tataatagca cagcctgcat atgaaagcat 420
ctctgctcgt gttttttgcc ttgactgggt ggcaactccc ttggttttct cggctgacga 480
aaaatttgac ccgaaataaa tcaattaaat tgaaagtgga gtgaaaagca aattccagta 540
aaaagggtgcc aggtgggagg ct 562
```

<210> 204

<211> 416

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(319)

<223> Area matching *Drosophila* EST AA439099. This EST forms a 1132bp contig with ESTs AA9493425 and AA940848. ESTs have sequence similarity to GMP synthase genes.

<400> 204

```
tttcggcttt aattcgcgaa aaaactgcag gaaatccaaa aggaaagtcc ctggaagcgg 60
ccataataac gcagccggtg aaaaccacag ggatttcac gccagctgtg tcgagcagcc 120
ctggatactc ggaaaagaag ctgcagcagc cgaagaaatt ttgagtgtgt gcgtgaggaa 180
ggaaaacggg ggaccgcaaa caacggatcg cgaatttcgt cttagacaa agtcttgccg 240
tgcttgctac ggtattccac ggccttgccg acggacttcc cggttctgga aaaccgcagc 300
caggctaaaa cgagagaagg tgagagtcgc aatatggcga aaaagatccc cgatcccagc 360
caaatcgcca tgcggtgctg ctccgcccac aattccgaac cccgcccgtt gaattc 416
```

<210> 205

<211> 550

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (21)..(377)

<223> Area matching *Drosophila* EST AA695424.

<400> 205

```
gcgcggacgg tcggtttttg taattttgcc ggctaacaca cctttcgaac gacgcgtaac 60
ggtggccggg ccattaaaat cgccacaacc acgggcaatt cgagtgcggc gcgctaatta 120
tgcaaggctg agaactagcc acaaaaattt ggggggcagc aataaaccag ttgatttaaa 180
ctagtttgtg agtgcgtgtg aaaaggccaa ggaatttggc cgaaagtagt agacaatagc 240
taggaggctg cgactgcgga ggattcaagt ccagaagttg tccgaccagt ttccggtgcc 300
cgtgtgctcg tgtgtgtgtg tgtgtgtcgg gattacttg attacctttt attttatggt 360
ggccggtgcc ttcgaagcgg agcgaatgag ttggagcagc tagtggccgc agagagatca 420
agagtgcgag agccagcgag agatgccctt cgtcagcgcc gtggtgcaac ccgtcaatgt 480
ggcccaagcc acgcggccag tttggggccac gcattcggac gattccactg cacgccgggc 540
aagtgccgga
```

550

<210> 206

<211> 590

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (152)..(590)

<223> Area matching *Drosophila* EST AA440949 (inverted).

<400> 206

```
caccaccgga tctggcgccc gatctttggc gaagcgagct acgtgttaag ttctcggcgt 60
gatgactata acaatgagac agtttactta tctggcttac acttcaatag gaaaacaata 120
```

cttttatata gcttctataa cttcgggggtg cgataagaac atgaatacag atacacggat 180  
 tgcaacagta cccaagccac ttgtttttaa caaatacagg ataatgggga gtaatgtaag 240  
 ctattgactg ggttacaatc aggggtctga taacaatcaa acattgtcca gttgcctttt 300  
 gcgaatatca atgaccactc acgagttgca actgataacg attatcgccg cacaatgcag 360  
 tgggtgggta tttcactggg gggaaactttt gggtccttag aaccagacg gattactcaa 420  
 tgaatatagg cgatatgttt gggtttacag cgaaagtgct attaatgtcg acccgatatgc 480  
 tctctttcga tgtgccagct ctctatttgc gggaatgaat gactatttta tgggtctggc 540  
 cgcgctgcta caatgctgca ttgctgcagt gggacatcct ttgacaggcg 590

<210> 207

<211> 312

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (132)..(312)

<223> Area matching *Drosophila* ESTs AI062455 and  
 AA440915.

<400> 207

gaacgcacaa tcacaagcgc cgctcgcgag aacgagaacg ggaactcgaa agaacggaga 60  
 tcgctgggtcg gagaaccgtg gaaccctggg aaccgtaacc gtgaaagtgg ggaatcgaag 120  
 atagaacgga gaggggtgta ggccgattcc ctctccccac tgcccgttga aattcagaat 180  
 actaagctct cggttaaacg cggcgaaaaa gaaagcaagc tctgagcggc tgaaaaaaaa 240  
 atgaagtga ataaaaactgg ggatcgcggc accagcaaca agtttttagtg gctcttcttt 300  
 gtgcgttttc gg 312

<210> 208

<211> 311

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (68)..(311)

<223> Area matching Drosophila EST AA816432.

<400> 208

```
ctcgtgtggc tctcatttgt ttgatttct cggttacata ttacttaact aattagaatt 60
tattatgaat ttttcattga atttcacaac gagaaatcta gtgccacgac tgcaccgatt 120
caccagcaag attgccgtgg atgttgaacc agctgtggtc tctgccctgg aacatgccac 180
actgaagccc agaaaacatc ccggagtagt gagaccaat catatggaac tgccgaaaca 240
attgaatgat acgcttaagc gccatcgtgg ggggatcatc ccgtcaaaaa actaatccac 300
gatggccagc c 311
```

<210> 209

<211> 359

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(258)

<223> Area matching Drosophila EST AA979191.

<400> 209

```
tggtgaacaa tatttttaaaa acatccaggc aggtgcttta tcccgtggca aggactttca 60
gccgcagcag caaccacggc aatgtgggga ccgaagctgc tgcgacagtg ggcgcacctc 120
cggcgacaag atcaccctt attctgccgc aagattacac agattgcttg ccggtgagca 180
ggaacacggc gcgccaggca tggattgaga acacggatgc tgtggcggag cgaaagggtg 240
gcctgattga actgctccgg gatgtctttg ccgccagcc gcgcgtggac atcatcagg 300
aagaatgttg gaagtgggca gagcaagtat cgttatgtaa gcatggcgca caccaaact 359
```

<210> 210

<211> 415

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (2)..(318)

<223> Area matching Drosophila EST AA391495.

<400> 210

```
tttcggcttt aattcgcgaa aaaactgcag gaaatccaaa aggaaagtcc ctggaagcgg 60
ccataataac gcagccgtga aaaccacagg gatttcacgc ccagctgtgt cgagcagccc 120
tggatactcg gaaaagaagc tgcagcagcc gaagaaattt tgagtgtgtg cgtgaggaag 180
gaaaacgggg gaccgcaaac aacggatcgc gaatttcgtc ttaagacaaa gtcttgcgct 240
gcttgtcacg gtattccacg gccttgccga cggacttccc ggttctggaa aaccgcagcc 300
aggctaaaac gagagaaggt gagagtcgca atatggcgaa aaagatcccc gatcccagcc 360
aaatcgccat gcggtgctgc tccgccaca attccgaacc ccgccggtg aattc      415
```

<210> 211

<211> 89

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(89)

<223> Area matching Drosophila EST AA441636. This EST  
matches ESTs AA820540 and AA817484. Evidence of  
alternative splicing.

<400> 211

```
gccagaagct tggtgctttc tccactcctc tttcatcctc gtcagtgtgtg tgagtgtgca 60
agtgtatgtg ttgctaggc ttagaatc      89
```

<210> 212

<211> 488

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (59)..(488)

<223> Area matching Drosophila EST AI295363.

<400> 212

```
caccggacgg ttgaaaagtg ttctgtgaaa aaatccaagg aaaattttgc ttgtttcaga 60
ttttgtcaag tcatggagct gccttcaatg gtggagcggt cgggtgatcg cttggtggtg 120
cgcagcttgg ttagtggtgc tccactttat cagtcactta ttgaggcgag agcaggtgct 180
gtgcttcta tgtcccaaag cgtgcagccg ctaataggta aggacttttt ggagcaacaa 240
ctggagcagt ataaggcgaa taactttatg ttccactat cgatggccgg gtttgtttac 300
gcagactctg caccaccggg ggacttgccc aaggaaaata tggagaactc actgccagat 360
ggtaatccgt gcaacaacaa caacgacgat gagctgccgc agtgcaagat accggcgtaa 420
ctacagctgc aaccagtgcg cattcttcac gcaaaatccg cgcagtcata tctcgcatct 480
gcggggac
```

488

<210> 213

<211> 170

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (51)..(170)

<223> Area matching Drosophila ESTs AI114059 and  
AA941565.

<400> 213

```
cgcgacgtaa ataccagacc cgagcggaca ttttttattt gtggagcgcg caacaagaac 60
gagaaaagaa accgaaacgg aaagcagaca aaaagagctg ctgccagtgt agaatcgcaa 120
agcaaagaaa gaagcaagtg cgtgtgtttt taaaccgaag ccgagagaat
```

170

<210> 214

<211> 480

<212> DNA

<213> Drosophila melanogaster



<220>

<221> misc\_feature

<222> (3)..(355)

<223> Area matching Drosophila ESTs AA801691 and  
AA441008.

<220>

<221> intron

<222> (356)..(442)

<223> Probable intron in gene represented by EST  
AA801691.

<400> 214

ccttagcggc gttccattca aaaactgcc aataagatta aaactctgga ttaaatggcg 60  
ttatcagtcg aaattgaaag ggtaatggac cagggcaact gcctgatgcc cgacatcaat 120  
atctgccaaa gcgacttggc caatcccacc gagcccattg tcaccaagat catggtgcac 180  
tatctgcgga gtttcggctt tcgcctggag ccgccctata aaattggcac cgaactcggg 240  
cactcgtcgc gggaggcgcg cgtctttctc atccgagtgt gccgccaagt ggagcgcac 300  
gtccagatca gctttcccaa caagacctac agctatatgg acataattaa accaggtgag 360  
ccggcagccg gtcttaagaa cattaatatgt aggaatttag atacaataag ctattattat 420  
taaacaattc tctaccatta gctggtaaaa aaacgctcgc catctgagct acctttttta 480

<210> 215

<211> 471

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (378)..(471)

<223> Area matching Drosophila ESTs AA950084 and  
AA978669.

<400> 215

agcctgccag taatgccggg gtggattttt gttcttgcct ctttttcaat tcaacttcgtt 60  
 ccattgcatt ttagattgat gttgttggtg ttgctttatt cgtttccttg cgggagaaca 120  
 tttccaattt tcatcctttt cgtgggtttt tctcaaattc ggggttttct tttcctcttt 180  
 tcgcgtcacg tacgccgttt gttatatccc tctctctcgc gctcttgccg tcttgccgctc 240  
 tcgtgctctc tcgccggcat gagcgcgcgc gagcgagacg gcggacgcag agatgagtga 300  
 aacagctgta agcgtcgatg agtataaaag gcgggcgcac cggcgagaaa ttcatagtag 360  
 cttcgaaaaa aacactgaca cagtacacaa gaaaacagac tctcgcagcc agaaaatcaa 420  
 atgaagcagc agcagcaaaa acgtgcatag ccagactttt tccactgcta a 471

<210> 216

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (20)..(236)

<223> Area matching *Drosophila* EST AI062945.

<220>

<221> intron

<222> (237)..(291)

<223> Probable intron in gene represented by EST  
AI062945.

<220>

<221> misc\_feature

<222> (292)..(439)

<223> Area matching *Drosophila* EST AI062945.

<400> 216

gtgcgaacta tacggcttca gcacgcgctg ggcaactact ggagcaccca ggcggacctg 60  
 ccggttcggg tgccgacggt gggccacgcg gacaacccca aaccaaagcc gacatcgagc 120  
 agcggagcaa gtgcatcggc atccgctgct gggggccacca agagtgcgga ctcagccgctc 180  
 gctacctcgt cagcttcggt ggacatcgca ccggcagcga ccaaggccaa gccaaagtaa 240

gcgataagag ttgcaagggt cgcgataaat agtaatatat ttcctctcca gattcgcaac 300  
gcttagcgac atgtcgaagg agtcgtctag tgacgatgac cagcaggcct tctatgccgg 360  
cggctcagat cgctccggtc agcaagtgtt gggcccggca agcgcaagaa cttccggggag 420  
cagctcaccg acatgatgc 439

<210> 217

<211> 312

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(312)

<223> Area matching *Drosophila* EST AA440345. This EST  
forms a 2293bp contig with ESTs AA201536,  
AA539993, AA942332, AA979174 and AA202096 and has  
sequence similarity to Human cleavage factor gene.

<400> 217

ggccggcaaa ttgttaaact ggctgaaatt gttaataatg ttttaagaaa ttgcgacacc 60  
aattaaacca ccgcaatgtt ttcgatgtgc aagcagacgc actccgccac ggcggtggag 120  
ttttcgatag catgccgctt ctttaacaat ctggatgaga acctggtggt ggcgggcgcc 180  
aatgtactaa aggtgtaccg gatagcgccc caacgtggag gcgagcccag cgtcaaaagc 240  
tgaatcccag cgagaatgcc gtctggcgcc caaatggcg actgggaaat gcctagccac 300  
atatacgtc ta 312

<210> 218

<211> 501

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (10)..(501)

<223> Area matching *Drosophila* EST AA696930.

<400> 218

ctgctgactg tcaaatgccg gcggccttag atttttcgac tattttcaat aaaattgtga 60  
aataccagtg aaaaattaaa gcaataaat aaaatgcagg agcaggagat ggaggtggaa 120  
gtgggggacc cggcaaaggc gtcgaatttg ctgcggctca tcaagcagct gctgctggaa 180  
aaagcttacg atggcgtgcg gatgttggtt caaagtgcc aggaatcgga aaagaacact 240  
cggctgctgc cccacatagc cattgggacg tataccttga acgtgtgctt ggaaaacatt 300  
tccgaccgag gtgaactccc aggagccaga actattcgac tgctctgacg agctgctcaa 360  
gctgctggcc caagtacgcc cactgcatg agcttatgct ggaactgatg gaacgcttgg 420  
aagagagtta gcagattcaa atggtgttcg gcgcctatct gcggccttac aaagttgtgc 480  
tgcaacgaca gggacgcaca g 501

<210> 219

<211> 586

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (8)..(437)

<223> Area matching *Drosophila* EST AA440135 (inverted).

<400> 219

ggtgcgaccg gcatgaaagt gacgaccggc tgcaatcatc aagccaatgg cgagatcggc 60  
cactgcattt ttcaccaccc cgggagtgtg gcccaatggg attcccctct tctggaactc 120  
cggaatatcc acaaaatcga ttccggagga catggtgctc acgcaacgca gctgggatcc 180  
agcagcatcc aggattccgg cattcagggg ctggtaatgg gcccaataga tggcatccac 240  
gccgggcacc ttctgcagga tctcatccct cgagggcggc acactctggc agatgatggt 300  
ctccgctcca cgggatcgga gcagttccag agccggtgct gggacatttg ggtgcgaaat 360  
cagcacttta aaagccctgg tcgcacgaga catttcgggg gaaaatatag cacttaatat 420  
caactagtag cggcgaattg caaggctgaa ctaaagtggg aaattttcca aatgaccatt 480  
caagcttttt ctgtgccccg ctcttaagct ttaaagggt ctcttaagct ttacattttt 540  
taatttggtc tcatcttttg gaaattcaca ttactatttt ctggcg 586

<210> 220

<211> 176

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (75)..(157)

<223> Area matching Drosophila ESTs AI063979 and

AA802032.

<400> 220

gaaggaagta agtagcaggc gtaattttat gtttcataag aatccgattt aagaatatat 60  
ctcaacaaaa ccagcgcgat ggcattcggt gactatccag ctgagtacaa cccaagggtg 120  
cacgggccct acgaccccg cgcgttctac ggcaaagggtg agcagggttac gtaatt 176

<210> 221

<211> 169

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(144)

<223> Area matching Drosophila EST AA699194.

<400> 221

cattaaccag aaccaaccaa tgtttgatct tcttatacgc aatataagcg atacgttttg 60  
ttttaacctta cattatttta tgaactgatt attaactgaa atggaaatac attgaacaca 120  
tctagcttgt taaacgtata atcgatcctc catgtaaaga taaacgctg 169

<210> 222

<211> 546

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (507)..(546)

<223> Area matching Drosophila ESTs AA441233 and  
AA392152.

<400> 222

```
caagctgggc gacttaaagc cgcataacc gataactgaa gtgggagagg taatggcact 60
tgggtctctct aaaacttgct gcggtatttg gcaggactag ttgggactcg aaccagggcg 120
tgaatctttg cttgccaac cggtaaacct aaccggttgc taaagtgggc caacattaat 180
aatatctttg ttgaatgttt cataaaagct attttaatat aaattcgcat cgttaccgat 240
tcaataagggt ttagtaaattc attatatttc tgactccata ttgatttcca acagcaaatt 300
aattaactcc ataacttccc ctctcccttt ggagcaaagg atgtagttaa tatcttaaca 360
tctaaacttg tttcgttttt ttattcaaat aggagttata ttaaataagaa atgtaaaaaa 420
caaagcaggt tttaagaaaa tgatgtcagg agatttgaac tcctactcat ggtccactct 480
aatccgcagt ctttgcaatt tactgtgttt ccaacttaac gcccccaagt taatagccgt 540
aatcat
```

546

<210> 223

<211> 474

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(79)

<223> Area matching Drosophila EST AA438352 (inverted).

<400> 223

```
gtaaataaaa cacaataaga ttgcttctga aaattatctg gaaactcaga gctccgaaga 60
gacgatgtga acacgacaag ccaactccggc agactgaccc aaacaaacgc cggcatttgc 120
aataatatta ttgtctaattc ggtatatata tatcatataa gtaaccattg atgtaacata 180
cttttggttg taaggaatat atagttgaaa agtaattcag aaaacatgca ataactataa 240
tttattaaat attaaagtat cttgctaaga ataattgatg gcaaatgcgc cttttgccag 300
agccatagtt atatcatatg cgttttgtat tctaaaatat caaaccaaat aagatgaagt 360
```

taatatattc gtagtacttt aaatcctgac ttacacgtca cttgtcgtct gcttagttgt 420  
aatattctaa atcttttgga ttaatcagtg cagagttctc aggatgacct acat 474

<210> 224

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (480)..(534)

<223> Area matching *Drosophila* EST AI455428.

<400> 224

ttgatgctgg ttgtttaact tccatacttg tctctctcgc tttagctctc tcttaggagc 60  
cccaactaac actaacagcc ggggtgttcgt cccctcttta accacttttt ctcttactct 120  
ccgtctctca ctgcgaaagt gcagcgtgaa gtgttgataa ggggcacggc gggggataca 180  
ctctccggga tattgcgctc tctattgggg ctctcttaca ctctcactac gcgttggact 240  
ttcagttcat tccatgtgca aaatcagaat ctgatatctg aaatacaaaa atgacaaaact 300  
attgtgttta gttttgaagt acttatecta acattgatta attttgcata gatatgcat 360  
tcatatactt acatttttat atgtttgtac gctatattca aattttaaat accgacaatt 420  
tcctgatttt actttacgct acgtgttgct tgaaaagaac caataatcga ttgattgtta 480  
tagtttgtaa taaattcgct ccgcaagctt ctttatttaa gtgaccaatg aaca 534

<210> 225

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (11)..(190)

<223> Area matching *Drosophila* EST AA246916 (inverted).

This EST has sequence similarity to Mitochondrial  
import receptor genes.

<400> 225

ggggattctt acgctcacgg actttcttct tgtactcggg atcgctcggg cgcttcttgt 60  
cgaattaaat gcattatcca ataaacagag ttccagctac tcccgtgca atgccgattg 120  
cagttttgtt catttcaatc atattactac ggaaatcctc tgtattaact tggctttatt 180  
ttacattccg catgtgccat cgatttacat aaaacaaaaa tcgatatcgc ctacaactac 240  
tggtgtttca tggtttttcac ttgttttcgca ctaatttgaa acggcggact ggaacactgt 300  
tttctttttt aaattttgct aagggatatt tatttaattt taagtaagag attttaaagt 360  
atttttttta gtttattcag aaatactgtg ggatcaagtt ataatacgct aagaaataat 420  
cgtaagctca cttcttgtat tatatttatt aacttgcatt attcgcttaa aatccccctat 480  
cccccaaac taatgttttt aattttc 507

<210> 226

<211> 376

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (233)..(348)

<223> Area matching *Drosophila* EST AA392258.

<400> 226

cgtgagtgtg taaaaaatac aggcagcata caaaataata atattgaaag cgatacaaca 60  
acaaaggccg tcccgtcgaa gacgaaacgt ccaaaacgga agaactggag agcctgtcca 120  
gttaattacg gagcacaaag tagaatcgaa cagcaaaggt gagagagaga gtgaggaggg 180  
ataggggtca acctggctct ctgcgaaaga agacgggggc gaggagcggc caaaatgatg 240  
atgatggaca ccatggacac ctgcgaatcg cagccgatgg acgtggctcc ggccgtagca 300  
gtggcagcca cttcggggcg agctcttggg ggactttacc gctgccattg gtgaagcatg 360  
gcggccaccg cctaag 376

<210> 227

<211> 487

<212> DNA

<213> *Drosophila melanogaster*



<220>

<221> misc\_feature

<222> (1)..(41)

<223> Area matching Drosophila EST AI296848 (inverted).

This EST has sequence sinilarity to Mammalian

40KDa V-ATPase subunit genes.

<400> 227

```
gaattcacac gccaggcaac ttttaagtga aagcagaaat tgatagatgg aacatgcggt 60
gataggtatt tctcggatga actgattctg atataaatac taaggattct agatgctaaa 120
ataatattta ttaagctaca aatatattta tatataatat ttaaatttc ggtggcggta 180
tctaccgatg cacgctagat ggcgctaccg atggtgcaag gctgccattc gtttatcctt 240
tttgacaata tggcagcgct ctaacggttt tttaaatttt aactttaaat ttgaaaagat 300
attatttggt tggtttggtc gttttaaagt gcatccaact agattatttt agttataaga 360
aatgcacct agttaagct tgctatttga atttcagata gctattttatc ggcccattct 420
aacgcaattt ccgcacatgc gcctggagga tgctgtacgg aaatacctgg tgctctgggc 480
catgatg                                         487
```

<210> 228

<211> 354

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (255)..(354)

<223> Area matching Drosophila EST AI388389.

<400> 228

```
tctactgacc actcacaaat ccggactgaa cactaaaaac tgaaaactga aaactcggac 60
tcgggcgcgt aaggagtcg gtcgtcggga gtcggtcgtc tttgttgat cttgaaactg 120
aaattccaat tgttgattta tctctcggct gctgcgccgc ggctgcgctg ctgcagcgca 180
gtcccactcg atttgaccag cgaccaagtt tataaaactt tgagccaaaa tgcagcggcg 240
cacagttggt accaaaacgt tgcacgcgtc gtggccctca tcaaaacaaa aaaaaaata 300
```

taagcgaaaa tgaaaacgaa attcgggttaa cgtccacaga agctgacaaa aggc

354

<210> 229

<211> 471

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (335)..(448)

<223> Area matching *Drosophila* ESTs AA441471 and  
AA540182 (inverted). These ESTs have sequence  
similarity to Mammalian RHO GDP-dissociation  
inhibitor genes.

<400> 229

gtacgaacca tgccactttt ttttcttctc tttttttgat aaagaaatgt gcacgaagaa 60  
tgttaaaacc ccagacgaat gaatcacaca caccagctca cacacacaca cactcacact 120  
gaggccggca catgaatcgt cactgatttt caagtagaat ttttgggagt gggtcttggc 180  
ctgcagtcac ccaactacat acatttgcta tcaatgccag cttgtattaa attaataataa 240  
taatattata aatatttttt ttatgtaaaa tgcattggaa ggcaccgcac tcacacacac 300  
acacagttgc aagttggcaa cgacgcgcac tcacctttta atatgcgaaa ttaatcaaat 360  
agtacgatct ctgaaaatta atcactgaaa agttactgta tgtttatatt tttaacaact 420  
ttttgaataa ctaacttttt taaaccaagc caataatata aaataagaat t 471

<210> 230

<211> 480

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (22)..(242)

<223> Area matching *Drosophila* ESTs AA439855 and  
AA567284.

<400> 230

actacaacca aacaaatatac taaaagtga tgacaagtgt gaccgcgggc gaaccgttaa 60  
aatatacgaa gaacggctga cagggctggc gagtgcattg gcacagtttg tgactgaagc 120  
cagaaaaaat actaagcgtg actaaaatta gttcagtgtg tacatgttaa aaattactta 180  
aatatTTTTg gcaatataag tgaaaacaat acttataccc gcacatcatt tacagtccta 240  
ttgacatttt aagttgtaaa tatcgaaact accaaaacga aatatttggg aaattatgaa 300  
gccctgacaa ctctgtagtc gataggcaaa agagctcgca ccatgagcct atcgttctca 360  
gctgttttga acccaaaaca aaggggaagg actatcaatt ggaaatgttt ctgggtgagga 420  
ataataagtt ctgaagaaat gcaaaatatt aaaaagctga acggtccagt tcatccagcc 480

<210> 231

<211> 625

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(141)

<223> Area matching *Drosophila* EST AA941606 (inverted).

<220>

<221> intron

<222> (142)..(396)

<223> Probable intron in gene represented by EST  
AA941606.

<220>

<221> misc\_feature

<222> (397)..(446)

<223> Area matching *Drosophila* EST AA941606 (inverted)

<400> 231

ccaaaggcat ccgatactcc cgaacttatg cgaaaaattg tgtcaaataa aaatttactg 60  
gttcgtttat tgtggcccgt gtgaattgtg ttaataccgt ccgactcatt gaaacctttg 120

gaatattcca agcttaaaac acttgaatag ttcgccgtca acatccaaaa aaagattata 180  
 tacttttaggc tcatgttcac aaattagata tcattgtaac aaatggggggg atatgtttgt 240  
 gtttatggga aacttgatca catcaaaaa acaacgtaac gagttcaaaa cattcttaaa 300  
 cacaacaaaa catttgcaca actaatcgt aatactcaac acaacattaa caaggtttct 360  
 gtagatacgg cttaagaata aataagagtc tgtaactaat taatgtaaca taaaatatgt 420  
 actaagtctg atagtaatgt agcgtacgga tcgcttaccg ctaataccaa atgtgagagt 480  
 tagtcgcagt gtggccacgt tacactttct acctgttgac actttcatgg tcaagatgtg 540  
 tccgccgtcc acccagtttt ttcactttcg ttataaaaat cctacgaaat tatatttcaa 600  
 cctttctaca cgcctttttt ttgaa 625

<210> 232

<211> 435

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (209)..(435)

<223> Area matching *Drosophila* EST AA392324.

<400> 232

aaaatactat cgtgatcatc tcccactcg ctctaccca ctgcctaaa ataatgggtgc 60  
 catcaagagc gcagcgcacc tgccgtatat cgttctcttt tgcactcgct cccgctcttg 120  
 gagcactcga cagcgcgcgc gccgagcgacg tcgagccggt cgagcattta agcttacgac 180  
 ttgacgaaaa tcaaatcaaa agatcgacaa cattcgacga gtgcagatca ccagctaaaa 240  
 gaaaaccagc tgagacatcg gaaaagtcgc cagattttca cgtaacgcct taaagatttt 300  
 ccgtgcggtt cccgaacaaa ctaaacatta ttaacaaaca ataaacgaat ttgtagtgtc 360  
 agtgactttt gaacgcacga acaaattccc aaacacacca ccaaacgtga ctgtataatc 420  
 agccccaaga aaccc 435

<210> 233

<211> 393

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(393)

<223> Area matching Drosophila EST AA264796 (inverted).

<400> 233

```
cgctattaac tgttttgatt atatcggcgg tgataaaacg accggcattt gttgttgctg 60
ctgctgctgc tgctactgct aatgtttcgt tctcgncgt tccccggccc gcttctgcac 120
ccaccgcccc gtgttcggtt cccctgccga agcttcggcc actgctgctg ctgctgctac 180
tgctaaatac gctcgtatta ctattaacac tattctcttt tgttttcgcc cgtttcgccg 240
acgactgcag cggcagcaat gctttgtcac acttgcgctg ttttcgccga attatggcca 300
ctttttgceg ttcttcgccg ggcgcccaa ttttggaagt agttgggctt tttttttgtg 360
aatttctgtg atttttccct tgcttttctt gtt                                     393
```

<210> 234

<211> 522

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(152)

<223> Area matching Drosophila EST AA540030. This EST  
has sequence similarity to a Rat calcium binding  
protein.

<400> 234

```
ccaatccaaa tggaatgcca ttcaatgctc gtctgcgatt gttgaatggt taaacaaacc 60
gatcggcgca caacacaccg tcaccatggg caataagtcg tcgcttttcc tgcggaacga 120
ggagatcgcg caaatccagg aggagactgg ctgtgagtac gatttctggt cgggatgtgt 180
gataaccttg ggctttttca accggagact ttcaatgcgc cgtactaaat cgaaatacgc 240
acttgगतat aaattaattg ggccacgagc aatgcaaaca acaacatcgc actggagtgc 300
taaaagcatt tcgggtccaa gaccatggga ttgccaaaat ggattcgctt agtttcgatt 360
cgtcatttct ataaaaattc caaatctacg aactatatgt tcgtgttcta aaaaactccg 420
ttcaaattat gcagaactga gtctgagcga tctgtgcccg ccttatatta gcggtatatg 480
```

gacagatggt ttgcagcaaa agcaatttgc atttcaatgc cc

522

<210> 235

<211> 596

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (85)..(596)

<223> Area matching *Drosophila* EST AI109898.

<400> 235

agtttcccca tgctcatcta acggtgagcg catggcccca aaattcaagt acaacacaaa 60  
cacaacacaa cgagggggcg aggtaaaaag cagcagaaaa gccagcagca gccgcccgt 120  
cataaatcta gcaagaaaaa cctaattaat tcaattaatt actacaaaaa tcataccggc 180  
atacgttaaa taaaaaccg ttcggtctaa ttaaaattta caaaaaatca ctgctttcat 240  
ttaaagcgat tttaagtga attctattga tttgtataat tacataaaaa gtgttgcgga 300  
aattgactct ctctatcttt ctctgcaa tttcacgcgc cgatgaaaat tcgcaaaaaga 360  
tctgtattaa atcatcaata aaaatagcga aactaacggt gcaatgaatc cagctgtttg 420  
aaatccgcaa cataaaagca aaaaacacaa aactataaaa caacacgcac cgaatcacac 480  
ggaaacaaca acaacaatag gcatgctcct tattaatatg tacgaaaaaa cattaacat 540  
aggaactgcg aaagttaata atggcatatg aatggggaaa agtgaaatac acacca 596

<210> 236

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (365)..(473)

<223> Area matching *Drosophila* EST AI259723.

<400> 236

acaccacctc aaaattgatt actcctaaca aaaaccgaaa aaatacttga aaaataccca 60  
 atcaacaaca gcacacaaca aataccaaca ttttccttat acaaacctca tctgattagg 120  
 ttcttcgtga aacttttcagt tacagcgccc tttttagagc agttagatca cagtcagtta 180  
 gtcgagagtc ttaggggttat ataaacacac catttacagg tcttcacagc actacaaacc 240  
 aaaaactgca agcaatcaca ccaaacaaaa gcgttatact ctaaacatta ctcttccaaa 300  
 ccaaacaaaa accccaccaa atcaaaaacc aatccaaatc gacacgaaca cgatcaacga 360  
 aaagatgcct ataggatagg ctacgatgtc ggtaagacgg caacttccat cacgaagaac 420  
 ccgcgggtccc gaatgggagt tacctacggg tggctatggc ctgatcgaac ccc 473

<210> 237

<211> 141

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(141)

<223> Area matching *Drosophila* EST AI294469.

<400> 237

ctaatgcttg attgtgatta tctggaatat tccactggaa aacgtgccgc ttcccactca 60  
 ctgcagtcac agtctacttt cggttgagtg agtatgtgtg agagaaaacc tgcgtcctct 120  
 gtcgcgggggt cttgacactg a 141

<210> 238

<211> 355

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (145)..(325)

<223> Area matching *Drosophila* EST AA140945.

<400> 238

ggctatgggt tattgaccgc tcgatgtctg cgtttgggat tgtcggtgag acgtaggaga 60  
 agtacgcgtt gttgcgctga attgagagtc ggcgttcgtc atgctcgcgc tgacgctggg 120  
 cgcgagtgtc attctgactc atagttttat tatttaagat aacaattcac tatgtattta 180  
 agcgatcttg catcgcatag agcgtctctt tcgctttcag attttttatt tagtttattt 240  
 tatttggcgt tcacttcact caaaacaacc gattttgtgc ggagcacgaa aaaaacgtct 300  
 tcacacgtcg gggatcgaat tatttatccc cgatcgaatt atttatcgtg ttctc 355

<210> 239

<211> 626

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(331)

<223> Area matching *Drosophila* EST AI259816. This EST  
 has sequence similarity to Human Epsin gene.

<400> 239

caatatcatc gcaatcgcat tcgagagccc tataaaccgc atagagtgcc aggatttttt 60  
 gatatccata tcgtgcgcgc agctatacta ttttccccct ttgttgacgt cgcattgtcg 120  
 tcatcgatcat cttgtgaccg tgtctattcg agtccgaaaa aagaaagaaa agaaagtcgt 180  
 aaaatataga aaagaaaact agttggggag gaggagtgc acacacagac acacacatac 240  
 acagccgagc ggagccccca cagcacaca cacacaacca aaggcgaatt gcagtgaagc 300  
 aacaaaaaca acaataacag aaacattgca ggtgagcgaa agagtaggtg ggagggggcc 360  
 acaaacatat tttctgtccc tctttctctg ttggggcttc tttttcttaa ataataattt 420  
 tccgtaatta tagatcccc ttgtctaaac gtaattcccc gctaaccgtt ttttacaact 480  
 ttgcttattg atagcgcttc ctttggcctt tgetctttgt tgtttttttt acaattgaaa 540  
 actgccgtta gccggtcaag ttgattagtc catttggatc cagggttgcc aggggcttgg 600  
 tgaaactggt ttattttggg aagggg 626

<210> 240

<211> 433

<212> DNA

<213> *Drosophila melanogaster*



<220>

<221> misc\_feature

<222> (209)..(433)

<223> Area matching Drosophila EST AA141103.

<400> 240

```
ttgggacgtg tctcagatTT ctatcgacta gacatcgccg atattcgaaa atgctcttcg 60
aattatcgaa atgtaggcat actgcaatTT acgcgcgcaa cgcaaaaatt caaataatag 120
aatatttggc tcaacaagac aggagactTT agatggaaaa atagaatcca caaaagcaaa 180
actatggaat aactaaaacc actttttcata aatagtacac acaatcgatt tatttcgTTT 240
ctttttgtat ggcaaaaatt aatacaaaaa attaaatatt aaatgtatgt atgtatgtat 300
aaaaagctta aagcaaaacta tataatgtaa atttaattgg ctgtttgTTT ctctcccgat 360
tgatctgtca gtatgggtaa gttagaaaga aaaggcaatc tcaagaaact catacggaat 420
ataattccac cac 433
```

<210> 241

<211> 401

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(98)

<223> Area matching Drosophila ESTs AA246767 and  
AA141059 (inverted).

<400> 241

```
ttcgtgatta tcagcgtaa ttgtacaata ttatgattta ttcgagctgt aaatcttcac 60
agcaagcaca aactgtaatt ataccactta gaattccatt ttaatggcTT tatttatggg 120
gcgtgcattgg gcagcattTT ctcgctTTTT attttttttt tcttgattTT tgtatattta 180
tgagagtgcc gtctccggcc acaaaaagTT aatcccacta aatgccgTTg atagtttata 240
ttacgattTTg ttgtgctggc taaaatgaaa gatattgggg cattttaatt ttagaattgt 300
gacaaatgcg caactTTTT ttaacggctg catatgcgac gaatgatcca agttctagTT 360
ttatgattga atttcattgt ttttcattTT gcttaatgag a 401
```

<210> 242

<211> 368

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (118)..(239)

<223> Area matching *Drosophila* ESTs AA441468 and  
AA142226 (inverted). Sequence similarity to *C.*  
*elegans* protein Z66496.

<400> 242

```
ggtggtacac aaaaatcgat gcaacatatt tttgggccgc ccaatgtcac ggatgttttt 60
cccaactttt taatgtgtta agctagtaga taatttatta tatatcctac aacttacaga 120
aggcggccac aatgcccagc aatcgacttc catatttgag ataccacggc tgctccggtc 180
caattggatc ttgttgattc ggccgtgccg gcagaccggt tatcttttcc gcaaacgact 240
gatccgggaa atagacggaa atagggagaa atctaaatgc aattaggaaa aatcgaagca 300
caattttgta ttgtgacgcg gcggggcgctt tttttaacac gcacacattg ccacgacaaa 360
aaacacac                                     368
```

<210> 243

<211> 321

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(82)

<223> Area matching *Drosophila* EST AA247070 (inverted).  
This EST forms a 1366bp contig with ESTs AA567381,  
AA568013 and AA540724 and has sequence similarity  
to a *C. elegans* protein.

<400> 243

aaccagatcc gcagctgcag ccattgtctt ccaatctcac acgcacacac acacaggaac 60  
aagcacgtcg gtggtgttgt tgetgttgtt tttgtgtcg tgcgtctga tgtacaatca 120  
gtgttggtca acaatttcgt gcttgaattg gtcacacacg gttgccgtgt acgcggtgta 180  
tcgataaccg atagtaaaca tgcattgggca ttggcgccac aacgacacgt ttaaacaatca 240  
accaaaccac accgaacgta tttagaactc caacaaaata tctgctccac gttgaattta 300  
aaaacatttt aattactaaa a 321

<210> 244

<211> 469

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (433)..(469)

<223> Area matching *Drosophila* EST AA802401. This EST  
has sequence similarity to glycosyltransferase  
genes.

<400> 244

ggccgagtaa caaggtcgat ttgggggctaa aaaacgccaa aagcgggcgc tgtcaacatg 60  
tgtttctaggg ttaccgcagc gcgcgcattt cgtgtgctaa aaagtgaatt ttagatttaa 120  
attgagatcg agttttttaa ataattggctt agattaccgt agtctttata tatatatata 180  
gcaacatagg tgaaatagaa aaagtaacaa ataaatattg aacgtaataa aagagggttac 240  
agaacatata ataaataatt aagttaatat aataataata aaccgaagat gttgaatact 300  
ttagacttaa atagcaatac ctccagcgaa agcctccctt tataatttat caaaaaaaat 360  
taacctatct atttgggtata ttcttttagaa ccgctttaga acattcatcc taccacgggc 420  
acactttcgc ccaatcagct gagaaaatat tttaaagttt taaataata 469

<210> 245

<211> 383

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(96)

<223> Area matching Drosophila EST AI135263 (inverted).

<400> 245

ggtggcacat gtgctcaaaa aggccgaaga cgggtgggaga gggagagcga ctacggcggtt 60  
gccagatctt tggtcgatga cattcaatag ttacttttaa caaaaatagc tagatcataa 120  
aatataatga attgcaggat acaaattcag ctgaactact ggtcagaaga atgcttgtat 180  
taatattaca catagataca tagttattga cttagaatta aattttgtat attgaattgt 240  
taggaaataa ctattctttt gtatcttaaa gaaaagaaaa ttattcatat taaacggatg 300  
ttgtcttgag actgctaacg attttaatag acctgttaag ttgttagcac ataaaataaa 360  
attattttga atccagcatt ttc 383

<210> 246

<211> 489

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (243)..(489)

<223> Area matching Drosophila EST AA695904.

<400> 246

aaccagaacg aaactccaat gcagtttcat tttgtcagtt taatcattaa acaaagaatg 60  
cgcaaccgat cgcaactagc tcgtggactc ttgtttctccc aataattggg atgttttcca 120  
ttttgcgtta acatggaaaa tgtgtgaaaa gctttttccc cctccaaaag aagcgtactg 180  
aactaagctt tcggtgggta gtaatagtag tcgttatatc ttatttttct tatttacgtg 240  
cagctgcaat cattggctgc gtcactttgg cgtcagctat aaactgggtg atcaactcgg 300  
cggcctccaa aagctgcgca tctgctccag acacttttagc caacgccagg agatggccaa 360  
aaccgcacac aagatgacgc cgctgcgcaa gtctctgtcc tccaagggca ttgtgctacc 420  
cattaatgcc gctggaaggt tcggtcattg caggcgcctt agcaggaaga agaagttcag 480  
gaatgggaa 489

<210> 247

<211> 417

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(317)

<223> Area matching *Drosophila* ESTs AA246386 and  
AA541060.

<400> 247

```
gccgtatgcg aaacggcgaa tgcgtcaac gcagcgctgc gcgaatccct tggcggcaac 60
tcctccgccg gctcgtcgac tgaccaggcc aagagcggcg aggacaccaa cggcagcctg 120
caaaatcaca tcgtggccaa tgccaaacgc atcctgatgg ccaaaatcga atacgaggag 180
gtgcccact accacgaatc ggtgctggag aacctcaagt ccaaatatat tgcatcaag 240
ccgggaaatc caggcgccat caatggcttt agtggcaaaa acaacacagg caaacttggt 300
gggcgcgaaat ggacatggtg agttacactg tgttaaagat acaacaaaat gttaaaatcc 360
aaaagttgct tgcaaagtgg cttttccctc gtcctgtgtc ctcctttgtg ttgcaat 417
```

<210> 248

<211> 427

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (311)..(427)

<223> Area matching *Drosophila* EST AA264961. This EST  
has sequence similarity to mouse Thioredoxin gene.

<400> 248

```
accctggcca aatgggcggt aagcttaaga tgagcgtgaa agcatagatt gctagtcgta 60
aacgctgaat gaattttaaa tgaatgaata tgtcaaatga gaatatttca tagttttaca 120
tattgtaatc cactaatata tcaataaaaag tttaaattatt aagtttcggt ttttttctat 180
```

tacacattaa tgggccctct aaaaatagga agtcaaagag ctcgaaatat cgataccatc 240  
 acagtgtgac cgcttttgaa ataccgcatt cgggtattttt cttagcacga atttggacta 300  
 aatgcatatt acaagtcatc tttaacaaaa aaaatttgca ttgaacgtta ataataacag 360  
 ttacttgctt aaatccaatt cggctgccga aacaaaagct caattaatag aaacctaata 420  
 ctatcac 427

<210> 249

<211> 459

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (136)..(293)

<223> Area matching *Drosophila* EST AA202880 (inverted).

This EST has sequence similarity to Calcium ATPase genes.

<400> 249

cggcagcaga atagggaaaa caggcgacaa tcacgttaca acaacaacag cggcacaaac 60  
 agttcccgag agtgcgaggag agggacgcaa cactactaac agtgggcgca tgcagcaccg 120  
 tttcttttga ctacgcgcac agcttgcaagg ggggcgcgga aggcttaatt aaatgtgtca 180  
 catggagcac agactgtttt gattcacaaa aaaagatatc gccttatttc acttatatgc 240  
 tccccgtttt cttgtcggtg gacacgcgca acgcagcaaa aatgacgaat gcgatcgagc 300  
 gacgtgtaca gactgagaag cgtgcgaatg cgagagcggg agggcgccac taacagcact 360  
 gtgtgtgctg ttgcgacgca agcccaaagt cgcgagagca gcctcgatgc agctgatctc 420  
 caattagaat ccattccctg ttattgttat tgctggatt 459

<210> 250

<211> 438

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (74)..(276)

<223> Area matching Drosophila EST AA263803.

<220>

<221> intron

<222> (277)..(343)

<223> Probable intron in gene represented by EST  
AA263803.

<220>

<221> misc\_feature

<222> (344)..(438)

<223> Area matching Drosophila EST AA263803.

<400> 250

```
gcccggagca ctggatttca cgagctccgc cctcgaagat ttgtgctttg cttgactaat 60
tggaatttat tgcaggtggt ctatatatat gagctgttgt gccggggcga ggatoccagc 120
agcgagagtc ccgaattttg gaacgagttc ttcttgctgc agccgaactt cgaggcgctg 180
gagaatgaga ttggcaaact-caacaacgag cagctgcagc tggtgaaacc gaacctgaac 240
accctcttcc agaggtgcat cgaaatgctt gacacgggtt agaccagttt gacctattaa 300
tatatacctc cagccaccta taatccgtga tttccccag aaagatcatc ctaagcggct 360
gtgcaacagc ctacacacgc tgtgctccct gttctacggg atctttaaaa atccaaccaa 420
aaccacatt aaacatcc                                     438
```

<210> 251

<211> 387

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (3)..(166)

<223> Area matching Drosophila ESTs AA202200 and  
AA202128 (inverted)

<400> 251

gtccactac tctacgctaa atggctatgc ttgttagaat tgcacatata ttttatgtat 60  
tttatttagc taaacacgga gacatatcct tacacgatat ctacgagcga cgcgaccagt 120  
gtgactgcgc ctacacaatt gaaacatgtc acatgcagtg tgaccgttct tggtcfaatg 180  
gaaaagctct cactcatata aaattcaata ataggttaat aaaaaaaaaa tactgactta 240  
ttttttaaat acaaacgtat ttactctaac aatataagta aaaagctaaa attattttta 300  
tgtttattta ggaaacctat cgatatatcg atacacatgt ttttttgccc accctagaaa 360  
ttgctaacgt atttttagca acaaatt 387

<210> 252

<211> 135

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(48)

<223> Area matching *Drosophila* EST AA439530 (inverted)

<400> 252

gtccgatcca tatttttagca cagaaattaa gtaaaatatg gcggtttagt ttgaagttct 60  
ttgtttttgt tgctgccag tgttaccaag tggttgaatt ccgcgtataa ttaggagact 120  
ggagagtggg tcaca 135

<210> 253

<211> 207

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (28)..(207)

<223> Area matching *Drosophila* EST AI109459. This EST  
has sequence similarity to GPI- anchored protein  
genes.



<400> 253

cccgagagga gcagacaagc gaactggact gggaaacagc agcagcagca gcagtcgttt 60  
gaattgaata tcattcccca tttcgagcta aacgtcgttg agagccaacc aggaagaatc 120  
caacggcgca ccatgccttc ggctgcaaat accgctactg ttaccgctgc aattgccacc 180  
accgtcgccg ccacagccag caacacc 207

<210> 254

<211> 574

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (471)..(506)

<223> Area matching *Drosophila* EST AI109779.

<400> 254

taccagacag ctgggcaccc gaaggagtaa gagagacgga tgtgaagaga gagtccctgcg 60  
agagcgaaca aatcggagaa ggagcgagcg tgatatgaat atatctaatt actttcacct 120  
ccttaagcat aaacttggtt caatttatga aatcttttaa gttactttct gcttgatagt 180  
tattcataat tgttatatta taatgaatct tcgcacatgc ggcattttctg cgcaagtgc 240  
tgaagagagt gaacaaggga gagagcggca agaacaagag aaatggcaaa caaacaaaag 300  
ccacagacac agctgtctta tcacagggcg gttttctgcc accccctttt gacttgatag 360  
caaagacaac cgttacttgt gggtttgtgt ctcccgataa gtatgtttat aaaaattcaa 420  
ttcttatatt ttatacata ttaagcattt ataacaagaa gagaatgcta tagtcgagtt 480  
ccccgaatta tcagaatacc cgttgctccc gttacctaaa ttaatatt atataccttt 540  
aaaaccgcaa ctgtagaaa cttgttgga aaag 574

<210> 255

<211> 247

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (147)..(247)

<223> Area matching Drosophila EST AA141054.

<400> 255

ccccgcgcgc aaacgaattt tctttttccg gtgaactagg ggtgtgggtg gaaagagaga 60  
gtgagaaaga gtgtggagtt ccgcttgccg gcgcttttct acaactattt tgtcattgcg 120  
cctctctgcg ctcttccgcg attccgcctc gttcattcat tcattagccg cgctctttct 180  
tactctctgt gcgcatgcct tgtgcggcgc tgcttctgcc ggcgtcgccg tcagcgctgc 240  
gttgttt 247

<210> 256

<211> 127

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (65)..(118)

<223> Area matching Drosophila EST AA141365(inverted).

<400> 256

gtatgcttct tcgtatgctt cctcgtatgc ttcgtgggcc ttatgagtgt tcctcctacc 60  
acaactcggc catcctgact agctgatccc ctgatcatgg tttacattga ttgcttagtt 120  
gtatgat 127

<210> 257

<211> 1022

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (144)..(549)

<223> Area matching Drosophila EST AI063643.

<400> 257

acaacccaaa ataaaggtaa ggggaatttt taattaaaaa attagggaaa ataacaagtt 60  
taagttgccg gaccagcca aaaaacaaac aaagcaacgc ttgtaaaaac tgaaaacaac 120  
atttcagttt atttcgcttc gtgccatgtg agcaacttca aattgatatt gaatcggaat 180  
cagtgtgcgg gtggtgctaa ttagcggaag acggcaattt attgaacgcg aaaaaagccc 240  
cacaatccaa cttccatttg gacacgaaac caaccacccg ccaaatcaaa tcgccgtcga 300  
gttgtgcatc aaatgaatgt gcgaaaagtg cagtaaataca atgtttttgt gagtgtttga 360  
aagaagaaga cggaaggagc gccacaaca aaagcaaaga gagcaagacc taacgggaca 420  
cccgaaacca aaaacctatc ggcacaacga cactttctca atagctatag ttttagttca 480  
tatgttcata tctcggaaaa tggacgaggt ctttagccta cacatggaga aattggacgt 540  
ttacgacggt tagtatctaa tttgccggaa gttctactta aacgtagaac atatgtatat 600  
gatggaatct gggttgtatt tctgattaat gagttcatca actttcaagg aaataataat 660  
agtagtagta gttgtaaaca gctgaagtat tgggtataaa ataacactga tatgggtaaa 720  
atcataatag acactttatt tgattcaaga ctgcgatgat tttagctgta tgaatcatgt 780  
cgaaaataat agaaatcact attactaaat atagataatt ttaaaattta gattcagtgc 840  
aacatggata cagtgattaa gtgttacaat ataaacaaaa gtaaaagaaa agtacaacaa 900  
gaaacaagta tttggtgaga aatgataaaa actcaccaat aatgaaaacc atttatgtag 960  
gattttaaca aacactgttc tcgtctgcat tagtgcttgt ctttgtaata gaattcgaac  
1020

tt  
1022

<210> 258

<211> 497

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(148)

<223> Area matching *Drosophila* ESTs AI107445 and  
AA390813.

<400> 258

acataaaca acggagctcc gatattctaaa taaatattat ggaaatcgca ccactgatca 60

ataacgccgt cgtgtcgtc acagcctctg cctctgccgc cgtctctgcc tctgctagcg 120  
 tcggcagtag cagcaaggat gataacggta ggcggtctc tagatgataa gcggtacact 180  
 tccagtgggt tcataataaa ctataaaaat aataaaatat atgtaaatac aaagcataaa 240  
 gtgtagtacg tgctcgaaag agtcacactt tctcgtaaa gaacttcacg ttctatccat 300  
 attatatgat tattatgttt caaaatcctt tataatcaaa agcgaattag acaatcagaa 360  
 tatctccac ccagcaattc ataatctata taaaatatag tcagaatatt gcaatcatac 420  
 caaaattaat accaacccca ggacttaagt ttttggttt aatccaaata tatccatttg 480  
 tttctttgcc ttaattt 497

<210> 259

<211> 411

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(75)

<223> Area matching *Drosophila* EST AI297362.

<400> 259

tgtgttggtg tggtgttagt gcttgtgcaa cttaaaaatt caattgttta ttgctgggca 60  
 aaactggtac cgtgtaccgc gtacctggaa aacaacattt aaagcgaacg ccaggcgaat 120  
 cgagagttcc gagcaagtgg gcaacaataa tgtgtcgtcg cggcgcctgc tcatttccac 180  
 cgtgataata atcggcatag ggttccgacg cgaaagccac aagtgaaagt ggaatgctct 240  
 gcctatccgc gttagttggc atagtcttca acaccagcg aattacatct ctccgactgg 300  
 atatgaagat atcgtgagta ttccctctg gaatcaatga aatgaaatgg tgtgcctagt 360  
 ctgtgatgat aaggcagcta ccaccaccac gtccatatcc ggatgcgagc c 411

<210> 260

<211> 230

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (96)..(230)

<223> Area matching Drosophila EST AA392916 (inverted).

<400> 260

```
tgtgggatat tatattaatg gaaagccaca accaaattat aactgtttgt aaactacatt 60
taaagacgta gttgaaatag aaagaggtaa acttacagat ttgaaatgaa tcagtaatcc 120
aataatgtgt tttgtttgga atatttccaa aatgtcttca acggaagagg caagaacaca 180
aacagaaacg gcacaaacac aaagagataa tttggcagca taaaagagcg          230
```

<210> 261

<211> 331

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(47)

<223> Area matching Drosophila EST AA201223 (inverted).

This EST forms a 2631bp contig with ESTs AA538867,  
AA439491, AA390780, AA390983, AA201661, AA391700  
and AA202007. Seq. sim. to Human nucleopore gene.

<400> 261

```
ctgcagcgtg tccagcgccc taagcggctt tcccacttca atgaactctg tgacgaagag 60
agcggcgctc agttaagaga gcacacgatt cgcgaagacg aaagtttctc ttcagacacc 120
gcatggaaaa ttttcagcac tcaccattag cccttttttag ggcgttttcc ggacgttgcg 180
tatagcgggc catttccgat cgctttactt acttgcgggc gcacttcaag ttgatttcga 240
tagcaggtct ggagcgtttt gagacctggg gctgctgaaa attgtataaa tcttcggctc 300
gcctacgtgt ggctgcaata ttaatgcaaa a          331
```

<210> 262

<211> 687

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (537)..(687)

<223> Area matching Drosophila EST AI454966.

<400> 262

```
gagaggggata atgggagatg gcgaatagtg ggaaagaggc acctgaaata gataagcaat 60
gagcaccact caatttaata tggacaactg ggccatttta agaagcaaata atgaatttc 120
aatttagttg tatattcttg agattaaatt atttagggta gcacaatgac acacatgcag 180
ggatgatggg taagacaaag cctttaagag agagggagag tttgttgacc tcattctcgg 240
gggggttgagt gacctgtttt cgagtagttt tgagtgattt gttcccagtg tccaggtagc 300
ttgatttaaa ttagactggt tattataact gcattgtggc ttttatatgt tttacacaaa 360
ccattcctaa gcgcctacc tatatcaata ttggtttgag agcagttgtg ctctcttaca 420
ctcaagtagc tcttttaatc tcttccactc attcgctact cagtcgccat tttcgccga 480
gcgctgactt tctgcggtg ctgcttctgt tcattcgtgt gttggatttt gagatgcgtg 540
cacagctgaa aagtaaaata atgcaaacgg ctgtattttt tatatcttcg ggtccactgg 600
gtacatacaa atgaaaagggt gcttgctggt atatacttcg aaattatcac gtttgcgta 660
gaccgaaatt gaagaaatcg attactc 687
```

<210> 263

<211> 441

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (10)..(441)

<223> Area matching Drosophila EST AA202767. This EST  
forms a 715bp contig with ESTs AA201231 and  
AA392823. Sequence similarity to Rat NUP84 gene.

<400> 263

```
agccggggcaa cgaattgaag cataaacaaa cgatgtcgtc caccgatgtc ttggaattga 60
acaaaacgga gttgttcgag aagattcgca atgggttgcc cgtgggtgcaa aggactcaga 120
acctgctgga ctgcaaggac gatctgctct ttgcctggca cgcaaggac agctgtctgt 180
```

tggttcgcaa ctggcgctca tcgctggcgg caaaggtgaa tatccagttc cagacactga 240  
 ttccatcgag cttggtgagc ctggaggtgg accgcgtgct ggctccaac gagggctccc 300  
 tcgtggcact aagttggacc gcgcggcggt gtcataatgg agctgccccg ccgctggggc 360  
 cccgatggat actacaagga tggcaagcca gttgatcacc tgccgcacgt tcgggctgga 420  
 cactcagctt ttcctaaaaa a 441

<210> 264

<211> 40

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (3)..(40)

<223> Area matching *Drosophila* EST AA201212 (inverted).

<400> 264

cccagtcgcg gcgatatac ttcggtacta cggattgtgg

40

<210> 265

<211> 564

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(33)

<223> Area matching *Drosophila* ESTs AI404994 and  
 AI260898. ESTs show evidence of alternative  
 splicing.

<400> 265

atctcaacga ctctacttgt tattttacat aacctgcacg gcgctaaaat gagcatgtta 60  
 tcgataaaat atcgatgcaa ggcgtgcagt taagaaattt atttaaaaag gtataggtga 120  
 atacctacaa atgtaattca tttaagttac tattaaattt tttctgacta tataaaatta 180

aattaaatcc tcagaactcg atatgtcgat atgtaacagt gcataactac gcttattggt 240  
acaggggtgg ataggctaaa gagaattgcc cgcataatth atttttaaaa ccattttctg 300  
ctaaacgtgg tgttaaatat ttatttattt aatttaattt atgatttatg atttatttta 360  
ttaaaagctg taagaattat attactgatt tctatgataa tcacgaagcc tataactttag 420  
cggttattca ctgtgctgcc tatcggtatc gaaagctttg ccggtttatt tacattttgg 480  
cgcattaaac caagcaaattg ttttaaaaaa cctcaatttc cgtgtttttg cgccacagca 540  
gcagcacaaa agaatcccga atcc 564

<210> 266

<211> 404

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(292)

<223> Area matching *Drosophila* ESTs AA539914 and  
AA201959 (1042bp contig).

<400> 266

gtctcgtgtg acgtgcgagc gcagaaagtg tcgtcttttag attttgtttg tgcacttttc 60  
gccatttccc tttgtattcc gtcgagttag gaacagcggg agccagggag cgcaagagtt 120  
gccgagaagc acctgcaaaa tagcggcacg agatcgccag aaaaccagaa aatcgcaaga 180  
agcaaaagcg accgggtcaa cacttccaca cgcaaatacc cagagcccc catcacacac 240  
acacacacac aaacatccaa cacttggtgc agtggtcgat gagaaggggc accacagcga 300  
taagaggaga agggacgaag gagcaggaag aagaactagt tgcctaagaa agacaccacg 360  
cgcatcttgc tatcagcgaa ataccactg caaacgttta gaac 404

<210> 267

<211> 454

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature



<222> (36)..(454)

<223> Area matching Drosophila EST AA440953.

<400> 267

```
ctctagaaag acaacaaatt ttttggcgag cggacgtgtc ggcggacaaa aagcttgcaa 60
acagaacaga acggaagaac acagaagaga acgacacgac acggacagcg gggaaagggtg 120
gcaattgaaa gaaagtgccca tacttagtgt gcgagcgaaa gagagagaga gcaaactggg 180
tattgcttgt gtgtgtgtag tagtttagtg gtcgtgtgtg tgggagtttg tgtacgaagc 240
gagtggcaaa ggaaaacaca acaaacatta ttccaaggaa atttccaatc atgtcgggtgg 300
aatcctccag ttcggcggtc caacagccgc cgtcgtcctc gaacctaccg ctcttgggcg 360
acaaccaggt tggttggcca cgaaccagct ccgcctcctc gggctcttcc tcttccacat 420
cgtcgtcctc ctctccggtt gggcggcgca tttg                                     454
```

<210> 268

<211> 253

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (145)..(253)

<223> Area matching Drosophila EST AA264591.

<400> 268

```
gttcggcgct cagttgcgaa tctgcgacca aaacgtttgg agttttctcag gtaagcactg 60
gactctggga actggttttc gctgttatca gtgcgaccag ttgcactttg cactttgacc 120
tgcacctctc acaccagtca cattccaggc acatctctgc accaccggca acatgattct 180
ctccaagccc ctgtactcgc tcttcggcac ttatctggag cagctcttca accaccgggt 240
ccgcaccaaa tcc                                     253
```

<210> 269

<211> 380

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (47)..(380)

<223> Area matching Drosophila EST AA539491.

<400> 269

```
gtttcggtcg tggacatgaa cggcattacg tttttcaact cggccgcgcg aataactcga 60
aaaaggcagc tccgcagcca aggcattttg aaaaacacaa gtccccgact cgaaacgcga 120
ccaaatattc ggtgtgtgac gcgaactgcc aatgcaatag ttcacttaag aattgcagat 180
taccgcgact ctgggcagtt ctcattcgat atttgaatgt accaaaagaa aagtgccaga 240
accagaaaac aaaataaaaag atcttctaac agaataacaa gaagtgtttc ctccgaaaga 300
ttaaaaaatc gcgaatgatt aagaatcgcg gcaccgtag ttccctctct cgcttttccc 360
ttttgcgctt ttctgcgttg                                     380
```

<210> 270

<211> 398

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (202)..(381)

<223> Area matching Drosophila EST AI403737 (inverted).

<400> 270

```
ctctgttcgc caaccaaca acaaatcaaa atatcagtg tggggcgaaa aaatgcgatg 60
agccatcgat agttcgataa catcccgoga acaatctagc ggatgcaatc gaatttaagc 120
taagtgttaa atggttgtaa atattacaaa tgtaatctta tcatgttcag ccacacatcc 180
ccaatcaacc tgatacagta ctttaaatat gacgtaattt tttaattatg cagtgaaaaa 240
gttacatcgt tgtgcactaa caaaagaaat accactcaaa gtggttaagat cacgaataaa 300
gctgcgtata aatattaaat aatttacgtt gtatttttgg taatgattga agaaacattc 360
gttggttaac gaataaggcc tcacaaggct tggcgatc                                     398
```

<210> 271

<211> 496

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (270)..(443)

<223> Area matching *Drosophila* EST AA567141 (inverted).

<400> 271

```
gctaaagccg tttttttctc ctgctttttg tttttcgtct gctttcgtgg ttctcatcta 60
caacatggca catcagtttt ttttttttta caatgtcaat taattctata cttccatttc 120
gaatgttttt tgaatacata acatacatgc tattttcaga caaacccaat ttattctgtg 180
tttctgccat gtgcttcaag tgttgccctc ttttcgcttc ccttgtctta aatccggcga 240
ctgtacagta gttcagaatt tatgcttact taattgctcc ttctttctct gaagtgtgta 300
cgaattggtg aatgccgcgc aaatcaaaca ctctcccg tcaatcgctt ttaggcgaa 360
taaaagtgtg aataatgcca acagtttggg cagttaaaaa atcggagata tctccccgcg 420
acacaaaaag ccgtgcggac tgcgcgaaac accaaacagc aactaaaatg agaaacacag 480
tccccgtgctt aaatat 496
```

<210> 272

<211> 546

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(478)

<223> Area matching *Drosophila* EST AI134670.

<400> 272

```
cccgtagctg tggagctagt aaatttcgtg ctggcgctc atttttattt tagttaacga 60
aacgaacgaa ccagcggcgc gctaagaaat ccaagaaata ctatagcaaa aacactcagc 120
cgaggcggaa ataattttgc tgtagttctt ttttgctagc gtgtgtgccg tcgaaaaaaaa 180
aagatataat acaaatcaaa tttataataa ttttctcta tgcgagtacc gaaacgaaat 240
caatgagcaa agaatcgtgg gttttttttt tgcccatata cgaacaatta aacgaactct 300
```

ctttgttatac agtattgcac aaataaataa aaccaatca cacaacgaac aacgaaagtt 360  
 agtaaagaga ataccaacga aaaagttgaa aaagtcagtg agttgaaaaa agttaaagtc 420  
 ctgcaagttt gaaaattgag gaaggcagaa agtaaagtct atatgaaaat atacttgtag 480  
 atattttcta cagcctgtgt gtgtgtctgt gttccgaaaa gcctctcatc ccaatctgaa 540  
 tcttca 546

<210> 273

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (413)..(534)

<223> Area matching *Drosophila* EST AA263763 (inverted).

<400> 273

ctacgtacta tttttctcca cataatatat atgtattaat actagttaga atatgaaaga 60  
 actgtttact caccagagcc tcgtgacccc aactgttgct cttttggtga tccttgagca 120  
 gctgcagcga tcggagaacc acttcgcccc gttccgtcgc gtagatgttt gtgtactccc 180  
 ttaaattttg ctccaaccag tgcgatatgg tgtacagctc ctgcgcgctc gtttgcgaaa 240  
 gctgccggaa tgaggtgtat tcategctgg aatcgctcctc tatgtagata agatccagca 300  
 actccaccgg cttcagcggg gcactgtgct tcttgaggag catactatag tgctgactca 360  
 ggccttcgca gccgggtgta aacaaactgg tgacattctc cagctccacg ctctgggaaa 420  
 ttgttgtgcc ggaagtaatc gttggcatcg cgcagtttgg ctagtgcgctc gaggaacacc 480  
 gagatgtttc cctccaccgg gcattgatga atcaactggc agacctcttg gaga 534

<210> 274

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(99)

<223> Area matching Drosophila EST AA568011.

<400> 274

```
atcttgacaa aaatttttgc aagcgcataa aattaaacaa attgtagagt tgtggacaac 60
aaatcgccac tagaataact ggaaaaaagc gaaaatggtt agtactagac aaacgcgact 120
cacttgctcc gcagcagaga ctttttaact cgcaccaaac cgaagattgc gtctttcggt 180
ttcccgtaga atttgcgcat tttttcggaa ctttcacagt ggcgttgcag cgaccgctct 240
tgggcggcat aagggttaag gggcatgtgg gtggctacgg gtggagggtt ccgcgaggca 300
ccccgtcgtg accttgccct catttgggac tacgacgtca cagctgccag ctccggcggg 360
tagatacaca tccgaattaa caccacgcgc tccgcacct ccgattcgcc gctctccatg 420
gaagtggaaa tggaattaca gccctttggt ccacatgcy gattttacct ggggggtggaa 480
aggaaagggt ctgaccatat agcatatgat catcggtatt ataggatagt ttctg 535
```

<210> 275

<211> 449

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (64)..(449)

<223> Area matching Drosophila EST AI107456.

<400> 275

```
gggtggacca cccttataag cgggctctcg ggccgcaaga ctctcataag cattcaagag 60
ttgcttaogt tcggttcgtt cgcatttctt ctctatctta tataatatta tattttctcc 120
taaatacaatt ttttactac caacaacaac aacaataata acaactcaac tattctcaac 180
tcgctgaac cttaacttaa ctttctcaaa aacaacaaac tacaactcta ccactacaaa 240
tctgtcaact ttccgttttt aaactgaaac tgcaaaccac aacatttatt ttcgtctcga 300
cggccattga caaagttttg ttttcaaaa acccgaggaa gaaaaattgc cagcccaaaa 360
agatttgaaa ggatacccca aaagattccg ttcaaaaatc gtcccccccg ttatgttttg 420
agtttcaatt cccgtgtttg aaaaacaaa 449
```

<210> 276

<211> 479

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (212)..(414)

<223> Area matching *Drosophila* gene Karyophilin alpha 1.

Acession no. AF074957

<400> 276

gttcaattca actagttcgc attccacgac gacctctacc tatatTTTct agattatttg 60  
cacttttcgtt tagcatttga tcacagtagc ggcgaaaatc aagtcgcact cactttttat 120  
ctgaaacctg tctttacgac ttaaattatt ctgttctcaa agaaatattt tttttaacta 180  
tttcaagctt ttgaattgcc aagacgacga aatgtctgcc agccacaaac agcggtataa 240  
aaatgccgcc ttggactcca cagagatgcg tcgtcgtcgc gaggagggtgg gcatccagtt 300  
gcgaaaaaac aaacgcgaac agcagctcct taagcgacgc aatgtgggtc ttgagccggc 360  
tacatcctca acatcagccg gagtggagag caacacccga taacgaacag cagggtttatt 420  
ttgatcaagt ttgggctgat agcatagtct taactatctc tccattccca atgcaggct 479

<210> 277

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(146)

<223> Area matching *Drosophila* ESTs A1295205 and  
AA141054. These ESTs show evidence of alternative  
splicing.

<400> 277

ctcccgtcgt tttgagatcc gctgctctcg caacaacaac aactataact gtagttaccg 60  
tctcttttgc atcgttcggt tttcgtttgt gtcgccaagt gattgtgtgt gtgcgtaagc 120  
ttaaagctga ctaacaaaac gaaacaagaa aaaatataaa ttataggaaa attgttaaatt 180

tataaccaga aagagagcgg cacttacgtg tgttattgtg tgcgtgtgct ttaaaaagat 240  
 ataaaaatag caatagaaag ttattaaagc gttggcaaaa aagtccaacg aacagcgaga 300  
 ggaaagcggg gaacgaaata gttaaagcca aagtcgctgc cgacgtcgca cttgaaaacg 360  
 tcgcaaaagt ttgtaaacac accagtgtgt gttcgtgtgt gtttttgccg gcggtgccagt 420  
 gtgcgtgctg ctagaaaaga gtcaagaagc cgaagaaaag gaagaagccc gaagaagcag 480  
 caaaagaagc cgacagcaaa aagtaaataa aatccaatgc ccctggcag aat 533

<210> 278

<211> 506

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (8)..(382)

<223> Area matching *Drosophila* EST AA567704.

<400> 278

gtgccgccga agtggacaca tcgccgcata cggatacggg aacgcatagg gacagagatt 60  
 cgaatccggg taatatagcc ttagccaccg atttggaact gcccaagggt ctgccgttat 120  
 cgttatcctc gcgacaccac tggaaccagc tgcagagcag tttgcacgcc cttcaccacc 180  
 agcaacagca acaacaacag caactacgtt catacagctc cactatcgaa acaaatttgg 240  
 aagacaagat gagcaaacc gattcgaaac tagataaata cgcgagcgc gatcgcttgg 300  
 gcctttgggg cactggtgac aatgaggtgg tcggcagcct ctccggattc acccgactct 360  
 tggacaagcg ctactcaaag gtgagttcca caagtttaga atatgcgaat acgcttttaa 420  
 gttgccccag ttccgttgaa cttagtggaa aaatgccagg caaaggtttt taagggtggg 480  
 ttcgcatcct gttttttttt tccgct 506

<210> 279

<211> 362

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (74)..(224)

<223> Area matching Drosophila EST AA539252.

<220>

<221> intron

<222> (225)..(296)

<223> Probable intron in gene represented by EST  
AA539252.

<220>

<221> misc\_feature

<222> (297)..(344)

<223> Area matching Drosophila EST AA539252.

<400> 279

gctccagcaa tcaagcaacc gagtatcggc gtcgcttcgt ttcgaatttc agttcgaatt 60  
tggatttggt cggcgacgct ctaatttggt taatttttgt tcgttaattg tgttaattga 120  
ttagttagtc gctgtgttaa tggaccacta agttagctgc gagcccgttt ctgtttagtt 180  
caagttatct ctgttttggc catccccctgc aatgagcgcc ttgagggtta gttgagtcct 240  
cttttcggaa ctccggcaat aattttccga gaaataacta gattaccggt acttacagat 300  
cacagtgcgc ccatcgcgcc taaagcaaaa gaagcgcgcc gaaggaccga gcccgcccggt 360  
cc  
362

<210> 280

<211> 548

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(347)

<223> Area matching Drosophila EST AI260759 (inverted).

<400> 280

gccaaagacga tggcaatcaa cttttcgttg ttgtttttgc agctcgtcgc ttgttgtcgc 60



tacacaggtg gctggctggt ggtgctgtgg cctctatttc ttgctatttc tctctatttc 120  
tctgtattga tatcgaaatg gatgtcaa at aagccgctcg acggggtttc ttcaggagaa 180  
agtgcacgga aatgtgtctc cgtctccgtc tgcgccagct gtgcgctatt cttctcgctc 240  
cgggtactta cagctccggt tatcgatggg tcattaggtg gtgcacactc atttattgca 300  
atgccattta tggcctaatt gatttgcaag ttgcgggcaa gaacaagtaa ttttgtagt 360  
aaatagaggg cagaatggcc actttgttct tggcgcagca tctggcaacg ctgcggggtt 420  
tgtttacttc gataaggccc cttttacact agtttcgaat tatcgcaatt gggaatatat 480  
ttcgactata tcttttttat ggcctaatat gcaaagcctg aataaataat tgatttaagg 540  
aacatact 548

<210> 281

<211> 199

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(77)

<223> Area matching *Drosophila* EST AI260646 (inverted).

<400> 281

ggtcagacgg aacagcgcag acatcgcggt ggggaagaaa tttcagtcgc aaatttcgta 60  
aataatcgag ttttcccttg atcgctggac ttctgacagc tgcgcagtgt gaacgtttgc 120  
tgcaatttgt cagctggccg agagggtagc cactcgatgc ggtatttttt cgggtatttta 180  
cctagaaccg ttttaattt 199

<210> 282

<211> 310

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (160)..(306)

<223> Area matching *Drosophila* ESTs AA202424 and

AA264609. These ESTs have sequence similarity to  
Rat hydroxymethylbilane synthase gene.

<400> 282

gtcccgacat tgcggctgca atatccggga tagcgggccg cacaggggcc ggcaaagcc 60  
caacgcacac ttttcactcg gcaaataagg gggcatcgaa ggccaccggg ggcagaaaaa 120  
gtaggaatgt ctaatttact tgcttcaatt gtttctccag gacgaagatg gtggcgatgg 180  
acgcacgctc taggcggaat actatgccct caatgacgaa acctttggat ccgctataaa 240  
tggcgactgg gaggaagccc atgagactat ggtacgcctg ggcgggaatg gcgaaagggt 300  
gcggaagcga 310

<210> 283

<211> 429

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (300)..(379)

<223> Area matching *Drosophila* EST AA802555.

<400> 283

cactggacgt ccacacaaaa attgtactcg cgacgtgtga gcgtgacgca tgctgtacac 60  
tcttaaccac acttaaatga gggcaaagca ctctcgcccg cagccgtgcg agtgagcgag 120  
atgactatac aagcagcatc tgggcatagc gaggcagggt tgctaagcc agtggtgtac 180  
aaccatcggc ggtcatcgtg agtgggcccg ttatcgctat cgtcgctcag ctgttacgta 240  
gcgtgtttgt tacgtcgtaa attttgtgog gaaaaaccgc agagttttca ttgccgccgt 300  
gaaaaaaaca taaataatgt ctgtgccttt cagtggcgca ttgcggcggt ccggcgccat 360  
tgtgtccgcc attggcaagc agctgaagag cgtgaatttg aagggcgta agcggataac 420  
cgtgcagtt 429

<210> 284

<211> 573

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (322)..(573)

<223> Area matching Drosophila ESTs AA802438 and  
AI063681 (1030bp contig).

<400> 284

```
ttgagaagca atggccgctg accaattgcc aggggttgcca gacatgccaa tagaaatggg 60
gaaggaagag cgcttttggg tgggtgttggg gtttttcaaa ttttttttc atttctttt 120
ggaggtgcaa ggatgggcaa tcttcaacac aagtattgtt ggggcaccca gcaagtactc 180
ataagttttg ttgttgcaag gaaggggtga aacagatagg gagagagacg gagacagtcg 240
agagcgtaaa aataaaatgt gtactaggca cgattaatag ttgtagtgc acttcccaag 300
actcaaacac acaattatta ttaaatatat atatatttat atatatatat gtgcacatat 360
ataagtgggg aaacaaatat aactttgaat gtcaaggggc gaggttaatt tgtgggttat 420
attttcagag ggggggtttt aatgggtcctt atttcgccaa tttaccgcca gaagctgcaa 480
gaacttggtc aatttgccc tgctgcgata taggttcgcc aacatcaagt tcaactgctga 540
taaaagctag ttctttgcgt aaaatgcgaa ttc 573
```

<210> 285

<211> 470

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (34)..(470)

<223> Area matching Drosophila EST AA438500 (inverted).

<400> 285

```
cacatgcaca agcacgcaca ctgcctcgtt cggcctgcgc tttgtgtatg tgtgcgagac 60
tcttcttctc tctaactgta gctgtagttt ctttcgcttt acgaaaacgc agaagatttt 120
cactttttat tggccccact cgctttgcta attattaatt tagctacctt aatttattca 180
gcaatcacca gttttcaatt gctcaacaca caaaggcgga cgcggaacac aacacgcaca 240
catctcgaag tcggacacaa aaggagtggc cgtcgcagtc ttgttcttcc agtgtctgtt 300
```

gttggtgctg ttcttacgcg ggccgaaaac tcccttcccg tatagttttt tgttagecct 360  
tccaggttc cataactata cggaagttat attgttgatt tgggttttat ctaagccgct 420  
ttcagagcaa cactccgaaa attaatactc ttgggttttc ccttcgcttt 470

<210> 286

<211> 444

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (14)..(153)

<223> Area matching Drosophila EST AI456286

<220>

<221> misc\_feature

<222> (216)..(348)

<223> Area matching Drosophila EST AI456286

<220>

<221> misc\_feature

<222> (419)..(444)

<223> Area matching Drosophila EST AI456286

<220>

<221> intron

<222> (154)..(215)

<223> Probable intron in gene represented by EST  
AI456286

<220>

<221> intron

<222> (349)..(418)

<223> Probable intron in gene represented by EST  
AI456286

<400> 286

gtgctgtgta taaattgttt ttaggaccta ggctaggaat tactggttgc acacactcag 60  
cgccacagct ccaccgacca cgcaccttgc aaggacccac catgaactcc aaggacaagt 120  
ccaagttaa gttgttcctc aaatcgctgc cggcaggtaa caaagtgggt gcaccattgt 180  
gggcaagata actcaattgg gattccgggg attcacaggt tacgtgggag agcggaccct 240  
gcggccggag tttagagagg aactgcgtcc ggagcagccg gtggcccagc gctgccggat 300  
gctgaaagag ctgggagaca cgcagctgca caacttcaat ctggacgaag tgcgttccat 360  
cgaattgccg ccatgccatg aacatgtttt tatttctcgt taattcgtcc ccacagaacg 420  
ccatcaccat tctgttcaat ctca 444

<210> 287

<211> 512

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (41)..(56)

<223> Area matching *Drosophila* EST AI062265. This EST  
forms a 1475bp contig with ESTs AA694862 and  
AI064128 and has sequence similarity to *C. elegans*  
UNC51 gene.

<220>

<221> intron

<222> (57)..(222)

<223> Probable intron in gene represented by EST  
AI062265.

<220>

<221> misc\_feature

<222> (223)..(353)

<223> Area matching *Drosophila* EST AI062265.

<400> 287

atctgagtgt caaggggacg ctcagcgagg ataccgtag actcttcttc gtgcaactag 60  
gtgagattcg aaaatcctat ataaggggta gccctaacta ataattgtaa aagatcaata 120  
taaaatgtaa cattaatatt actttagaac aacgaaatgt attataatta actatcagaa 180  
gatcggaagt tatagtatac cattatttcc atttccgtaa ttctagctgg tgctatgaaa 240  
gcactttata ccaaaggaat tgtgcatcgt gatctcaagc cacaaaacat tctgctatcg 300  
cacaattatg gcaaaacatt gccagctcca tcgaaaataa ccctgaaaat tggtaagtct 360  
tgtaatcttg taaaatctaa gaaacaaaat ctgttacctc ttttgaaagt tgttacttaa 420  
aaaactgggt attactacga aatcttcatg ttaatcaaat acttccactg ctacttgta 480  
cttatactgc ctgcaacttt tctttattac ag 512

<210> 288

<211> 465

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(429)

<223> Area matching *Drosophila* EST AA247020 (inverted).

<400> 288

gcgtgggtgca cctgcggccg cttaaagatg aagaggaagt ggagtggag gaggaatgga 60  
acaggaggac caggagccag gaggtctctt tctcttcttt ttctcgttca atgacacaga 120  
aatctttcct ctctgtcttc gctttgtgcg ctcttcttc caatatacaa gcgagctttt 180  
tatatgtgcg agtgcgactg cgaggccatc gctgcgttta tctccctctg tctgtgtgtg 240  
tgtgcgtttg tgtgtgttgg agtgcgtgtg gctacacaca aagtaatatt ttcaagcacg 300  
tttttcatgc acttcgagcc gttttttgtc tattgccgca tagaaaacga ataaacgcca 360  
ctttcatcta caatttggtg ttacaattcg tgcattttg tgcacttttc actatcaaaa 420  
accgtttaa tctgtttcac cttgcgacaa gaaaaattac acacc 465

<210> 289

<211> 285

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(143)

<223> Area matching Drosophila EST AA264635.

<400> 289

```
gccagtagca gcaacaattc cagttccacg gacaacaatc acggaggcca caatccgctg 60
aaccgactgt cctgaagtc cgccggaaag cgtaatcagg agagcatgtc gcattcccag 120
ccgaacggcg gctggataaa cggttaaggcg gaaaacccgg aggaaaatca tctaaggagc 180
cgactgtttt atggttggtc gagagggggg ggagggcacg gcaggtgcac tgcgtctgtg 240
agttattgat ttttcacaca acttaagcag tgtcccaggg gagcg 285
```

<210> 290

<211> 575

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (58)..(491)

<223> Area matching Drosophila EST AA201749. This EST  
forms a 877bp conmtig with EST AA803278.

<400> 290

```
tcgtagccct tatgtttcct gcaatcgatg tttctacett cactttcggt tccggcggtg 60
tgcgtaagtt gctccgcgtt ttcgcaattt taagcgatta tcactttggt tgaactctag 120
gccggccatg tgcctataag ttaacagcaa agcatatcgt cgccattggg accaaagtaa 180
ctctcaaadc tggttcaatt ttaatccgta gaaattttac atcatggaca attctggaaa 240
taaccgctac gagctgttgt tcatggacga cgatgactcc tctgggctcg cacagcccac 300
agattgccgc tgtagtcgcg gcgcccgaaga agccggaacc ggcaaaggcg ccaaaggcac 360
caaagagcaa gtcggagaag gagaacaagc cggttgtggc tgcccgcaag gccaacgctc 420
cggtaggctaa aaacgctagt ccagtgaag gcggcaaggg tcccgtgtgc ggggatgtgg 480
gtcgtcccaa gaacccaaca gcaaacggtg ccaacaacca gggcagggtc aacaacaacc 540
aacgctacgg aaataaggag tcgaacggag aattc 575
```

<210> 291

<211> 460

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(162)

<223> Area matching *Drosophila* EST AA392551.

<400> 291

```
cactggcccc aagacgttgg aattttgtga attgttggtg ctgcagccca gcaataacgg 60
tacagaggac aacagtatca gcaacaaata caacaaaaag gaatgacaaa gtgaaaccga 120
ctgcgctgcc ccacaaacta cgacaacatt aataacaata ataacaaaac gaaataggaa 180
gagcaaaact gtgatctctg cttaactttt tttatTTTTT gggcaattgt tcaatttggc 240
tgtgctcaaa agtaaattaa gtcaactcgt tacgcgtatt tgcggtgttt ggcaacgctt 300
tttccaaccg acgactggaa aatcaattct tcggattgcc aaaggggaac aacaactagc 360
agttgttgaa gttttccttt atattttttg cggccacccc caaaacaaaa agcctagttt 420
ttagaagaaa gaagaatgga agaagaaaga aagaaccgcg                                460
```

<210> 292

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(379)

<223> Area matching *Drosophila* EST AA438539. This EST  
forms a 1200bp contig with ESTs AA201773, AA263752  
and AA439563. This contig has sequence similarity  
to Human ERF 1 gen.

<400> 292



ggtagagtg taataatgaa ataaccagtt ttogaatttc gttcacaaca aaagtgcggg 60  
 cctttcatgc caaaatactt tggtttcgaa ttgtttttca aattcgaatc gaggttttcc 120  
 agctttccag tttgacagcg agagaacgaa agagagcgag ggcgaattac ggtgttcgcg 180  
 ctctgcttgt gctttccact ccactcccct tcttaacttc cccccacca gcctatatac 240  
 tctgtgtgca tgtgtaaatg aatactttaa aacgttttta atcgttgagc tgtattcatc 300  
 gccagccacg ttaaaaggaa gaacgtgtta tgttgaatac gaccatcaga agatcttagc 360  
 gaaaggattc caggagccca aattcttaat ccccatccca cacacacaca tatactcgca 420  
 cgtaggcac gctctcttgt tgagaagaaa gggtttaaata taaagaagcc acc 473

<210> 293

<211> 446

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (297)..(446)

<223> Area matching *Drosophila* EST AA141715.

<400> 293

gccttaccgc tttttattta tttttctttc tgtttgttta agttccctct tttctttgct 60  
 gattgtttcg ctttctgctt gccagtgtga gtgcaggagt aactgtgtgt gggcaatgag 120  
 ctctcttttc gtttgtcttt cgctgtcgtc tgtttatgta tatttaatgg cctgacttcg 180  
 aaattaaagc caccgacatc ggatgacgca ctggtgactg ggcctacaat agtggtagtt 240  
 gcgctgctca cattcttgct catggcgaaa tatttctttt tgtagagtta ctttgagtta 300  
 cgatcacagg gtgcctagtt tcatgcgaat agttgccaat tgtgggcaac attaaaaata 360  
 aattaaccga attggtctta tttgcctcta atttgcaaata atcagagttg aagaatgtgt 420  
 agcgaaatag gtatctcaaa aaccgc 446

<210> 294

<211> 161

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (80)..(161)

<223> Area matching Drosophila EST AA695862.

<400> 294

atttaactta accacttata attgcctcct cgcagtccca tgtaactca gtttactgag 60  
aggcgctcgag gcgttcgtac ccttagtat cagtttcacg gtcgttggtc gtaagaacg 120  
catttcacaa ctggcaacaa ttaagccaaa ttaattgtat t 161

<210> 295

<211> 132

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (2)..(132)

<223> Area matching Drosophila EST AA201517.

<400> 295

ctcgagaaaa cgtgggggttg aaaaaccttt gagcaacgtt gtgccaattc cacaattaaa 60  
ccgcagagtt tgcacaattg gcggttacac ctcatgtct gcccttattt accaaaccca 120  
ttaaccgaat tc 132

<210> 296

<211> 238

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (176)..(238)

<223> Area matching Drosophila EST AA202297. This EST  
has sequence similarity to vacuolar ATPase genes.

<400> 296

ggctagattg accagcaaag cagcgaagag gaggagagaa gaaagcggga gagaaaagag 60  
aaggcgaaga gaggacggca cttagttggt gttttgaagt cgaactgggt tacagttagc 120  
agtttagcagt tgcctctcag ctggctcagt gtttttttag tggtcgagct gtgcgtgtga 180  
actgtgatat tgcgatattg ggctatcgca attggaaact ggacttttgg ttgaattc 238

<210> 297

<211> 51

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(33)

<223> Area matching *Drosophila* EST AA567483 (inverted).

<400> 297

ctctgggggt tgcgccgct ttctgagcgt cacggtgtcg ttccggaatt c 51

<210> 298

<211> 468

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(209)

<223> Area matching *Drosophila* EST AA817479.

<220>

<221> intron

<222> (210)..(270)

<223> Probable intron in gene represented by EST  
AA817479.

<220>

<221> misc\_feature

<222> (271)..(468)

<223> Area matching Drosophila EST AA817479.

<400> 298

```
gttcacagca cttaaaagaa cacttgggaa aaacaataaa aatatttcgc aaattatggc 60
gaagcgataa gtcagccaaa aattgaatcc atcggagcga ctgccttgga gccacagccc 120
acccatgatg acgaccgact tcgcggggcag ccagttcgtg tccagcaatc ccaacaccag 180
ctgtagtgca tcccgtctggc taacggagga ggtatttgca tggatatgca atttgaaaat 240
gatttgattc acatatttct gttgttctgt aggtctttaa actaatcgaa attgtgcagc 300
gcgacgaagc catctacaat ccgaagcaca aatactactt ttgccgcccc gtacgttggga 360
aaacttttgg ccgaggttga tttgaaactt ggaaaagaat ccgggcgccc agtctggcca 420
attggaacaa tttgcgcac tcgttccgac aaaaattcac cactatct 468
```

<210> 299

<211> 365

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (17)..(139)

<223> Area matching Drosophila EST AA441327. This EST  
has sequence similarity to Rat sodium dependant  
dicarboxylate transporter, AB001321.

<400> 299

```
gtcgcgcatt tcaccgtttc cgaatcggac gaaccggggc tgattgctct cctgctgctt 60
tcgagatcga gtcccagataa ggatataact acaacctaaa gaggaatcca agcctcctcc 120
tgccgctagt ttcgaaaagt aatagagta cttgttatca actgggaagc ggagatacat 180
agctccgata ttctgtgaa agccagacaa acggatacca acgaacaatc gccatgtgcg 240
tcgtcgtccc ttctcgtttc acacatcgtg cgataaaaat accgctttgc tttttgtgtt 300
tatttaaaaa ttttggttag gaagttgaac tccaactcct tgacgtttgc attttcccca 360
ccacc 365
```

<210> 300

<211> 432

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(391)

<223> Area matching *Drosophila* EST AA698011.

<400> 300

```
ccgtcgcttt cttcgcttat cgggtgtgtgc gtgcgcctgc ctacgtgtgt gctgtgcatg 60
cgatttgtgt taacaaaatg tgattagcaa aaatacaaag aaatcaggca tagtggaaca 120
aggcattgtg gctgaaacaa cagtcggcgg cagtaacagt cgacactaaa aaacaacaaa 180
atatacacat atacatatat taataatagt acatacgaaa catatctttt gagatataca 240
cgaaatgcga aaatttgcac aaaaagcaat gcgctggcgc ggcaacaaag cgcggccgta 300
aaaaaataag ttacgccaac gacaattctg aattttgtgc tttatccgca gcagccagca 360
caattaaatt aatatttgaa ctacccccaa agttaacaaa agttagccag cccattaaaa 420
aaaaatacac ac                                     432
```

<210> 301

<211> 207

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (67)..(207)

<223> Area matching *Drosophila* EST AA951986. This EST  
has sequence similarity to Human nucleolar protein  
p40 gene.

<400> 301

```
gtgtatctca ataatcctcc cagtaagccg cgtgaaggtc aactgcaac atcgatagcc 60
```

gatgactagg ccagcaacaa tcgataattc ttacccccgc acgtgttgaa attgttttct 120  
tttatttgga tcagatttaa tttagctaata ccagacatgt cggactttga aatggaggac 180  
agtgcctcgg gctacgactc aggggat 207

<210> 302

<211> 186

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(186)

<223> Area matching Drosophila EST AI295731. This EST  
forms a 2018bp contig with ESTs AI258429,  
AA696170, AI109519 and AA391348, and has sequence  
similarity to Mouse APG-1 gene.

<400> 302

ggccggacgc tagaaatttc cattcgcagg cgaaaagcga atccataatt gatgtgaatg 60  
tgagaagcat atatcgaatc gaatgttctg gacttggttg tcaaacgaaa agaacagatt 120  
gcaagccgac acgtgcgtgg ctgtgtgttc agtatacatt atatctaatt cccgtctccc 180  
ctctct 186

<210> 303

<211> 82

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(82)

<223> Area matching Drosophila EST AA201430.

<400> 303

agaccgacca actggaggcc agatacagat accatcattg tcatttccca attgaccaga 60

gaaagaaacc tgctgcgaat tc

82

<210> 304

<211> 54

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (15)..(54)

<223> Area matching Drosophila EST AA263209. This EST  
has matches Drosophila ARP gene Accession number  
AF132912..

<400> 304

ggccacctaa cgccaacaat tcggggacaa aatcaaactg catgcaaaga attc 54

<210> 305

<211> 1004

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(140)

<223> Area matching Drosophila EST AA541045.

<400> 305

ccccaccgc agccactcac acacgcaaac atgaggctgt ttgcggcagc aacagttgcg 60  
cttgtattgc ttctgggcca agcagctggc gaggagcttg cggaggagcg agcgggacag 120  
gcacagggcg atgcggaggt gagtgtgcgt gtgttgtttt gttatgattc agcagcgcg 180  
ctatttcac atcaaaacgc ttctggggag caaaaagtaa cgtaatcccc ttcaaagtga 240  
ctaaggcttg tgggcaggga ttacggttcg acattaagcg ggaaatatgc aattttacag 300  
ttaactctca ctgcgtctca cccgcttacc caaaaacaca tacacaggag ctcacctaaa 360  
ccgaacacac ctatactcac acacattcgc catattggct gacgtccctt gttttttcct 420

ctttgaagta cactgacaag aaaggatgtc aactgtccag cctcagtggc tgaagtgcaa 480  
 tttcaacaat gattttcatc ttcaatgaaa tctgcgatat tccaaacaaa aaatgtttta 540  
 ttgcgagttt taaaaaatag cccattcttg ctcttttcgc ttttctacgc ctgttttggc 600  
 ctttgtttat tctgcgacgt gtcagctggt tgcttatttt gaccgataga accccattga 660  
 tccccagact gccgttgttt ttgcaactgc ttcttatcgg ggtattttta taggccccac 720  
 tagtccgttt aaaattgctt tgtgcccga attgctgttt aatttctgcg ttaagtgtta 780  
 cttccccaca agcggaaggg gaatttaaatt ttgcaaggct tttttttacg tccgttcaaa 840  
 cgcagccact gttttttctt ttgcggaag cctgcaatcg aatgatgcta gcaagtactc 900  
 atagggtagt tatgaagctt acgaaagaat ggggatcatc ttcacagcc cactctatat 960  
 taagtttgcc accatccgtt ggacattaac ggtcacttag tatt  
 1004

<210> 306

<211> 566

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (392)..(501)

<223> Area matching *Drosophila* EST AA390337.

<400> 306

gaccagggtca ttgaccccaa aggattactt tccgatagtt ttgtcgtgca gtattggtga 60  
 acttggaat tctttcgaca cttaacctat aaacttgga aggaacgcaa tgtagcaaaa 120  
 ctactgttct tggtagacagg gggtttaagg tagactaaca aggacaattt tatgacactg 180  
 aagccctatg gagtaagaat caaagaactg ctgtattttg gtttgtataa atgaataaaa 240  
 cgttctacgc taattgaaga gcattcgaag aggtttgaat acagcgccat agggtagacca 300  
 gcttgtggag cattgaaggt atttcttggt ttaagaatga tcacgggatg gtcacactag 360  
 aaatacagcc aaacaaaaca actaaaagca tttcgagcgc taacaaatat atatctttcg 420  
 acttgactca ttcgcattcc ggttgaccgt gtcgcgcctg cagcatgtct gaaaagccga 480  
 ctgttctgat tttgggtggc taagttggtc ccgcctgcac ctctcatcg tcacctgccc 540  
 ccgctcccat ccacacttcc gctta 566

<210> 307

<211> 440



<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(202)

<223> Area matching *Drosophila* EST AA141555 (inverted)

<220>

<221> intron

<222> (203)..(272)

<223> Probable intron in gene represented by EST  
AA141555.

<220>

<221> misc\_feature

<222> (273)..(440)

<223> Area matching *Drosophila* EST AA141555 (inverted).

<400> 307

```
tgtagaactt tattttcgat ttagttttgt ttactaataa acttcgttag ctatgacaaa 60
tctacaacgc tggctatattt acgcatcgct ctttgcgatt ccctatctct ccgttgtttt 120
gggaacagtg caaacgccac taactaccaa gtatttcctg cacattcagc ttttaccact 180
tttgctcctc gtgatttttg gtgtgagttt ttggatatga atcaatgcag ataacagctc 240
ttattgacta ctattatata ttaccctcag atatattccg tttggactgt tctatataga 300
actctgactt ttaacgattg tcccgaggcc cgccaaggag ctgcaggatg aaattcagga 360
ggctcgcaag ggatttgata tccaagggga tttcggtttc gagattagga gacttccaga 420
acttgtgcat ggtaaattctg                                         440
```

<210> 308

<211> 402

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (158)..(252)

<223> Area matching Drosophila EST AA263730.

<400> 308

```
ggctacacct ggctgcgtta tcgatagttc gggccgatag ttgccgatgg tcagctaate 60
gcagtgaac tccgctagct cacagcaata acacgaggag taatgaagtc gctctagaat 120
ataaataaac aattcattaa ttaaaatagc gacatgggtca actggaggaa gtttatcttg 180
tggttcgccc aggagcatgt cgactttcgc gtgcaggagt ttgattcgct ggtcaaaatg 240
tttggacttc aggtccggcg gcttacagaa cacaccaggg taaagtgttt tagtaccaga 300
atthttgaaaa cgcaagatta acaaattcca ccttccttat aactttttaa acctgggggg 360
ttaatgatat atcccaactt gggaatttta attaatatgg tt 402
```

<210> 309

<211> 573

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (324)..(370)

<223> Area matching Drosophila EST AI259832. This EST overlaps EST AA990765 and has sequence similarity to Human ubiquitin conjugating enzyme 12 gene.

<220>

<221> intron

<222> (371)..(447)

<223> Probable intron in gene represented by EST AI259832.

<220>

<221> misc\_feature

<222> (448)..(545)

<223> Area matching Drosophila EST AI259832.

<400> 309

gagcagactg ttatcgggtg caaccatcga ttaattacac atategctgg gcagaaacaa 60  
ggaaaggata gaaagcactc gaagtgattt ttacatcag ttctattggt aacggtaggc 120  
caaagattca gtgaaacaat tgcccttaaa cactgacat ttcaaacaat gcaacctgtc 180  
cctcaagcag caaaagcccc ccagagagcc agaaactttc gagcacagcc aaacgcggaa 240  
gacgaaaacgc cagcgagacg aggacgcca gatgattaaa ctattcacgc ttaagcagca 300  
gaagaaagac ggcgagcaaa agggcagtca gcagaagaaa gcgtccgccg gccagctgc 360  
gcatacagaa aggtagtctt caatccagca cctggtatga tcaactcttg cttattactt 420  
atccatcttg ggctggtttc ttccccaga tattaacgaa ctgaacctgc caaacacttg 480  
cgccacagac tttcccgatc ccaaggactt gcttaacttc agcttatcat ctgcgccgac 540  
gaggctttta cgaaacggcg ctttcgtgtt caa 573

<210> 310

<211> 483

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (75)..(483)

<223> Area matching *Drosophila* EST AI514268.

<400> 310

gctgagctat gggcagcagc cgacgagtgc tctgctcggc acggtcggca gtcattctaa 60  
tcgacgcctg ctgatgcgga cgcgctcttc ggatcgaatc gaatcgcctt cgaatggctg 120  
gtcgttgggt gatcaagtgt cgcgtgcgct aatcattaat taagtgtctt aggaaaaagt 180  
cccaattggc tatcgaaaacg ggtttccatc taccagtgc tttgcgagct gccttgccctt 240  
tgccggcaggc tcatttgtga aaaagaaata tcgttgccgc cagttagatt tcacctgaat 300  
acctgcaatc gaacgcaatt atcataccgg caaatggaa accacaacac ctgtgctcga 360  
cctgtgatgc cgcacaactc aactactgtg gcgcctcgaa agcgctctat gcaaatcgaa 420  
atcgctgat atggtgtata tcatggttct ggcgttttgg caattcgctg gcctttcatt 480  
tgg 483

<210> 311

<211> 435

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(435)

<223> Area matching *Drosophila* Genomic sequence

AC006562. This EST matches the genomic sequence

20bp 3' to NPS0411. This EST has sequence

similarity to Human molybdenum cofactor

biosynthesis protein gene.

<400> 311

```
atcatatgga cgagctgcca ggcagcttt cgccaaagct tttgttctag tgccagtgtt 60
aggcagcatt tgaaatTTTT tgccggttga ttgattgtat gggggggggg gggggagcca 120
ccaggggggtt gacgcttcag agctttgacc tgcaaaaaac ctagcagaaa tgaagatgca 180
gtgacagcag tttacttata agtgaatgga gtttaatttc atttatttta gtacagtata 240
caataaatga ttaatatTTG ctatacagat gtaatgcctt gcaaagagtt acaagtgtta 300
taaacattca agcatctaaa ttttgacatt cttagtttgc ttttaaattt tttttttaa 360
ttttacccaa acttaaacat aaaaatgatc aaatacgaga tataaagacc catattaaat 420
accaggccct tctta
```

435

<210> 312

<211> 442

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(71)

<223> Area matching *Drosophila* EST AA201987. This EST

has sequence similarity to aspariginase genes.

<220>

<221> intron

<222> (72)..(147)

<223> Probable intron in gene represented by EST  
AA201987.

<220>

<221> misc\_feature

<222> (148)..(435)

<223> Area matching Drosophila EST AA201987.

<400> 312

```
agttgggcca acaacaaggc gcgagcataa acagcgatac caacatggcc ggcttcgtcg 60
cgggtgcacac gggtagctat cttggccatg gcggttcgga tccgccgggc agacagccag 120
atgattgatg accgctactt gctctcaggg gctgggaact gcacgcacga aacgaagtac 180
cagcgggtga ttaaggaggc ctgcctgcgc gccacggaga tccttcgcaa cggcgggatcc 240
gccgtcgatg cctgcgaggc ggccattgtg cggctggaga actgcggcta cacaaacgcc 300
ggctatggct ccaatctctg catggacggc tctgtgcagt gcgatgcggc tataatggga 360
tggctcaacg cttaactttg gcgcctgcac cgaacgtagg tcggggttgaa agaaccccat 420
acagttggcg agaccatatt cc                                         442
```

<210> 313

<211> 408

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (12)..(408)

<223> Area matching Drosophila EST AA540020.

<400> 313

```
gttttagtggc gagtttgtcg gcgcgaaacg ctcgttggtc cttttgtttc gaaagagatc 60
ctattcgaag atccccgac cttgcgagga tcgtctagtg caatatatag actagttaat 120
ttacttttgg aaaaataagg acaccagcag ggccgccgat ttgtgcccct ttcttgaaag 180
tcgcaaaaaca aaaacaacga cgacaacaac aaagcggaga caaagaatcg acaagtagcg 240
```

ataaacgaaa tcattcccgg ggaaaacctt ggagacgggt gattcactgc caataccact 300  
 gccaatgga gactgatcac ggcagccatc cttggcgctc ccaataagcg gagtcaccgg 360  
 aacgcgtggg aagccatata cggaatgcag cccgccggag cttcgaga 408

<210> 314

<211> 467

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(38)

<223> Area matching *Drosophila* EST AA201670.

<400> 314

ctgtggacgg tcgtcaatgc gtgaatatc ttctatgtgt aagtgggtgtg cgtgtatgta 60  
 gatttctggt taagaaaagc cccaaaaacc aaagcgcccc gcaaaatata tattgagtct 120  
 tcttggccca acaacaaatc tgccgccgga ctttcgccgg agggcgagtg aaaaattcag 180  
 tttctctcct ctcgacgatg cactttggag gctgtgtgag tgtgtgtgcg agtgagtgcg 240  
 tgtgtgtata catatgcaaa tgattggatg tcgaatcctt gcatcatcat catcttcata 300  
 aacacttggc gaaaaaccgc aggaaaacgc aagcagccga acaaaaaaag agagcctctc 360  
 aagacaacgg cagcggccaa aagtgaacgc gcaacaaacg ccggccaagc aggcgcggca 420  
 attatttata aatctaaagc cgtagcccc cctctctctc cactcac 467

<210> 315

<211> 464

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (15)..(404)

<223> Area matching *Drosophila* EST AA201957.

<400> 315

gcggtggcct ttgtttagt caaattaggc gaaaacgaaa caaacaaaaa tcagaaatat 60  
 agatcgaatg ctatggcgca cgtaaagcgg tatcggagggt cgtctaagtc ctcggaggaa 120  
 ggcgacctgg acaacgagga ctacgtgcca tacgtaccgg tgaaggagcg gaagaagcag 180  
 cacatgataa agctgggcag gatcgtgcaa ctggtttcgg aaacggccca gcccaagtcg 240  
 tcaagcgaga atgagaatga agacgactcg cagggtgctc acgatgtcga gacctgggga 300  
 cgcaagtaca acattagtct gctggaccag cacacagaac tgaagaaaat tgccgaggcc 360  
 aaaaagttga gtgcccgtcg aaaagcagct gcgagaggag gaaaaggatt atggagaagc 420  
 atttggtcca acagaaggcc cttatggggg tgtggcaaaa gttg 464

<210> 316

<211> 477

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(353)

<223> Area matching *Drosophila* EST AA695344.

<400> 316

gcttagacaa tacaattcaa aatgaatgta ggcaagataa gcgttgtcac cagacttcct 60  
 gccctccgct cgtgcgcca gtactcgagc gctgcgaaag cggaactgcc ggcttccttg 120  
 gtcggcgacg tggatgtgga accaacatat cccagacgg tggacagatc cggcctgcaa 180  
 ccacaacaca aaaatgtgct ccttaacaaa ttgccatacc aggaacctca ctctggatt 240  
 catttgaccg agaagtacca gagacaggca ttcggccggt atggggccca gagcaatgtg 300  
 aatcccaaga tttgcttcga ttcccacgga gagaaagaca gcaggcagggt tatgcaacta 360  
 gaaacctcct gaaaatgctg gagaagaacc gcgcgcagaa ggcagaggag ctggcaagga 420  
 taaatgcccg tgaagaggac attgcgaaga agatggagaa gttgaccaca gtggaag 477

<210> 317

<211> 451

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(450)

<223> Area matching Drosophila EST AA441018.

<400> 317

```
ggcgggagct gtacatgaat ttcatttggg aaacaaattt attcttaaaa tggtaagaac 60
acggccggtg ccgtgtgttc cgtcgccaga tgtgaacacc gcaacgagac gcaatcccgg 120
gcgtcccaag aaacagtcca tcggagctga cttaagcaca acgataagca aaccggggcg 180
tcccaagaag ctgtccatcg gagctgattt gaccacaata cgtaaaccgg ggcgccccaa 240
gaaactcgga gctgatttga ccacgataat acgaaaaccc gggcgccccg cgaaactatc 300
aaacaaacaa tctttgacag ccctaaacga gccagaagtg tcgcataaga aaatgcgtgg 360
taaaaataag gcgcattaag gtaaaaaacg gtgtcgtatt ccgaaatttc tcgaatgatg 420
cgctggatg tgggatgcca gcacttttga a                                     451
```

<210> 318

<211> 334

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (301)..(334)

<223> Area matching Drosophila EST AA202301 (inverted).

<400> 318

```
gtatatacta tacgcgagag ggagcaggca cacacaaacg aaaagcctgc ctccaattga 60
ttagtattag tacttcgaat agtattacta tggttattgt tttcatctag ctgaactttca 120
attgtttggg gctgatattt agctagattc ccaggtgcg attactcatt tggcttttgt 180
ttcgagacca ctgtgccaga tttctgggtg agagcgtggg gagtttcggt tcaactcacc 240
acagaaactg ttgttgcgcg tcgcgtcttc tatttaggcg gctctctccc acacacggtc 300
aactacagt ccaaaaatga acgaatatac caca                                     334
```

<210> 319

<211> 393

<212> DNA



<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (245)..(393)

<223> Area matching *Drosophila* EST AA735819.

<400> 319

```
cctaaattgc aacaaagaaa attgtatgaa atatacgaag cgaagagcag agcgaaagcg 60
acgatgaaaa agaggctgct gcttgaaaaa taagaagagg tggaggagca agaagaagag 120
cagcagcagc cgtcgcgagt tttttacacg cgtgtgttag tgtgcataca attgtgtatg 180
aaaaagaata aaagctaata taaagtgtca aacgtaatct tgtatatctc cgtgtttctt 240
gcagcgcttg acaacgaaat ttatattaca tagtaaatgc gaaatacaac aaagggttaat 300
catattgctt aatcagagta ctgcggtttc aaacgtcttc gtcttcccca tcttctaaac 360
tggaatgcac ccaacaccaa acaaccaaaa ccc 393
```

<210> 320

<211> 147

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(147)

<223> Area matching *Drosophila* EST AA440886. This EST  
overlaps EST AA95395 and has sequence similarity  
to *C.elegans* UMP kinase.

<400> 320

```
cgctgacgca gcaccaattg cgacattcca aggccagcaa taggttcac accaccacct 60
ccacagcccc accacacaat atcggaatca tgagcgtaga gaagccaaag attgtctttg 120
ttttgggcgg tcccggggcc ggcaagg 147
```

<210> 321

<211> 602

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (76) .. (217)

<223> Area matching Drosophila EST AA8033640. This EST  
forms a 859bp contig with ESTs AA803683 and  
AA803676 and has sequence similarity to Human  
Ribosomal L28 protein.

<400> 321

```
accagtgttt cggcaagcgc agccaacttc gcgctatgtc ggctgccata ttctttcttc 60
ttgatttcaa cgagaaaggt ggcatttgcg ttgttctcga tttgggtaag ttctagcggt 120
ctctcagcgt cccaagcgct ccgcaagtgt agaggataaa tgcctgcacc acgtgttgcc 180
gtctatattg ctgccggccc gctaaacctc ggaggtaaatt tgagtttacc cacacgtgca 240
acgcagcggg caaatagtga ataaaatttg aattaattgt agcgaacca taatggactt 300
aatcaaatag tctatattac taagcgaacc tgcgttgatc aataccaaat ttaatatcgt 360
ttctctttct ttgcatgctg cttttcctac tgctgattta catggatctt tcaataaagg 420
taagaacacg tgtggtctta aaatgcgtga ttaattctgt gatgaatgat tgagcagaag 480
agttcttgaa gactatattc atcaccaga ctgatataca gaaatctcgt gctttattca 540
agaaacataa tctaactgcc gactttcttt tagttccatg ttcacctttg gctgctaatt 600
ca 602
```

<210> 322

<211> 1073

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (472) .. (786)

<223> Area matching Drosophila EST AI257267. This EST  
has sequence similarity to Chick glycine cleavage  
system h protein.

<220>

<221> intron

<222> (787)..(841)

<223> Probable intron in gene represented by EST  
AI257267.

<220>

<221> misc\_feature

<222> (842)..(1073)

<223> Area matching Drosophila EST AI257267.

<400> 322

ttttttttgt agagctgata aggggaataaa tcgggccccca gcaacgattt tattgggagt 60  
agataagaat accggaggag catcgacgtg gttgtcggaa attaagatga ctgctttaat 120  
ctttagtctg atctccaaca tttagaagag ataaaagtca agcacctggt ataaaaaat 180  
acatttttga tgtttgattt ctttacattt tttagtattt caaatagaag caaccatttt 240  
gacaacttat gtaattgaag tattttttgtg gtgtactatt ttctaattaa atcgaaagtg 300  
cgaaagctca aatttaatta taagaaatac agtcctccaa taaactaaat aaatcttgaa 360  
gttttcaatc tgcccgcgga aatgttgggc agtgcgataa ccggtaatct attatcgcta 420  
tcgatatgca tgccttacgc catttttagg cacattttga agaagccgct gtttactcgg 480  
gtcaacaaaa gttcacgaat tatattctgg attgtgataa gccgggcaat attcgacttt 540  
catccccgatt gccgggcatt aaacgtagcg tgtgtgtttt caaatcggat cacttgtcac 600  
cgaaacaccc ccgggaacgg ttggaaaatt catctcgccg gcagttgcct ttgtttttga 660  
ctgggaaaat atggtattca taacgaaatt cgcaaggatt gggctgcagg ccgcccgcga 720  
gcttagtgtc acgccccttg gcgccgtcca ggctcgcgcc attcacctga caagccttct 780  
agccaaaggt aaggcaattg tttatgcaat agccactgaa tctcaaactg taatccccgc 840  
cagaacgccg atacacaaac aaacacgagt ggggtggaggt ggtatccggc agcaatgcc 900  
tagtaggcat cttcagctac gccaggagg ctctcgggga tgtggtggtc gcccaacttc 960  
cagaacccgg cacggaactt aagcaggatg acgaatgtgg ggccctggaa agcgttaaag  
1020  
cggctacgag gtgtattcac cccgtagtgg caaggtaatt ggaaagaatg ccc  
1073

<210> 323

<211> 501

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(75)

<223> Area matching *Drosophila* EST AA539327.

<400> 323

```
ctctgggtcg tcttgcagtt agccggagct gattcgcccg aggaggagca aggcgttcgc 60
tacgcaaacc gctgcgaagc ctgcaaaatc ctggccaccg aattggaagc tcgacttgga 120
gagaccggca agtcgcacga cgtcatcgaa atcggatact ccgttgacga tgtgaagccc 180
aagaagcgcga ctgaataccg ggcgagcgaa ctgcgactgc tcgagtcctt ggagaacgtg 240
tgcgagcgag tgttgggagt acaatctgca caaggaacgc tctgacagca cgagattcgc 300
caaaggtatg tcccagacct ttcagacgct ccatggccct tgtggacaag gggcgtcaag 360
gtgggatctg gggaataccc tacgaagctt gtggggacaa gcccccggtg ggaaggtcac 420
cccaaataaa aaccccgagt gcgaaaacct actggaaggg agtacgagga aaccatcagc 480
gactgggtac ttttaagcac c                                     501
```

<210> 324

<211> 468

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (419)..(468)

<223> Area matching *Drosophila* EST AI539327.

<400> 324

```
gtttaaccca tcgccgcca gttaacccat gacttcggcg gcgagtcacg gatggcagaa 60
ctgtgcggaa tcgaaatgcg agttcgaacg cagagtgcgt gaaaatgagt attatgggaa 120
acattgccac aaattgatgc actacgcagt gctaccttta attgaattat taattatgta 180
ccttaatgaa tgcataattg aataataaac tacgtgcaca cccccccaca attgttgtgc 240
gcacggcgag cggaattgtt cgccgttttt tttttttggt ttttggcctt ctctcgacca 300
```

gccactgtta acctttaact tttgtgcacc gaaccgaacc aaaccgaccg gggcgaacca 360  
 atgtttcgcg gtagtaaaca taagttgggg ctcattaagt aatcacatgg aatattcccg 420  
 cagccaatta aaccaaaaag cgcagaagg gggttgcggg gcagcggg 468

<210> 325

<211> 422

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (92)..(265)

<223> Area matching *Drosophila* EST AI402854.

<400> 325

gtcgaggcgt aacatttcgt gtctttgaaa tgcatacat cgaagtcacc agtttcagtt 60  
 ccaagtttca gtagatttcg ggacatcgtg cggatcgaac gtctggcgct gcgttcacgc 120  
 gactcgtagc ctgcaaggaa tcagttacca gtgaccagta aacagtgatc ggtgaatgtg 180  
 aacagtgact agtgaatgag acagtgaacg agtaacagcc cgaaaattgt tgcatttacg 240  
 agaaatcgca tggatattga aaaaggtata gccaaagatg tatggtaaac aaaaaaaaaa 300  
 aaaaaaaaaa cgcgtgccgt tgttttttag atacacgtgg acagtgggaa tttgtatcta 360  
 gattgttttg gttgggtttt gcttttagca aagtgtactc acccgtgtgc taaatgcata 420  
 cg 422

<210> 326

<211> 354

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(222)

<223> Area matching *Drosophila* EST AA441362. This EST  
 has sequence similarity to mammalian proteasome  
 subunit HsN3.

<220>

<221> intron

<222> (223)..(290)

<223> Probable intron in gene represented by EST  
AA441362.

<220>

<221> misc\_feature

<222> (291)..(354)

<223> Area matching Drosophila EST AA441362.

<400> 326

```
tgcccgtcat tctccggcag cgacaaacat ttcaaagtct cgcgttattc cagtctccga 60
ataaattagc atgttgaaca actacaacag cctagcgcag cccatgtggc agaacggacc 120
cgctcccggc gagttctaca acttcacggg cggacagacg ccggtccagc agctaccgcg 180
ggagctgacc acaatgggac cctatggaac caagcacagc acgtaggaac tgcggatatg 240
tttatatgca gatgtaccac ttgtttacac tccttttact attcccgcag tgcttccagc 300
accacgggca ccttccgtgc ttgggcattc gctatgatta aggagtgatg ctgg      354
```

<210> 327

<211> 227

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(219)

<223> Area matching Drosophila EST AA202487. This EST  
has sequence similarity to Yeast YFY6 gene.

<400> 327

```
gtcgcgtgtt ttatgctcaa gcaattggat gagtacaaaa acgcagagat tttccgcagt 60
cgggacaaca aggctttgaa ggagaagtgc gatataattg tgcacgtggg cggcgtttat 120
gatcatgcc aaaaattgta cgatcaccac caaataacct tcaaggagac ttttagttcc 180
```

gttcgcccag atgtaagcga ggactacaac gttgtcaggt gaattcc

227

<210> 328

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (328)..(455)

<223> Area matching *Drosophila* EST AA263590. This EST  
has sequence similarity to human hRNP F.

<400> 328

agctcgactc acttttcttg ttcttgctac ttttcacacg ggtatgacag atctgagtga 60  
tggttgga cactggcttt tccagggatg gacacgttta taactgtcgc tgtcacggaa 120  
cagtgaata tttaaaatgt ttctgcttca gtatatttca aattcgggta agatcacagt 180  
tagtttatca ttttccttat atttaatttc ttctatcttg cccaaaaaaa gcaaaaaaaa 240  
aatcaaaatc aaaccttggt tctttttcaa cgggtccacat tgatgctggc tactgccagg 300  
cgggtatttt tgatgattta attgcggtca cactgcatct tcaacttgac cgccgtgcta 360  
tttgattaat ctctctgaaa aataagtcaa attaaccgat taaagtttaa aaaaagggcg 420  
atattgggaa agttgaaaca gaagcagaat acgggttagtt cttctgggtc cgcaccaagg 480  
tgtggacatt tagaaaagcg ttatattggg gac 513

<210> 329

<211> 247

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (50)..(113)

<223> Area matching *Drosophila* EST AA201496. This EST  
has sequence similarity to human oxoglutarate  
dehydrogenase.

<400> 329

gtccaggccg tgcgctagca ttaacagtc caccactaac gcaaaagttt tcggctgtaa 60  
aaacgtaa atttaaactt taagcaagtt tagtgtaaaa ataatcaaat catgtgcgtt 120  
aatttgcaaa aagtctgcgg ggctatggtc catttagact tagtactgga ttcagcggaa 180  
aactcgcatt tcgctgtgctt ttcacttgtc ccacattcga ggtccgcttt tgcacatgt 240  
ggaattc 247

<210> 330

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (281)..(510)

<223> Area matching *Drosophila* EST AA391430.

<400> 330

ggctggacga gggctgcacg tgaattgatt gatgatgagc agaactgggtt cgttgaacta 60  
gattatggaa ttaatcgatt tcgtactttg tgtgaaataa acttgtaatg accttttgct 120  
taatatttat taaagattta ttcaattttt tgttttattt ttaaattgcag ttttaaatta 180  
ttgtttgttt acatatgtaa cgacagccct ggtgtttcct gtctaattggc aacgctctga 240  
aattgcgcag caaccccatc tggccacact gaccatttag ttttttggtt atgttgggtt 300  
gtcggaaaaa tcggctgttt tccgtgtgtc ccgtctgcca tgaaaagctg ctaaaaagct 360  
aaatataaaa atcagcgcag cacacacgtt ccgtgcctg cattgggtgc ccattctaata 420  
gggaaattat gtgagtgccg agtcaggaaa acgcacgtg ggtggtatat atccttatat 480  
ccttaagtat gtaactgcgc cccgttggtt 510

<210> 331

<211> 432

<212> DNA

<213> *Drosophila melanogaster*

<220>



<221> misc\_feature

<222> (1)..(50)

<223> Area matching Drosophila ESTs AI292722 and  
AI534704 (inverted).

<400> 331

```
ctgtaagggtt agaatgcttc ttcttaacga tttgtcattc gcctttcttt agagatgggc 60
ttacgcgaaa cacaactatc gcaagccaaa acgaaaatgt aggggtgttc aggtgcagat 120
aattgttttag aaatacctta ttgattaaaa ataatgttct tgacaaccta gaaataaatt 180
taagtcaatc aagttactca atgtcggtat ggtcacaatg cgtacaatta gttaaattag 240
ttagtttggtt caatattaaa aaaatccttt ttttaattaa aaaatagctt taatattatg 300
tatcggaataa tttaatggaa catagataac actatttata atattatacc gtgttataat 360
tgtgataggc atacacaaat ttataagggg aaaaataagc cagggaagg cggcccaggg 420
tggccatttc gt 432
```

<210> 332

<211> 65

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(65)

<223> Area matching Drosophila EST AA439393 (inverted).

<400> 332

```
aatgagccta acttggtttt tcgatcacac gcggcgacgt ttgtttcaac gataattcgg 60
aattc 65
```

<210> 333

<211> 529

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (299)..(512)

<223> Area matching Drosophila ESTs AA820797 and  
AA438876 (inverted).

<400> 333

```
gcgctgtccc aattggaaaa cgaagagagc tcgacttgcg gtaatcgcag cgcagctttc 60
accatacga agacgatgag ctgacgttgt tagaataact tattggaacg tgtccattta 120
gtttgttggt ggcggcgga gggtagagc aggagagcgt ggtaatcaca tgtatgtcta 180
tgccttcgcc ttactggcac tcacttacac acatacacac gcgcacagct gcaggtggaa 240
aattaaaaaa caagagcgga aagagtgcga tttaaactcg ctggcaagcg gcacttacct 300
tgtttctttt tacgtggcca atagtaaag gtggtcggta tcaatattag cgccaagaac 360
gataacacca aagtagtagg aacgttcgc cgtctcatc atactgaaac ttttgaccgc 420
ccatctccga cagcgactat atgtatttg attttgtgg ttttgctggc actggcttg 480
gctcgttcgc ttccgttctt tctctggcgc gttttcctgc cttttcttc 529
```

<210> 334

<211> 486

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(52)

<223> Area matching Drosophila EST AA697891 (inverted).

This EST has sequence similarity to Bovine gamma  
COP.

<400> 334

```
ggtaaaacaa ttgaaatggt tttctggctg cgcttacacg tcactcagcg gtgcccagtt 60
ggttcacatctg ttatcgatgt gaaaactcca gttaagtatc gatagctccg atgttggtct 120
tatctttaaa agaccacctt tttctgcgt tttgtaggca gtatatattc gccgataatg 180
cacattataa ctttcagttt tcaattaact cgacatcgag atctggtagt tttttttgt 240
tcttaaaatt tcttgtttg cttcactgg attgaaaagg aactagttga gattcactta 300
ctgggttcgat tgtatttatc gatagattat cgattgtgaa tgggcggaaa aatagctaag 360
```

ctttgaattt gctccacgtt gactttataa cgaaattgct aagaaattgt atgaatataa 420  
taatggttta aaatttattt acattttcat aatttttacc attaagttgg atccgttttt 480  
aatgg 486

<210> 335

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (31)

<223> Area matching *Drosophila* EST AA696845 (inverted).

<400> 335

ctccagtctg cccaatgcgc gccgcacacc tcggagccgc aaattataaa cacgactgtc 60  
ttcgatttaa cgggctggcc tatcggtcct atcgatgact cgatagtgcg agctggagtg 120  
tgaccatttc ttggtaaaag caaaatcgtg aagagtaagt gtgcgatact atcgaactgt 180  
catatactca accaaataac atctgaaatc tgtttctcac taaaaccgaa atttccatca 240  
gggttaggaa aatatagttt acgcacatca agttgcatag gtcaatccta cgtaaaaaag 300  
gctcgatata ggtaagggtg gacctcagcc tgaacagggc ctaatgcaaa tacattccga 360  
taaatagatg ttatcgataa ccatttggtg tataaccagta aatgctttgt tttggttttc 420  
attcagaaaa ttgacataca tttcttagtc tgcctaaagt tccttggtt gaa 473

<210> 336

<211> 384

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (384)

<223> Area matching *Drosophila* EST AI259031.

<400> 336

atttaaacca aacaaagggg tagtttagag ggttcttcat cgcgagaaaa aggtactacc 60  
 atgtcattgc ccacgaccag agccaccacg gccacgacca ctcacgctgt ggtccaggct 120  
 gtggaaacgt atattcagaa ccagaatttg cttggcgaga tcgctgagct ggacgacatg 180  
 ctgtacgatt tgggtgtccat gcacaaagac aacgagctgg ccctgaaacg ggtgcttgca 240  
 gtgcatccac aacctgttgc agacgaacag caagttaaac gtccgctttg gccaaaagtg 300  
 tttcacaac tggtctccgt ggtgattgcc gacagtcgtg aggattcggc agcccggcgt 360  
 caaatggtgg ccaatttact ggtc 384

<210> 337

<211> 314

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(82)

<223> Area matching *Drosophila* EST AA803464. This EST  
 has sequence similarity to Huamn hypothetical gene  
 KIAA0258.

<400> 337

cactggactc tctcgcccg ggcgtagatg gccgagtcg cacgcagcag ttctgcctta 60  
 atttcaatca tttatttact tttttatttg gtcgcgactc ccgtagagt accgtctgca 120  
 ggaattgttc gataggcccg ccgtagtgga tagcagccgt gcgcgtacgc caaccacttt 180  
 ttaaagtgtc cacctctgat aagtcgtgtt actgaattta aattttcttt ttactctagc 240  
 agaatcccag gtaggccttg ggtataagct cgaaacattg tcattgctgt cgcgcacgag 300  
 aacaaccaga attc 314

<210> 338

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (169)..(489)

<223> Area matching Drosophila EST AA539974.

<400> 338

```
ccctagcact ctcgcgcact tttggcgctc tcctaggcca attcgctcgc tctttttctc 60
ctctgctctt tgtcgtggtg cgatcatgtg tgggggtccgg ctcgcgctcg ctaaactctt 120
aaccagtggc tttttaacca gtttaagttt acatttgctg gagcgcagac gtgtccggaa 180
agcgaacgga agacaagtgg aacggaacac ggccgtataa tcagaaatca aacagagtag 240
tggtgtcgtc acttttgga ctctccataa aaatccgtct gccagtgtt gttgcttctt 300
cttgagtgcg gggttttcat gtatcgccgc cggattccg ccttcgagcc cagcacaccc 360
cgcgtgggag tgctaccctc tccgccggct caatatgcca acccccccg cgacactgcc 420
gccccgaaaa cgccaccaa ctgagcgtac actttggacc ccaatttgcc gaagaaaacg 480
attgcaaca
```

489

<210> 339

<211> 524

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(46)

<223> Area matching Drosophila EST AA941993.

<220>

<221> intron

<222> (47)..(431)

<223> Probable intron in gene represented by EST  
AA941993.

<220>

<221> misc\_feature

<222> (432)..(524)

<223> Area matching Drosophila EST AA941993.

<400> 339

```
ctcgcagcatt tgtgggacga gctgagcgga gcgcacaaac tgccaagtaa gtggagcatg 60
tggatgaaag gagttcccag aacagtgttg ccaacaaaaa aaaaaaaaaa gttaaaaagt 120
taattttaat agtgtaaata aatatgaatt aaattaaatt tttatgtaaa cagtattagc 180
tttcatgag attaccaaatt tgtgagtgtc tgtgtttgtt tgtcttttaa aaacttttaa 240
agcacataaa gaaatatatt ttaaatttaa ttaaaaagtt cgtaaaaagt aacaaggtag 300
ctaaattaaa aagtttccta ttcaaatacag atttggcgaa caaagagctc aagttggcaa 360
cactgacaat gactccaagc gcgaacaaag cgatttctat cgttatccca ctctctctcc 420
cagaagtatc ggttctcaag gccaaatggg aaggggactt cgagacaatt ttccgggtng 480
gagtacaaaa ggataccgcg ggcgataac ggtgatttta tggg 524
```

<210> 340

<211> 431

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (43)..(431)

<223> Area matching *Drosophila* EST AA803074.

<400> 340

```
ctcccaacga atcgaaatca gttgttcggt gtgcgtgtgt ggaaaaagtt cgagttcgcc 60
gagagaagcg tgaaaatccg atatcgaaac tacgtttttt tttagtcata ccgattggct 120
atgcaaattt aattgcggat ctcccaaata atcgaaaagc caacaggtcg cccctcaacc 180
aaaataaaca caacaatcga gccgcaaatg aaacgggcaa aaacagcaaa ggcaactggc 240
gaaccgctta accggtttcg aaatatccat cgtagcacag tttcctcgtc catataatat 300
tccgattgca gtggatcaaa atataaacac acacactcgc atataaatte gcagatatac 360
gttgtttgtg tgagtttctg tttgtggttc gcgtgaaaaa tagttttgac aaatatatac 420
aaagccacac g 431
```

<210> 341

<211> 589

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(197)

<223> Area matching Drosophila EST AA695870. This EST  
has sequence similarity to mammalian/yeast signal  
peptidase 18KDa subunit.

<220>

<221> intron

<222> (198)..(267)

<223> Probable intron in gene represented by EST  
AA695870.

<220>

<221> misc\_feature

<222> (268)..(534)

<223> Area matching Drosophila EST AA695870.

<400> 341

```
actcggccta aacatacgtg tcggaaattt tctgtcttcg tggacgaagc cgagaagttt 60
tgttaaggac cttttcaatt gcatttaaaa aggtattttc ctccacaagc accgcaataa 120
cagccgcagc catgggcgta gccagcatgt tgcagattga cgagatgctg ggcgacttca 180
acagaatgaa caagcgtcag gtgagcagcg ccgctttctcc gggcaatgca cccatatatc 240
atcctgattc gtgccctttc cctcccgtag tcgctgtacc aggtgctgag cttcgccatg 300
atcgtctcct cggcgctgat gatctggaag ggcctgatgg tggtcaccgg cagcgagtcg 360
ccgatcgttg tcgtgctcag tggcagcatg gagccggctt tccaccgagg cgacctcttc 420
ttcctcacta actacaagga ggagccggtg cgcgtcggcg agatcgtcgt cttcaagggtg 480
gagggcaggg acatacccat tgtacaccgc gtcacaaact gcacgaaaag tgagtttctc 540
ggggctacgg atatggaaac caatccagaa agcgtcttta agatgaatg 589
```

<210> 342

<211> 911

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (775)..(911)

<223> Area matching Drosophila EST AA433251.

<400> 342

```
agtgagccaa aatgggcat aatgtgattc ctgctccgct tagccgtatc ccgggcacca 60
gccaggcgaa ggagaagcac agcaaggacc tgaagaccct cacctatccg cagctgctgg 120
agattaagga caggcagtct cactttctgt cggtcaagtg agtttttagtt tccacctgtg 180
gagttccctg tgaatttate ttatttaatt ttatctctat ttagaaagcg tttgcaccaa 240
ctgccggaca agggaaagcg tctgcaggag tcgtacgaca aattactggc cgagatcagg 300
aggcgggatg aagtagagga agcgactcga atgttgagcg gtctcaacat tgtcgaaaag 360
ggcaaaattg ctctcaacaa tctggagtgg gaatggcaga aacacggacg agggcgccca 420
tgtggacgac attctggtac agcgatgatg aggtggagat ggatccgttg cggattatag 480
cgcagggaac aatgcacgag aagaaggtca aggttttgcc tccgccaacg agtctcatta 540
cggcagatga cctggcggat atcgaggagt ttaagaaacc aaccgactcc ccagattccg 600
ctttggcagg acatagtgc accagttccc ttccagccga aatcgtagaa atcgacgcca 660
gtcaagtggc cgcaaagctg agcagggagc tgcctccga tcagcatgcc ctctacctca 720
tcgataagac ggaacaaaat gtgaatactc ctagggaata gtttatgcca ttccgcacca 780
cgaagtccaa tgtccacaat cccgacaagg agcgcgtgcg caaaaagggc aagcattggg 840
aaataacggc agcaactccg acactcatcc agcacaatag aggcccaagt tgggtgccatt 900
ggctgagtcg g
```

911

<210> 343

<211> 1176

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (718)..(1007)

<223> Area matching Drosophila EST AI297203. This EST  
forms a 1122bp contig with AI455195 and AA438815.



<400> 343

ctgtggtcgt tgccgccatc ggagatctta cactgaaact tgaaggcgga ttctgaatat 60  
taattcttct tgaaaaaagg cttttatata tatacataga tctatagctc cctcaaaatc 120  
attgcagctc attatcaaac atgctttaat gctgattcgt ctgtataaat atttaattat 180  
tgtctaccaa gtcattggaa aattttcacc actatgctta ttcgccaaca ctctcggaat 240  
attttatttt ttccatgggc tattttgtata atttcttacc ttaatgcca gaccatttga 300  
atatttatac cctgtccttt gctgttttgt tctcttatca atgcccttcg cattgacctg 360  
agttttcaga tttccttgcc tttggcatca ttaatccctt tcaacatggc caaaagccat 420  
tcaaaactga attgttgaga gctgtcactt ggcattttat tgccatcaga tagctgtact 480  
cacaacaaaa ttctacgaca acccaaccga caaagccac acgatgatag ttaattaa 540  
agttgttggc acactcagaa tatcatgcaa aattagcctg gctaactggc cttatcataa 600  
ttatcagcaa tccccaaaca aaactttaca acatgataat tattaaataa aaagcaaata 660  
accactaaca gtagaaccga attaacattt gtgagctcag aaaacaaaag caaaatacag 720  
gtgaaacaaa atgcagcagc atccgtttac taatttatac gcaatctcaa ataatttaca 780  
aaacaaatgg ttaaccgaaa gaaatatttt aacaagcttt cttgaggcat tacaaaaatt 840  
aaaataatat atttcagaca gagcaagata tctattttaa tattatttta tacaaaatga 900  
agcaattggt aaacaatttg gacaacgc atgcaatcgacc ctatttgtaa ttaattgat 960  
caaaagcgaa tgtgtcttaa agcagtacct ctctactaca cgcttggagg taattgaatt  
1020  
tttgcatttt tattttccgg gtcttttaaat atatataata taatatataa ttttcagctg  
1080  
atttattgag tttgggtttc tttgattaac tatatgtgag ctgtgtggac tgctacttta  
1140  
agggttaagct aatcattttc atattttata atatttc  
1176

<210> 344

<211> 106

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(106)

<223> Area matching *Drosophila* EST AA694869 (inverted).

This EST forms a 1632bp contig with ESTs AA735812,  
AA568063 and AA695306, and has sequence similarity

to mammalian transketolase genes.

<400> 344

gttcggcatc tccgcacgtc acgtcgtcaa cgccgttaac gagatcctca aggattagg 60  
gaccagtcgt gatctggcta cattcattta ccgcctacag gaattc 106

<210> 345

<211> 143

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(99)

<223> Area matching *Drosophila* EST AA392932 (inverted).

<400> 345

accagtccta tctaaatttc tggttttcag atactagaat atgcgtgcaa tttgcggatt 60  
tggacagatt ttggacccga aaaaaaacta atgcggatcc agtgtgacca ccgctcgacc 120  
gttcaaatat accatgggaa ttc 143

<210> 346

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(260)

<223> Area matching *Drosophila* EST AA391707.

<220>

<221> intron

<222> (261)..(309)

<223> Probable intron in gene represented by EST

AA391707.

<220>

<221> misc\_feature

<222> (310)..(510)

<223> Area matching Drosophila EST AA391707.

<400> 346

gtctggacta cacagcattg ctgctataag gagtcgggac cagaggagta agaaggaagg 60  
aatcccgtcc ggtagggact actagcattc gcaagtgacg tccagcaacc ggaggacccc 120  
caactgtaga atcagcatca ccataccta cccaacaaac caatgacatc ttgagacctc 180  
accagccatg gatcccttcg tgttcttcat agtactggca tcgctttatg gcgttcttta 240  
ctttttcgac cgcttcttca aggtgtagta tatccagcca aagttcgtcc agatacttaa 300  
tgtaatccct tagagttgca tgcactaccc gtacgatgcc ttcctcaaga acaccgggct 360  
tgagtataaa tttcatgagc ctccactggc acaacgagtg cctttaacag gaccctctac 420  
gctgggggat ctggccggta acagctgcac ccggagagta atgatcacca gtttatgtta 480  
ggagtccttg gtcacctttt ctctgttccc 510

<210> 347

<211> 528

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_difference

<222> (45)..(141)

<223> Area matching Drosophila EST AI294564.

<220>

<221> intron

<222> (142)..(444)

<223> Probable intron in gene represented by EST  
AI294564.

<220>

<221> misc\_feature

<222> (445)..(528)

<223> Area matching Drosophila EST AI294564.

<400> 347

```
atctgttcta ttattgtttt ctttttgta agagtttgat tgaatcggat tggatagaag 60
cctggtgaaa agacaaagaa ccagcgtaaa gatgcctcgc cttgtcaatg gccgcgaagc 120
cgcgccacg tactcgaatc tggtaagttg aacttcaatg tgtggagcca gcgactcctt 180
tcaccaaaac aaaggattgt atgcatttgc tgcattgttg ttatgctggt tgcgcaacaa 240
atgtgcattt ttacaaaagt cagaaagatt tgtgcttata tttttgtata aaacgcctta 300
agtacatata ggtgtgccag tggaaatata agaactact ccataacgcc cacttgca 360
atctttgcgt tgtgtgcact tattttcggt ccacaatctg aacacctgtc gctccgtgag 420
ttaaaatttc cttttctatc cacagggttg cttcatatc attttcaatc taatcgttgg 480
aaccggagcg ctgacgctac ccggagtctt tgccagggca ggatggat 528
```

<210> 348

<211> 551

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (345)..(460)

<223> Area matching Drosophila Karyophilin alpha 3 gene,  
Accession number AF152928.

<400> 348

```
gacagaagtt tcaataatag cgatgacact cgtaatggta tctacagttc gcagggtca 60
aagatatcga tactttgcta gggttgtgta atagtaccgt cagcacaagc gcctgottga 120
aaaaacctaa ataatatgaa ttgctataat gctttttaag acaaatgaaa tatttcctaa 180
ataatgttca actggttcat aagcttacaa ctccaactga gtaaaacttaa aatttctaaa 240
tttaaaaaat aagtcgacat aaattcagat ctgacgattg gtgcttcaat cgaccctgcc 300
tattaagtgg ggcagtcccg aattgccaac cgcagccaac ttcttcacgt tcgttgtcac 360
tgattgcaat tttaataaaa aggaaaggaa ttttatcact tttaaaaaga cgtagaaagg 420
tgtgtgtggt cgtgggagaa acccgattta cttgctaaaa ccgtaagtat cctctaccgc 480
```

aggaccaaga gaaacctttt tcggcccggtt gcattgctat tttcatggat ttttcgcat 540  
ttcctttttt c 551

<210> 349

<211> 177

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(177)

<223> Area matching Drosophila EST AA540743. This EST  
forms a 1129bp contig with ESTs AI064582, AI519458  
and AA568024.

<400> 349

tgcgtaatta acgctaatta ggcagaggag acaatttagt tttattcgat cagcaataaa 60  
gtgcggttgc acacgtcacc gaacatttgt tgcccaacac cgcactgcga acttcagctg 120  
caagtggagt ggaaaaactg ctgataaccg atgaaccag agacaactaa ctagccc 177

<210> 350

<211> 328

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(325)

<223> Area matching Drosophila EST AA539054.

<400> 350

gcccgcgcta tccgagtgcg ccccatgatg cgtggcatcg cctcgtcgtc agtgtggaac 60  
cggaatcgtc ccgttcagag ttccctgatg caatactgcc gggatcggtc gttgcgcctc 120  
cagcgggtcc acggagccaa tttgatgggtg cagcgcttct acagccgcaa gcgggatgat 180  
tccaacgggg atattattat gggaccgatg cttatgtccg atcaagatac ccattctccg 240

gcaactgtgg cgggtgcccgg accgtgtggc cacatgttcc gttgttggcc atgcgcaaag 300  
aatcctctct tccccgctt tattgaaa 328

<210> 351

<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(73)

<223> Area matching *Drosophila* EST AI062939.

<400> 351

acccgagcca accgaaagcg ccacaaagag ctcttttctc tcccggtcg gttgactaaa 60  
aaaaaattaa aagggtgaaag cgcgtctcgt gtgcgtctttt ttcacattat tatttttttt 120  
cttaatctcg tgaatgctac ctactactgc agcatctcat ggaaaaccat tcttaagctt 180  
tttttttttg gttttttgga atgcaaattg cgcttatata ataggccatc gcgagccctg 240  
tgtgtctgtg tgtgcgagtg agtgcaagca tgtgtgtgtg tgtgtgtttg tgtttcaaga 300  
atcgaacttt atgctttggt tacatttccc tttcacaatg accaaatgtg tgtagagaac 360  
ataatttggt taaaggtttc cgttttgtcg caccaacgag tcgcattgcc acccctgtga 420  
gaaggggctc catagccccc aacacccatt cccacccct gtctctctgc tgctgcgccc 480  
ttaaaatttt caattgaaat atgactgcac acaggccagc cccaaacgca g 531

<210> 352

<211> 1109

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (927)..(1070)

<223> Area matching *Drosophila* EST AI109224.

<400> 352

gtctgcctt tcgacggagc aactccgatg gcctcagcac cgactacgcc cactcccttc 60  
 ccaagaagga cgatcagaac gccctctcca gactgggtgca gaatactgcg atgtacgtag 120  
 ttgatagtgt atagggtcca catttggtcac tatcatatac aattccattg attggaatgc 180  
 tagcatttta cagcgattgc tatactatac tatactatag tagtatacct acgtagttat 240  
 agcgatggca ggatctagta tgtagtatgg ttatacccaa gcatttatcg ggatgttcaa 300  
 tgcaacaaag caacacagcc ctaattatcg cttatctata ttatatttgc attcgcttat 360  
 acgctacttt gctctccaga aacatgataa acgttggagc catggactgt cacagcctgg 420  
 agcaccagga gtacgccgat agaataagat tgtactcgca gcggttgcac caacagtggg 480  
 aacaacggcc agcagccag tatcgcccaa aaagggttgc aatatagcta gattgaaagg 540  
 gtgaatgatg actaacaatt aaatgaacaa caggtctcct taaagatgta ccaagccatc 600  
 agttctatct gtctaagcca acctatccag atgacactgc tcaagtgagt tttacttttc 660  
 gcaaattgct tgttgcttac caatttcgta tgtttttaga tgaagctctt caccgagaag 720  
 gcacacatca gtgtctcgca catacagatc gaccacaaag aggccgtggg tgttcccttc 780  
 cggattccct gattatcgta tcttaagtga aataaagtga taaatttata taaaatcaaa 840  
 atctatattg gtactaagta gcccttgaat aaccaggtaa tcgacttatt ttcattaagt 900  
 gtacagaagc aaataaatac atactatatt cttaacacgg caagacattt tttttattta 960  
 ggaaggcaca cacacacaca tatagctaaa atccaaaatg tcgttcgata ttaaccataa  
 1020  
 attttgggtc tacacgcgca aggaaattgg tcaattaatc aagaagcaga ccgctgaaga  
 1080  
 agatgaccgc agaggaaaag catatcgat  
 1109

<210> 353

<211> 382

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (43)..(146)

<223> Area matching *Drosophila* EST AA696728. This EST  
 has some sequence similarity to isopentyl  
 pyrophosphate isomerase genes.

<400> 353

ggtaatcctt ttattacaag gtccataatc ctctgtatcc ttagataacc ttcccaaaca 60  
 cctacaccaa cgcggtgctgc agccatccgc tttacgagat cgaacaggaa cgtcaggagc 120  
 gcaacgcaca gggcatccgt gtggccgctc aacgacgtct caactacgaa ctgggcattc 180  
 ccaaagagga actgcagcca caggactttc gctacctgac ccgcatccac tacgcagaca 240  
 cgggcgacgg cgtgtggggc gagcacgaga tagactacat cctgttcctg caaaaagacg 300  
 tgacgctgcg tccaaatagc aacgaggtct gtgaggagcg ctacttgccg cgcgataatg 360  
 attgacgagg cggtggccga ag 382

<210> 354

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (59)..(533)

<223> Area matching *Drosophila* EST AI518328.

<400> 354

ccctggcctg agttttcctt cattttcacg cgaagttcac actatttcgc gccaaatggc 60  
 aaataagcat aatttgtgca aaaaaagaag tttggatttg agcgaggaat caacaagcga 120  
 aagccatgcc aagcgtcagt gcaccgaaaa cctcttttgg ccggagggcg aagacgacga 180  
 cagcttcttt tccaacgcgc atctggagga tttgctggac ggacgaaagg aggagctctt 240  
 tggcacgcaa gcaaccacaa gtaccaacaa gatgacgcaa agtgggtcgg atgatggact 300  
 gggactcttt gcggacacat cctttccaag tgcacaggag tgttccaccc aacagtgcct 360  
 ctaaaccgga tgaagccagt gcaccaactg ataaacatca aatcgacctg gcggacgagg 420  
 aaaacgccga caagctgttt aagaaaatca acctcaacga tctgagcatt gccgaaatgg 480  
 aggatatttt tcatggcgcc gatgatttta gtgatcccat gggtcaaaac aca 533

<210> 355

<211> 457

<212> DNA

<213> *Drosophila melanogaster*

<220>



<221> misc\_feature

<222> (43)..(432)

<223> Area matching Drosophila EST AA263622.

<400> 355

ggtcaatctg acgccagttt atagaaatct tttaacgttt cggtcgtaaa tcggctcgaa 60  
tgctagtaga aaattagtaga ccagcgcaaa acggggtcgaa aggcaatgag gcatcaaaaa 120  
gttaactaaa ttaatcacaa ttaccgtgag aaatcagaca gtgcagcgcc acagcgactt 180  
taattcagaa aatttgtaac ctggagcgca ttactaagaa ggactgttgc ccataggaat 240  
ttgacagact ctggcgactg tcaaagtgtg atgtaacatt tttaagttag gcgtgatcta 300  
ggaaaaattg tgaaaaactgg ctaccagcga taaattgtcc aaatatttcg tgggcatgga 360  
cgaagaggag gaggaggagg ttaccggatc taaagctgca attgttcac aattacagta 420  
cgcgagcaca ttgtaagtgt ttttctggat tgaattc 457

<210> 356

<211> 489

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(164)

<223> Area matching Drosophila EST AA539661. This EST  
has sequence similarity to Human proton ATPase  
like gene.

<400> 356

gcctgggtcaa tctgttctgc ggcattgctg tgggcattgt gggttcgggt gccgccctct 60  
cagacgccgc caatgccgcc ctgttcgtca agatccttat tgtggagatc ttcggttcgg 120  
ccatcgggtct gtteggcctc atcgtgggca tctacatgac ctccaagtcc aagatgggag 180  
acaaggagta ggcgccgtcg ccagccatcc agtgtgagta tgaatcattg cagagacagc 240  
caagggtcaag agaatagcac tcgcgacgga gcaactgaag ctttatcact tgtaggctgc 300  
attgcgcgat tcgctgctaa gagaatgttg taacgcactt gttcttgctg ttgataaact 360  
cagtaataag ttaatttaac cgcataaaca tagaggagct accagctctt ctctgagatg 420  
cattttatga aacctaaagc aatacactcc tgattgccat ccttcggttt tgccaagtgc 480

tatagctcg

489

<210> 357

<211> 1043

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(152)

<223> Area matching *Drosophila* EST AI388964.

<220>

<221> intron

<222> (153)..(213)

<223> Probable intronin gene represented by EST  
AI388964.

<220>

<221> misc\_feature

<222> (214)..(579)

<223> Area matching *Drosophila* EST AI388964.

<400> 357

ccccatgtca agttcagatg acgatggggtt tgaccaggat gagaacaaac tgttgcaggg 60  
cctggagaag tccttgaagt ccctggagct gcagaagaat gaggagtaca tcgaatgccc 120  
cccatctgag cgtaaatagcc ccccatctga gggtaaatac caccttatgg ttaagcagcc 180  
ataatattgg tactatcaag ctttttgatt tcagtggggg agtacgtgat gcaacatata 240  
cggttctccc tgaccgagtt aacaaatgcc ttaaaaatgc cagccatcga catgttctta 300  
tactttttgt ccgataagcg agatctcttc gagaatcaaa gtgttggcca ctgacaatgt 360  
gaaacgagtt ggccgtgttcg tggatgtcct gtggtcgctc tgtgaactcg aattgggagg 420  
attcgatgaa gtctttctgt ccgcattcag ccggcagacg gcgcttctgg acaagatcaa 480  
gaatcttttg caggccaaag ccgctgtggc aaaatgcgat gcggagtcgg cactgatatt 540  
aagccatagt aagtggatgc ttctacgagc ccataagcat ggccctctta gtcaccaggg 600  
ctacgaattg gtggaacttt ataagaaatt ggcaccttcc tttaaaagcg acatgattga 660

tgggtcttgaa gcattcaccg gtaacttttc acataacgtc aagggcctaa tttatccaac 720  
 gctggagacg ttactgggca aagatgcaac taaggctccc aatgaagaag aggatgaggg 780  
 cttggtgtcc gacaaagtag tcaaatatgt gaatgcactg cgaaatttac taagggaaga 840  
 ttttttagca ccactagttg agtttgtgca acagctgcgc agcgggaacgg atgtcgatga 900  
 gttgaagcaa cagggccttc tgtgggtccga tgtgcatctg actttaaatc cacagtttgc 960  
 caacgctcag cgtcatagcc ttgttttttt gaaggttcaa tttactaaag aatccaagaa  
 1020

tgcctataag cttggctgaa ttc  
 1043

<210> 358

<211> 536

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (365)..(462)

<223> Area matching *Drosophila* ESTs AA438987 and  
 AA264877. These ESTs have sequence similarity to  
 Human FXR1 gene.

<400> 358

atcggagtga acgaacgaac gaagcatttc ggcggcgaga gagagagaaa aagagagcga 60  
 gagcgcacac gcttggtggt ggtcatgtgt gtgtgaggcg gcggggtcac acacacaaag 120  
 ggagagagac aaagaagaag aggaagcact gcgctgctgc gctgccggca aagccgacgt 180  
 cgctgccggc ttcgccgcca gctgcattta gtgttttagct aggaattatc tggcccccaa 240  
 aataacttca aaattttctt caactatatt ttttattagt gtgtcaatat atagtctccc 300  
 tctccagata caaaaattca aaaataccaa aaacaaaacc attccatatt atcattgatt 360  
 acaggcaaca tttgaagcag cagccgcca gcaaaagact gatttgagta caaggaacta 420  
 gaagcaggaa cgcgagggtt ctgccactgc aactgaatt gtgagcatac ccaccatac 480  
 ctagctatat ctatagccct aatatctcca ttcttcccc tcaggagccc cagata 536

<210> 359

<211> 257

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (6)..(257)

<223> Area matching Drosophila EST AA392117.

<400> 359

```
acctgagcaa gggtttatgc cgatgatctg cgcataaacc agcagcagct tatggacgag 60
atttcggccc tcttgacagaa cacagcgaag ccgagcgccg ccaacgcact gcagctgaat 120
caggagctcc agcgccggct catgcaagtc cggaccaaaa ttctggccat gttacaagta 180
gtaagggccc gcttctctcg gaacgaggac atcctggtgc gccggctgcg acctagttcc 240
catttcggcc cgaattc                                     257
```

<210> 360

<211> 591

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (45)..(120)

<223> Area matching Drosophila EST AA821194. This EST  
forms a 987bp contig with EST AA736168 and has  
sequence similarity to Human 40s ribosomal protein  
s29.

<220>

<221> intron

<222> (121)..(544)

<223> Probable intron in gene represented by EST  
AA821194.

<220>

<221> misc\_feature

<222> (545)..(591)

<223> Area matching Drosophila EST AA821194.

<400> 360

```
ggtcgggtg ccacgctag ttcttttct ttctgaattt ctctggaaa acgccaacat 60
gggtttcgt actctctgt actcgcatcc ccgcaaataat ggccaaggct cccgatgctg 120
gtaagaattg tgttgccgt tgtttttcgc acgttttgggt gtacaatttg tttaaagtgt 180
tgtcccgtaa ccccgatatt tgcacgattt ttgcttggtt gtagaaagtg gggttatacc 240
cgaccgctt tttttttaac gcatggcgtc taccaatttg tatttgcttg tattgtcaat 300
tgtttcaatg ttccaaaggc ttttgcccc gggtgagtag ggaaatacgt gtttagcatc 360
tagaacagtt tccttaatta aggggtggcca aagtaagagc tgcgcgagggc aaaacgagcc 420
atttcogaat ggatttggtt cagccaagt cagcgacagc tttgctttta atgaaactgt 480
tccatgctac ggagattctt tgatggaacc gatctaacta tgatatacca tctcattttc 540
agcccggtgc tgctctaacc gcacgggtctg atccgcaggt atggcttaac a 591
```

<210> 361

<211> 555

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (12)..(469)

<223> Area matching Drosophila EST AA539752.

<400> 361

```
gttcggacgt gctacgggt ctctctgtg tgtgtgaggt agtgtgctg agcggagcgg 60
cgaaaaagca caattgaaat taaatcgagt cgttatctgt ggattcggcg gatacaatac 120
aatatcgat cgttatctat ttacaaacaa atcgacgtgg attaataaaa tgccgcacac 180
gaatgcttaa agcggcctat ctgtgtgtgt gtacgtgtgt gtctatgtct ttgtgtgttt 240
cactctctct ttgaaatagt aaacaaattg cgtataaagt ttacagcaaa gtaaaagaca 300
aacaaaaata tttatataaa acaaagtata ttctgcagtg cgtgtaaaat atttcgaaaa 360
gtagccgcaa aaaggcagcg gcgtcgacgt cagcagagcg cgggctgcaa gtgtgttggt 420
gaggcgata tacatacata ccacgcataa agtgcataa taaggggggt acataagcag 480
tgtaattaat taagtgaat ccaaatagtt ttgtgcatgc gaaattggaa aaatcgagag 540
```

gagttccgca caaca

555

<210> 362

<211> 526

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(382)

<223> Area matching Drosophila EST AA803203.

<220>

<221> intron

<222> (383)..(455)

<223> Probable intron in gene represented by EST  
AA803203.

<220>

<221> misc\_feature

<222> (456)..(484)

<223> Area matching Drosophila EST AA803203.

<400> 362

ctccccgacc gtactactcg accaactgac ttgtgtgcag aatttcctcg gctaaataaa 60  
accaaaaatt ggcaaagcgc cgtgtcagat ctagccgctcg attgcacaat tccggagcag 120  
gacgtcgtcg ctggagccac cgaagcggag tcaccatcag aagatcacca gcaccaggag 180  
aaccacgtgg acagtctctc tctttttctt ggctgccgag gcgtcgcgtg tgcgtatctt 240  
tcagcgggtga ataaccacgc gctttttgtt ttcggccaga ggaggagcgt gttgcagtcg 300  
caaacgggaa gatgggttaa gctaaaaagg gcaagaaaga gatactgacc aaggtcgaag 360  
gcggttcctc ggtggacgaa atgtgagtct tgtgcaagtt catgcccacc tgccaacttg 420  
gcaaactttc tatcgcaaat tattcaatct tacagctccg atgtggacag cgaccagttg 480  
agcctcaaca accagcagaa tcatgccctt gaagggcaat caagct 526

<210> 363

<211> 401

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (105)..(154)

<223> Area matching *Drosophila* ESTs AA802887 and  
AA820871. These ESTs have sequence similarity to  
*C. elegans* protein B0336.11.

<400> 363

```
cgccagacgg gaagcggcag caacaacagc tggaagaagc tgatcgagtg tgagcgagac 60
agcagtcacg gagcgagctt ttgggtgtgc tttcaattca gtagtatttt cacttttgcg 120
cgaactagtc acaaaaacct gcaaagcaat cgcaatttac gtttgtttct gtcttcaact 180
tgccgtaatc gtcattgaaa tgtgcaatct gtaattgtta ttaacaaagg agcaaacata 240
agtggaaact gcattgttat cgtaccaatt gatattcact actcaaagtt taagcaaaaa 300
caacaaaatg cccagggtat gtgtgtgtga gtgtgttcgt gtagaatgtt ttttgtgttt 360
catgttcatt gaatttcgct taagaaatcc tgcgtcattt a 401
```

<210> 364

<211> 177

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (22)..(177)

<223> Area matching *Drosophila* EST AA817394. This EST  
has sequence similarity to Dead box DNA helicase  
genes.

<400> 364

```
ggccaccccc agtaagcgga ccgcattttt ttctgtgaaa gtcagaaaaa ttagccgaaa 60
aagactgtaa atatttatta atatcagccg aaaccgcacg cgaacaaatc gtgaacatgg 120
```

cgcgcaagaa tgcccaggcg gaggacctct ccaacgtgga gtttgagacg agcgagg 177

<210> 365

<211> 546

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(77)

<223> Area matching Drosophila EST AI064638 (inverted).

<400> 365

ctcccggttc tttcgatcct gatccctccc ccaaactaat aattttaagt gatatttgttt 60  
ttatcaatga gtttctacgc ccatcaaagg actgcccact cgtttgcata acagatgtct 120  
ttaggttgct tatcggtttc tggtatcgat gatatttatat aaaaataata caaataaaga 180  
caaataatag aggtaaagat aaattttaaa ttctgaggaa gccatatatt tattgttggt 240  
cctttaataa gcaggaattt tcaagtattg attcagaaaa acgcttataa ctggaaacaa 300  
tctacaactt aatgggagta tacaatttaa tgattagttc ctttcgatga tgtggattca 360  
aagttgctca accaaagtta aaaatctaaa atcgaaaatt taaaaactta tcgagtgaga 420  
ggaccaatcg actactcgac ttagcaaaca tcgaaatata gcagggtggg acctcacatc 480  
gccatctggt ccacgctag ttcattcttg gttcatcgcg ttcgggtcag tgcacggaac 540  
gatattt 546

<210> 366

<211> 547

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(37)

<223> Area matching Drosophila ESTs AA736157 and  
AA140746.



<400> 366

```
acatcaccat aagcattttg ttgtgtgacc ggagtttagt gttgccaaat accaaagcat 60
gaccgcctac cagaatgttt gcactacgat agataaaata ctaaaagtta caaaaaaatg 120
atatatatct ttgtttaatt tttttgtata tttgtttttt tttttgtatt atattttgca 180
tatttgtaca tttctctatt ttataacggt tactccgtaa atttacttat atgtaaatta 240
tatttataca ctaaactttc tttaagacaa tttcctattg ttcattttat tgcgatatat 300
ggattttatgt gccagtggat gtctcagtag tcaaataact gatttcttgc attggtggta 360
acagaaatat catcaagtca gcctgtatat aaaagaacat atgtagatga aaattttaa 420
tgattgtatt ttaaagacaa attattttcc ctgattttgt agagtgggat tttttattta 480
actatgcggt taagtgggaa aagggtctata aacaaaacga gttgatagca gagtgcctg 540
tgagttt 547
```

<210> 367

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (7)..(369)

<223> Area matching *Drosophila* EST AA820427.

<400> 367

```
atgtaaacga aatgcgagtt ttaggaaagt gcactgtttt ggtcaggcaa acccgagct 60
tatccacgcc atctgggcgc cgcagagtgg tggtcacggg aagtggcgca gtcactccgc 120
tgggcaacaa tggaccggat tcttggcgac gcatcctggc cggcgagtcg gcaattttctc 180
ggctgagtgcc ggagtttaag ggcttgccct gccaggttgc ggctcaaata cccgagggaaa 240
acctacagct ggatcaacac ctgaccaagt cggacattaa gctgatgagc cccgccacgc 300
agcttgccgt attggcggct gaggaggcct tgtcaaccgg aaagctgtgc cccaagcaat 360
tgagcgagga ggagcttgag cgggttcggag tgtgcgtggg catgggcatg ttccgaccttg 420
cagaggtcta tggcgccctgg aaccagctgc aacgaggtta caacagagta agccccctttt 480
tcgtgcccag gctgctgccc atatggcggt gtgggtcacat aacatgagac atggctttta 540
gaggacctac cacttcggt 559
```

<210> 368

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(533)

<223> Area matching *Drosophila* EST AA391736. This EST  
forms a 1692bp contig with ESTs AA202259 and  
AA820861.

<400> 368

ctaccgactg tctgtgtgta agtggg'gcgcg aacgtacggt cgaaaaggaa gtgaaaatag 60  
tgcaaaaagg ccaagtaata ataataataa taaaataggc aaaaagacag gccccaaaag 120  
agaccgacca gaccagtttc aaaaagcgcc tatttccagg ctctttgtgt tatgtgtagt 180  
ggtaagtgtg tgagcggcaa caacaacagc agcagaagca acaaaaacaa ctagcagcga 240  
ccacatacgg tggaaaaggc cttttttcaa ggagcgaaag gcaatgcgcg aacgagcaat 300  
aagaataata aattacactt tgctataata agaataaatt tatacatata tacacacaag 360  
cgggagaggc ccacacacac atgtgttttt cctcgttgag agtgtgtgga aaattgtaat 420  
actaatatga accgcagaag cagcagcaca acgagaacca cgagagaaaa tttcgaaata 480  
tcgcatgtgc cattttaagc tttaaataaa ttataacgta cagtattaca aat 533

<210> 369

<211> 612

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (158)..(470)

<223> Area matching *Drosophila* EST AA567184.

<400> 369

gctccgggca agaagtccat taccaagtgc gccgtgaatc agcgccagggt ggtcatcacc 60  
ttgtcgggca gggagttggc ctacttcgaa atggatccgg taagtaattc tactactata 120

ttacactcaa cttttgactt cttgctctga tgacaaaaaac acgaaaagaa caatcatggt 180  
 gagacactat gtgtcctgca gtgctgagct tcaaaatcaa ccaagagcct tatectcggt 240  
 tacttaactt cacaactaat gaatacattt tatgcttgca gactggggag ctgaacgagt 300  
 acacggaacg ttccgagatg cctgctgaga ttatgtgcat ggccttgga actgttccgg 360  
 agggcgagca gagatcctgg ttcttgccg tcggcctggc ggataatata gtgogcatct 420  
 tatcgctgga tcccaacaac tgtctcactc cctgtccat gcaagccctg ccttcgccag 480  
 ccgaatccct ttgcctgggc gaaatgggtc acacggagag cagactcag ggaggtttgg 540  
 atgacgatgc ttccgctcag cgcagtggca acaataaggg aaccatttac ctaacattgc 600  
 ttgacaacgg tg . 612

<210> 370

<211> 462

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(122)

<223> Area matching *Drosophila* EST AA735277. This EST  
 forms a 1176bp contig with EST AA697907.

<400> 370

gcccaaactg ttggcattat tacaactttt attgcctaa aaggcgattg accgggagga 60  
 gtgtttgatt tgcgcggcat tcaccaattc gtcagcactt cagagaaaga aggagcaatt 120  
 aagtaagcat aaattctgaa ctactgtaca gtcgccgat ttaagacaag ggaagcga 180  
 agagggcaac acttgaagca catggcagaa acacagaata aattgggttt gtctgaaaat 240  
 agcatgtatg ttatgtattc aaaaaacatt cgaaatggga agtatagaat taattgacat 300  
 tgtaaaaaaa aaaaaacttg gatgtgccat ggttgtaaga tgagaaccac cgaaagcaga 360  
 cgaaaaacaa aaagcaggag aaaaaacggc tttagcgaac cataatgcc gaagtgacca 420  
 ttttaaccga aaccttttca taaaaccgaa attcgacagt ca 462

<210> 371

<211> 616

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (514)..(616)

<223> Area matching Drosophila COP 9 complex homolog  
subunit 1-2 gene. Accession number AF129080.

<400> 371

```
gcgtggtgcg cttcttcttc tgaaattagg gatgggaaaa atatatcaat ttatcgatat 60
attaaaataa atgtaaatat ttatatcgtg atagtctttc tatgatatat caaatatcgc 120
tctttctgta aaatatttta ttggacacat gtggattcat aaaaaactga aaactaagtt 180
attattctta aaggatcact aaattattat atttatgatg aaatatctga tgataaatga 240
taatatatta taaaatgtca agaataatth gtttgggtac tttatcattt tgataatttt 300
tttaaagtaa aagtgtctga taacgacctg tagtcgcgga ttataaaagt atttgatata 360
ggaacttagc ctaaaaccaa ctatctttgt taaatatttt aaaactgata tcagtgttat 420
tttttggtat attatttggt ggaaaagtgg aaaatggtct tctcctacag ttgtcatcta 480
tcgacaaagc cgttggtcaca ttgccatctc tagattatcg gtgtaaaata atttgcgaa 540
cggaaaaatt aattgacgaa taaacaaaaa cgtagcttaa atttttcatt ttccctggac 600
tttcggtgca aataga 616
```

<210> 372

<211> 322

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (140)..(189)

<223> Area matching Drosophila EST AA202581.

<400> 372

```
attcagacaa acacggcaat gcacttttgg tgttatcgat aagcagtgtt ggacagcacc 60
ctgcagctgc ctgcattggt atgcgcaatt atcgatatata acaccctggg gccatcattc 120
tcgttaagcc atctctagtt cgccactgaa ctcgtaaaaa agtgtaaaat ttgtttacat 180
tgaaaaaagg taaaatattg ttcttgaggg ctacctacgg tgctccctgg ctcttagatg 240
```

ggtcagccaa gacaaagggc cgtgtgcatg tgtggcgcgt agccctttat aagtgcgggg 300  
ggtggcggga acagctcagg gc 322

<210> 373

<211> 607

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (41)..(377)

<223> Area matching *Drosophila* EST AA390775.

<400> 373

cactgagcca aacaaaatcc gaaattatcc gcaacatgga cgagtcggag ctgctattca 60  
atctgtttta tattctgttg tgcattggtga tcatctaccc gccagaggag ttccaacgcc 120  
tgggattcac cattgaacag ttgttcgctc ggttcctggg agaagagtac ctggactttg 180  
taggetacca ccagcgccgt acttcgctga atctcttcgt gcactcctgt ctgcccttct 240  
cctactttct tattcatagg ctcaagttct ccgtcttcgc cacgcaggag cccttgagg 300  
acttcgacct ggacccgat ttcccatgc ccaggaagc ggtagcggtt aaaacgcttt 360  
acgtggaaaa ccgcccagcg gttcagtgtg ttggcgttc tggcgatgcc cgtctgatct 420  
tcaactgggc accaggaaaa tgggcgtcgg caccctgatc agcaaggcgc tcttcaagta 480  
ctccatcacg ccgggcagct acagtgcctg ggctagcgaa attggtatta gagttccggc 540  
aaccggaaat ataccagaag aactaattca ttagcttcgg tgattgccac gcagactggg 600  
atataaa 607

<210> 374

<211> 488

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (169)..(488)

<223> Area matching *Drosophila* EST AA539898.

<400> 374

cgggtgaagtg agcgggttggtg gaacgtgagt ggatgctaag agcaagctct cacatacgcg 60  
gacatagctc gcacacacac acgcacagac cgcctttttg cgccgccgaa acgaacactt 120  
ttacgaaggc gacggcgaat cagtttcagt tgtcagttcg catccaacta gaaagcagtt 180  
aacgagtagt ctgtgttttt tgcgttgagg ttaaaagcca cgaggtcggt catcgttcat 240  
cgttttcctt ttcaacttca agcaaagcaa atataaacca atgcaaaaaa cgcagtgate 300  
ttttgaggcc caaatcgttt ggggccgaac accgttgatt ctaaaacgca aatgtagaaa 360  
caaatcaaga aaagtggaaa ataaatatgt ttcgctttca aaacatgtgg aatgtgcccc 420  
aactcaaaac tgaaaacgta gaaggaaccg cgttcgtttt ttacatacga caatcgtatt 480  
aaaataag 488

<210> 375

<211> 597

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(127)

<223> Area matching *Drosophila* EST AA390453.

<400> 375

gatgtgtgca taaaaatcaa gcgctgcagc agccaaaaag cgagaagaga gcgcgaggca 60  
gagagcgtgc aaagcgggtca gcgagagagc ggggtggctgc tgcaccttca taactgttgt 120  
tgcaaagggtg agtgcggtgc gaatatgtt tttggttcag aattgtttat ttaagtgtac 180  
totcaaccag gccaacacac tcacaaccac acgcccgcac gtacctgcga cccacgaacg 240  
tgtgtgtgcg tgtgtgttgg cctgcctgct tattttttat gcggaaaaaa cattgatcca 300  
aactttttcg ggcctcaaga acctcatttt tggctcgccc cacaaggcat taatatctgt 360  
tgtgaaccga aatgggttta aataaaagct ggtcagcaga taaaagtga tccaatatat 420  
atgtacgtac atatgtatgt ctgtaggag cctttgttca tttcagctac aaacatctga 480  
gaaagaataa agtattaaga aatattttac tttggtaatt acttaaacag aaccagtttg 540  
gcctctgtgg catatcactt gccagttgaa tccgcggaat taattcttga agacaaa 597

<210> 376

<211> 328

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(321)

<223> Area matching *Drosophila* EST AA568061 (inverted).

This EST forms 1356bp contig with ESTs AA264532  
and AA441674.

<400> 376

gagtgggtga tgcttttccc gttcgttttc ttggcggact ttggtcggaa tcccgccttt 60  
ttctgactgg cgattgattg ccattcctgg cctttcgggg tggactctga tcggaatccc 120  
tgtgcttttg gcgtggcgga gactgatcgc catctcgccc tcgtctgggtg ggactctgat 180  
ctgagcttcc cgcccttctt cgcccccttt gaggactctc ttctcgcttt gctggcttac 240  
tcgatctcgc tgggcttaaa tccctagagc tgctgcgctt ttcttgctta attctgacgg 300  
gtgaacttcg tctggatggt gagaattc 328

<210> 377

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (102)..(311)

<223> Area matching *Drosophila* EST AA141908. This EST  
forms a 794bp contig with EST AA802528.

<400> 377

gcacagcgta agacgacgag atcctctctt cgaaatctat ggcatagccca gcatcaaaac 60  
aatcacgcag ttcgaatacc aaaatccatt gcatacttgc aggcaactc cgaaaatgcc 120  
gcacaaagac gaaacagtcg gtctagttag aacagtgagg acaatgaaaa cagcgcgtcc 180  
ggcaccggtta gggaacagcg tgacgaggcg gcgggccgca ccgttctcca gtgggcgtgg 240

catgtggtca aatccacatc cgtggagccc acaatgttcc tgtacatggt cgccttcattg 300  
 atcacctcgg gtggtggagc agaacttctt cctctacaag tcctgtcggg ttaacaggaa 360  
 atttcacgga gggagatctg caggaaatct caacaagccg gagaacgaag gagttccgaa 420  
 cgaaggcaat gttgaccaat gcctgggtcc ttcagtgggg agaacatttc tgcccacggt 480  
 ttccccatta ttctggcct tttctgggt cttctcggat cgacgggccc gaa 533

<210> 378

<211> 612

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(100)

<223> Area matching *Drosophila* EST AA539224 (inverted).

<400> 378

gtcccagcga aaaactttgc aaaaggtgat tttccaact acttcgcgag agagactagt 60  
 ggaaaaggca agacgaaaac acaactaagc gaagtgggtg gttggccagt gtggccgcag 120  
 gtggcgacc gccaatagc cccgcgcga aaaataccac tttctttaaa ataccaatgg 180  
 gtcttaattt ttgattcta ttcttttagt tttatttttg ggcccaaatt ttcgaggata 240  
 atagttgaat attgtcaagc taatacctat ttcgctatat tattattatt gttaaaacta 300  
 atgatgaaga attgtaaagc tgaaccattg tttaaaagta ccaaacaag ccaatttact 360  
 tggctttact ttacttttct tctctttaat gaagaaaaga gtttacttat gccaatgcct 420  
 gcagagcctt gctgtatcat cagtttctgg atggaaatgg agacaaaaca caataccaat 480  
 ctattaaatg acaataacta tcaattaaat gactaatatt ggctgtcacc aagtaaccta 540  
 tcccatctat ggaagagtag gcattctcct ggggtgaatt aacaaactct ttgggggcta 600  
 ttttaatgaa ga 612

<210> 379

<211> 837

<212> DNA

<213> *Drosophila melanogaster*

<220>



<221> misc\_feature

<222> (431)..(622)

<223> Area matching Drosophila EST AA246367. This EST  
has sequence similarity to human ribosome S6 PK  
gene.

<400> 379

gtcagtagtt ttggatttgg cccaaagagc gaacaaagcc gggttgagtt ttctgggtaa 60  
tcgtgtcaag gttaaataca tgtgctccac ttaacaaag aacgatagag acggcacttc 120  
atctggcatt gaccagccac cctctgccga catttcaata aaaccttgag acatccaccc 180  
ggttaaagtt atcaattatt ccaccacact accatgtttg ataagctctg tggcagctgc 240  
cttaaaatgg catgaaatat tcacagggaa gaagttgccg gtttaatttg atatggacgg 300  
gaattattaa actatcatat ttaaccataa gtacatcctg acctgcaact tgtaacaaat 360  
tttcttatct agcttgtgct tgcagttggc cgggtcttct ttatcactat cattgagtgg 420  
aatgactcac cgtagtattt cagatcgggtg accgcctcca ggtcccgttg atgggcctca 480  
ttgtccagat caaggggtgt actattgctg gtgggcatgg cgtaggaggg cgtgggtcgac 540  
gaggaggcct tcgaggctgc tgctgccgct gctgcagccg ccgccgccgc cgctgcagct 600  
gcattgttgg acttggcctt ggacaagctg gagctggatt catcgatctc tatcccgttc 660  
ggctcactct cctccatgtc ctggtccgta gtactcccgt cggaatccg cgctcgtcct 720  
cgctctccgc atccgatatg caaacaatat ccgccacatt tgtggtggcc gggatggaag 780  
gtgtgggccc gtgatatggc tccgggaaag tgtaatccct tgcaaagctg aaatggc 837

<210> 380

<211> 654

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (46)..(319)

<223> Area matching Drosophila EST AA817295.

<400> 380

cgtaaaacca tggcgttctt ttcagtttca cattggcggt cgttgagcgc ggacgtgagc 60  
atgtatttct gtttgagtgt gtgtgagtgt tagtgtttgt gtaagaagtt cggcggcaac 120

gaaaacgtaa aatagtgaag cataaaggca caaagtgaag aaatactcgc acataaaccg 180  
 atgttagtgt gtttgtctaa gcccttctac ctcttttttt gctacctgcc aatttggttaa 240  
 ctttattggt gctaccgctt gcgtgccgtg aatcaaagta acaacaaccg ccacaacaac 300  
 aacatgcaca aataaatgta agtgtgtaag tgaccgtgga gcgatttaat aacagtgcga 360  
 agccaggaat agcaactaaa atctgttttt aaacgcgcga cgaatgagtt taaaatcgat 420  
 tgcagctcgc aaaaattggt caacatcaca aatagtagaa tgcaccacac aatgcccttt 480  
 agttatatac catgtacatg tagatgtatc atatcccggtg actcatccga tttgcttttg 540  
 catatgcaat ctctacgcaa attacttggg tgaccaaag aaactattat aagttgcgtt 600  
 gaagatacat aattgtcgac cgaaatttca taatcatggc gagatattaa taat 654

<210> 381

<211> 387

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (35)..(383)

<223> Area matching *Drosophila* EST AA439743.

<400> 381

gtgtggcagc cagttagtcg tgctccgcta gtcgatgtcg acggttcgct gttttctgtg 60  
 ttgctcgccg cccgttcccg cctctccgc cgcatatcga agtctcgct attgagtctc 120  
 gaaaacaagt ccaatctgat gtacggccgc attccaagg actccctttt aaacactaat 180  
 tcaagcacgg catgccaggc ccaataggtc gagtagcagt gggcgcggt ctgcaacaat 240  
 tagagcaata attgttgagc gccagcctat gcggtctaca tagaaaccga actaccggac 300  
 tatcgcccg taaccaccta tagtttacgc ctggcttttt tggtagaacc ggcccaaaag 360  
 cccgttcaac caaaaaaaaa aggtaaa 387

<210> 382

<211> 548

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(264)

<223> Area matching Drosophila EST AA441568.

<400> 382

```
catacgccca ttctgcggga atcgccccca catccaactg gtcagtgcgg attgtgccag 60
cggtgagtgg agatggcgcg cgaggacgag gaacgcacgc tggacaatga ggaggtgtcg 120
caaccgacgg aggaggacca agtggtcagt cgggccgggc gccgtgacaa tgaactgagc 180
cttccgtccg gcggctgctg catgccctcg agcacgagcc accggttcat ggctctggtg 240
ttcatgtgcc tgctgggatt cggctcctat ttctgttacg atgcacccgg cgcctgcag 300
aactatttca agaaagatct taatctgacc tccgcccgat tcacgctcat ctactcgatt 360
taactcgtgg cccaatgtcg tcctgtgctt cgtggggagg tttccttacc gatcgactgt 420
ttggggcattc gactggggcac gattatctac atgatgatct gctgggtgggg gtcaattgat 480
cttttgccctg cgcggcattc tggacgcttc tggatgatga tctggggacg ggttatcttc 540
ggattggc
```

548

<210> 383

<211> 579

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (337)..(408)

<223> Area matching Drosophila EST AA247082.

<220>

<221> intron

<222> (409)..(478)

<223> Probable intron in gene represented by EST  
AA247082.

<220>

<221> misc\_feature

<222> (479)..(568)

<223> Area matching Drosophila EST AA247082.

<400> 383

```
attcaagcta aaaaatagtt gtttcgccac tatttggtt cggtgttatg cctatcgtgc 60
aactgcgtcg ccggcatttc cttatttggt ctgctgcgca aagaagaaga attgctgcga 120
acggccgttg aaaaatcgaa gcagagagcc aattggaaaa gcaataacaa cttggctctc 180
tcgcaaaaca aacagtttagc ttgtgataag ggaaattaaa ttactttgtg tgcgaaaaaa 240
gagcgctaatt cttaggtgga attaccaata aaacagtaaa agaaacaaac tgcaaacgct 300
ttccagcgct ttgactcatt tagtgccaat atttcagagc ctgcaggtga caaaatgcgt 360
tgcagtttgc aaaaggactg cgcagctccc acgcaggaaa attttcgtca agtaagatga 420
tacatgctga atacatttaa actgaactaa aaactattca ttgcatttac tgacattcca 480
gcagatgcgt tccaattgt gatttgcttg ctttgctgct tttctgcagc ggtgaaagtg 540
tcgccgttga cgcagccaat cagctggtaa gtgggccgg 579
```

<210> 384

<211> 828

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(321)

<223> Area matching Drosophila EST AA201685

(inverted).This EST forms a 868bp contig with EST  
AA540405.

<400> 384

```
ttctcggeet tttttgttgt cttggctgct ttttcttcca ccaaacgaat gcgctgcgcc 60
tccagttccg cctcatcttc gctgtcgatt tggagtgcta catccggcag atcgctcttc 120
tctcgtctt cctcatcttc ctctcttct tccatategg actcatcgga ctctcgtcg 180
ccgtttgctt ttttcattgt ttgcagcgga tttgcaccat ttgccattgc cattttcagc 240
atgtcagaca cgaaacgctt gcttttcttt taacaaatcg gcaaaaactg cggcgcagcg 300
ttcagaacaa atccaaatcc accgacgcg ctggaaattt ttatttttct gcctctctct 360
cactctctct ctctctgtgt ctcttttagc gttcttacct ttgtttgtgt tcgtgtgcga 420
gcgtgcgaaa ttcggcgtag atgtgtgttg gtgagcgtga tcgcttgcaa cactgtttga 480
```

gcgtgtcagt gttatacagc gccttcccaa aggacagtgt tggaagtcgg agctgccgca 540  
 cgcgctataa ttcaaataaa aaggagcggt aaatgcgaat tgtaaagta aaagagcagc 600  
 tgccgccact aatgccattht tgatagatat ttgacttttg gcgcagaagc ggccaactat 660  
 ttgtgtattc cgttcacgcg ctcaaattggc acgtattttcc caatgcactt aaaaaaaaaa 720  
 ccatgttaaa tatacatthaa aattctaaga aggaccaaag ttttggataa tatactcctt 780  
 ggaagcttct tttaacattc ctttggagtt agccactttt ctatataa 828

<210> 385

<211> 472

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (83)...(218)

<223> Area matching *Drosophila* EST AA540693. This EST  
 forms a 1450bp contig with ESTs AA441321, AA440080  
 and AA392794.

<400> 385

gccgccgcca aagctgccca acacatacac gaatgttaga cacttcgctg tcggtcggca 60  
 gaaacaggca attttatacg ggcgaaaagt tacaaaaaat aattttccca cttttcgggtg 120  
 gcgaaaacga agaaactgta aaaaatggac cagagattta agtgcaaac atagaaacat 180  
 cttgcgataa agcgtgctaa tccggggcat aaaactggta ctgccattat ctgctttttt 240  
 taattgcttt tgtttatttt ttgtatagga cacagtataa tttttctttt gcgctgcgctg 300  
 cgtgtgagtg agtgtgtgtg tgtgatttgg ccactcgctg gtttctatgg tatgtgcccg 360  
 tategccgaa cagagttgcc gccttcaggc caaatcataa aaaatatatt gggctgtcaa 420  
 ttgaaaaata ttgaaaaggc ccaagcaagt gaattatatg ccgataagcg gg 472

<210> 386

<211> 1082

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (452)..(1044)

<223> Area matching Drosophila EST AI295950.

<400> 386

gcccagggca ttatcagttg agttaccagg aactcgtttt gtggccccga gagacaagca 60  
tggaagactc aaaccggcat cacatttgct gctatcagcg ctatttatac gcgccatcag 120  
cggaaaaacg agttgggaat cataaccagc cgaacgcgat atgaatagca caccccaatc 180  
cgaaagatac ggggttcaaaa cccgcgcggg gcgaactcat taaatatttt tagatctatg 240  
tgaaccacat gtttttgtgt attttattaa atatacattt cccatttttg attgcagggga 300  
atcacttggg gctgcgccta cagaataaca ggcagcacgg cactggatta tctcaagcag 360  
cgggagtgc cactgggtaa gttaaactgaa ttgaagagaa gtggggacca tcatttgagc 420  
taaccacga tgactccaac aggtggctat gcaacaatcg ataccaagtt cttcccgcgc 480  
gtcgcctcgc aggacacgcc cttcagcggc gaggcggtcg aggtactggg ctatgtggcg 540  
acgccagaga atatctattg gttgggcgat gacccggtcg aggagattgc ccagcagatc 600  
gtatcctgcc gcggtcccag cggacacaat gccgagtacc tgttgcgcct ggccctgttc 660  
atgcacgagg agattcccgg cgtgaggggac gatcatctgt tcgagctgga gcaattgggt 720  
ttagaggaa tgtaccgccg ccaaatacct ctgtcatctg tgatgggccc caatccagat 780  
aggatacgcc gcgactcgca cgaggacatc cgccgcccgc catccttcga gttcacctcc 840  
cgtgtgcccc acaccaagct gcgttgccctg aacatttgat ttctgggtgt ctggcggcca 900  
agtgttatgc aggtcgcgtt ttttgctaca gcaaattcca aattattgat cgacatttta 960  
gcttggtagg taaccagagt ctattgcaa atttgacgta tttctttaa ttgtaaataa  
1020

tcctaggcct aatcataaca gcaactctca taagtgactg attagccata actaggatta  
1080

ag  
1082

<210> 387

<211> 505

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (2)..(339)

<223> Area matching Drosophila EST AA439667.

<400> 387

gtcgggtacgc ggttcagcgt ttttgttcaa cggattagcg caagttaagc acgatggcgg 60  
cccagacgat actgtttgat ttcacgctgg acaaggacaa gacggcggat gaggaggcgc 120  
gcctccaggt ggccaaaatc ctgcgtaacg agctggagca gctgttcccc cagctggagc 180  
tggcctactc gatggagtcg ccggaaaacg gctactttgc ggtgctgcac gagaacaagg 240  
acacggtgat tacctgccgc atcttcagc acggcctgct gacgctcaac gtgggagtac 300  
ttcctgcccg atggcaagga gccgagcata tccttcgacg gtaccgtagt tcagtgccat 360  
tttaggttcc tttaaaaaac tcaaaaaaca agcaagcaaa caccgacag cagcaccacc 420  
accacatct ttcttacctt cccattttcc gtgtctcgtc tgaattattg gggaaagggg 480  
tttttcacc acccgggtna aaaat 505

<210> 388

<211> 637

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (12)..(394)

<223> Area matching *Drosophila* EST AA539198.

<400> 388

cctcggcgca tttttttcaa agcgaaacgg cagaaaaatg ctctggcatt ttacggattt 60  
ctaattgtat tatttatgtg agaaaattgc aaataaaagt gagtccatca tgccacccaa 120  
gatggagccg attagcgtgc gcaccgcgcg tctgaacaac ctgattctgg gcaaaggagc 180  
tggcgtctgt gcgaagcccg ctggaagcgc ctccggatca ggtattcccg cctccaccag 240  
gagaagcatt gtaccctga gcaccactag cgccgcctg gccgaggcca tctgcgcga 300  
gggactcctg gacgccttct gtctgctgta caacgagtgc gacaaggata cgctgaagaa 360  
gcgcgatcgc aacatcgccg agtttgtaa caaatgtgag tcaactgcat tggtcagcag 420  
ggttttogga tggactatct accattctat agaaatggaa ctcagaaccc catttttact 480  
tcttgggtct gagaatctac ttttgcta catattccat tattaaagcc cacaaaatta 540  
ttgggagtag aatctcttat agatttacct gtatgttccg ggttccctct tgaaatagac 600  
tatgcctagt taccattat attactatct aatttct 637

<210> 389

<211> 518

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (83)..(227)

<223> Area matching *Drosophila* EST AA696927. This EST  
has sequence similarity to *C. elegans* ADP carrier  
protein gene.

<220>

<221> intron

<222> (228)..(497)

<223> Probable intron in gene represented by EST  
AA696927.

<220>

<221> misc\_feature

<222> (498)..(518)

<223> Area matching *Drosophila* EST AA696927.

<400> 389

tgttgggggc tctgattccg gcggttcttc gctcgccagt acgctccact cgcagttagt 60  
taatcgcgga acgaggacga ggtggtttcg actcgggcgg attggattag atcggcttgc 120  
attgatgagc taattagacg cgggaattgc tcgcggaaac aacactgaac cagaagcagt 180  
caaagctaaa aaacaggaat gccgttgacc aagagtttgc caaatgtaag tttcagctgc 240  
gattgccgag cgactgacac gtgttgcttt tgcaattgac tgtcagacgg gagagcgcag 300  
aaatgagagt gcgactgaga cagtggcggg tagcgaaggg ttgtttgtga actaccata 360  
aagataaaag tataagtaaa tacgtacata tatacagcaa aaagatattc aaactaatca 420  
agtagaggag aagaaacccc aatgaagcaa ccctttacca caactaatta tttactttgc 480  
aattcttctt tgcagtctcc gtcgcttttg aagcgcgc 518

<210> 390



<211> 500

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (360)..(500)

<223> Area matching *Drosophila* EST AA438961. This EST  
has sequence similarity to Human KIAA0160 gene.

<400> 390

```
catgtgagtt taccgtgcag tgtgccccaa tatggttttc actaaatata ccagcaaatt 60
gtgtcggttg cacatggctg taactggcgt gctttacagc actgacccaa acagctgtct 120
gaaaggtgca ctaattactg tctttcattc aatttactaa ttaaaatagg aaaaatatat 180
aaagtataac ctttaaaaaa tgttttgtac taaacggaga agtaaagca tatgaaatca 240
aattgtttga aggactatca aaacagtgtt ggcaaacgcg caatgtatta ggactggcgt 300
tttacatgat tggcatgacc gcaaaaaaat aatgctttca tttgcaatgt ttgtaagcga 360
ataaagtgct tgaactcatc aacttaaaca agtacaatgg gcatatgaac aaattattta 420
gtcagagtgc aactggtgaa cagtaaaaca aaaaaattcg tcatgcagtc gtacgtttgc 480
tagtgcgccc ataataacgc                                     500
```

<210> 391

<211> 641

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (53)..(260)

<223> Area matching *Drosophila* EST AA735138 (inverted)

<400> 391

```
gatggatgga tgaatggtca gttcgcattg ccagctctag cgattcactt acattgctgt 60
atgagactcc caaaagttga atcaacatct cgttcggcga ttctcgcct tctcgcgga 120
tctcgtctag gcgctgcagt cgctcactct gcgccaggca gaccggcac gtctgtgggg 180
```

taagctcgac gcgcattctg gaatcctgct cgaaatttaa tttaaagaac cgctcgcgta 240  
 gtattgtagt gttaaaattt gtgttgctaa agtggttggt aaagcgactg aaaaaagaaa 300  
 cgaaaagaca tcgccatttt cttaccagg gctgcatagc atcggcgaac acgatgtggt 360  
 tcattttgct gggtccggga agcggatttt tggttaaata tctgataaac atgtttgctg 420  
 cttgtgacaa tacattggaa atatttgctt ctttaacat ggctaaacga tatgatatga 480  
 taactgaaag tattccccag tgtgcctata aacaccaacc acttgtaaaa tgagaaagaa 540  
 aatattaata cttcaaatat tcaaatatta tgaaaacaat tatatatata tttatatatt 600  
 tctttcatat ttaccgtata tttagataga gtaaagaatt c 641

<210> 392

<211> 287

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (237)

<223> Area matching *Drosophila* EST AI064414 (inverted).

<400> 392

ggctcgacaa aaggcatttt ttttaattggt taaaaatcat ttgactgcaa cgtttaaaac 60  
 aacaaatatt aaccagggtt gcacgatcag cgggttcacg aatatatgta tcttcaaaaa 120  
 cggctgattg gtggcaatgg aaaagttggc gaaatttggt tttttatttg aggaaacttc 180  
 gattaataat ccaacagttt aacaacaatt cggaaaatac gttggaggga aatctttcga 240  
 taggttacta ccagggttgg tcgagggcag ttaggaaaat ggaattc 287

<210> 393

<211> 543

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (67)

<223> Area matching *Drosophila* EST AAS40712 (inverted).

This EST forms a 809bp contig with ESTs AA440879  
and AA440431, and has sequence similarity to Human  
Cyclin G associated kinase gene.

<400> 393

```
gctgtaatcg acaagtgata cacctaaaat atctggcgcc cgttaactga actaaaacat 60
tttcgtagcg ccgtggccac aaaaaataa aaagaatcca gggctgcgga ggagcagggtt 120
cctcagcagg gtggagcgga atcagtttgc tccgatagct tgatcgcgca ggcctggctc 180
accatcgata tgtggcgctg tgctcttata gatatttgac gctgggctct tatccgatgt 240
ggcgcgcgga taactagatt atgaatttcg actaaattta gaggctttt aagcaaacat 300
tttgtagtgt gactcttcaa aattcaagac gtttaatcct ggctttaaga ttgcacctgg 360
aggtggattg tattatatatt aaaatgcgtg gcagtgccaa cgcccttgcc gaggttttaa 420
ggagatcaca gtttttgctg aagcagtcac gtcaagatat atgctctaaa agagttcttc 480
cggctagttc atactcttca acaagtaccc atttagcttg ataccggtta aaagagcgca 540
cac 543
```

<210> 394

<211> 682

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((596)..(682))

<223> Area matching *Drosophila* damage-specific DNA  
binding protein, Accession number AF132145.

<400> 394

```
ctttggacta gtcagccgcc acgaggataa aaatcgtttt cgctgacttt taacgcgcta 60
aaatgtttcc tgacacttag tgtgaccgtt caactgttaa gaactaatac tgtccggctc 120
aggaaaatat actttttatt ttggaaggta ttccatttat gttcaatata aattatgttg 180
cagagagcgc gtggatttta taagcttggt ttgattcttg tacaagcaaa tgacacattt 240
aagatttcca taaaagtcta gaagatcatt tacagtcac gcataagcca gaaaaaacg 300
aatatcgata tgtgtttgtg ttgccccaac tctctctttt ggcaagaaaa atcgatttcg 360
tttttttgca gctctgggac gccttcaaat tgcgggttaa ctgaaactgt ttgaaaatag 420
```

cttttgtaat aagtgccttt aataccacta ttaccacac ttacttaaa tttctaaagc 480  
aatcattggt attacatgac aggattgttc agatattccc ttacaagtta ttacttggtt 540  
acttattttc ttggatggaa tacgtataat taaatataat atactaatta aaaataaata 600  
cgaagacaga gaaaagtcta aatagaatga gctaatttaa gtaaataaat atatagctta 660  
cttagggccg tgggtggttg gt 682

<210> 395

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(513)

<223> Area matching *Drosophila* EST AF007159.

<400> 395

gcctcgacgt tcgctaacag agctgagcac tgtaagcgg cgcttcgtga ctgtgagccg 60  
aacgcatacg aacgacctac gccagcgcgc tcaaacctgt tggccaactg agtgtgcaac 120  
aaacatgttg tgtttacgtt ttttccttgg cctaagcggg ttgagcgtgt tgctgtcctc 180  
catcaacatg ttgcactttt cgggcttggc aacaagtgct ttttgtttcc aactaccaga 240  
tactctttct atttaactgt atttatggtt gtagttatat tatgccgtta attgtgaaat 300  
gttaccaatg agtattgcat ataaaaatca tttaaaattt acatattaca aactcaagct 360  
gattttatta aaattaaatg tatatatcta agtcctattc aaaaaaaaaa cgtatcaaca 420  
gaagctgcgt aatatattgc ttaattcaaa ttggacattc agcccgataa aaatattttt 480  
gacagatcac taggaagctc tgacacggaa aaa 513

<210> 396

<211> 958

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (13)..(235)

<223> Area matching Drosophila EST AI511691 (inverted).

<400> 396

```
tatgtaacca accttttttcg ggtttcttag aagattcagt ggaagtggcc agaggtgcag 60
gagtctgcaa atcaggaact tcatcaaaac gatttttgccg cacagaaaat gctgccgcct 120
gcaactcgct cagttgcgtc acaataagta gcaacaaaat aaataaaatg cgactcatta 180
tgcgtttaat gaaacatttg ttggcttata cttaaaaaag aatcgacaag ctcaacctaa 240
tcgtgttaaa ttgaacttaa aatgccgccca ttttgcactc gataccagga atgctcgata 300
tcacagcaag tcgaaagcag tgtactgtaa ttctcgtacc gtgtgctgtt aatgtcagta 360
acattttact gttaagcgca acttctctta ttagcaaatt gtgcaagcag ttcaaaaaat 420
aanaaatggt caatatagaa tttcattaat attataaaaa aataaacaaa tattttttta 480
gttgatatcc ttggcaaaaa atatttttaa aacctatgag tagaaatccg gaagccagta 540
aatcgaaaac ctagtgttct accaaaataa atttaataaa ttttaacaat gtttgtgaca 600
atgatcaatg catagggcga ctattgatat ttagagtttc acaaaaatta aaatgtattg 660
catcaattaa aattaataaa agaatttggt tttgtggatt aattacgttg atgttgttta 720
cgtctatttt aaaattgctt atgccggtag ttttgtatgg gaatcgataa taagcaaacc 780
aaaaatcacg aatatatccg gatgtttaac tcccttgga ttgccataag ttctgcccct 840
ctaactctca ngtggtttgt accggggggg tataaacttc ataattggat tactctctta 900
taacttccca aattttataa tattatatta ttgcaattat tgcaatttgc atttactt 958
```

<210> 397

<211> 289

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(61)

<223> Area matching Drosophila ESTs AA264883 and  
AA392712 (inverted). These ESTs show evidence of  
alternative splicing.

<400> 397

```
gtctcgcttc ttagcaaaaa tggacgacga tgcttgctg acgggacgtg aacagagtga 60
ccgcgatggc accgttaata ttggttgccc tgctaacgga tctataccaa aaaatacttt 120
```

atggttctac caaatatagc aaaaacttca aataaccgaa aagtctgggg agaacatttt 180  
tcaattgcat attctatgta ctttcttgag tcctataacc ttaagtcatt tgtagaaagt 240  
tagattttcc ttttcttagc attattgcat ttttattttt atggaattc 289

<210> 398

<211> 538

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (30)..(451)

<223> Area matching *Drosophila* EST AA438399. This EST  
forms a 821bp contig with EST AA439438.

<400> 398

gttttagagta caaattgtgc agcactagca agaagcagtt tagttacggt tactccgtag 60  
aagcgcgata caaaaaagtc aataaaaggg tgaaaagcga acgttctaga cacagaaagt 120  
attcaaaaat actgactcag tcctggcgca gcatcggtga caaaagagc ggctcttcac 180  
ggtgaaaagt ttccgcaaaa tcggcatttc tgaaagttgc gcgttcacgg tatgcgaagc 240  
gtggcggtgtg tgtcgagttg agttacctgt aattgtgtgc gcctgcgaga gtggaagtgg 300  
agtaaacctc gccaccgttt tgaagttttg gaaagatata gggataaccg ccagcggttt 360  
attttaaacat atgtcggagg caactgtggc caaaagccg gaggcggtgg aagatgtgaa 420  
tgcgctcgacg ggggacgaga agcagactcc cgtaagtagc cgcacatata catatttagc 480  
gacaattaac atagcacggc gatacgcaca ccaacacggc ttccgtttgc tttgccga 538

<210> 399

<211> 627

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (600)..(627)

<223> Area matching *Drosophila* EST AA440272. This EST

forms a 1324bp contig with EST AA438941.

<400> 399

```
attcaggtat tctcgcaaaa taaatgtaca tatgtatctt tatatatata tgtgggggtcg 60
tccctctgac gtaccaagtt tgcttgaata gccaaacaaa caccttttgt tgacgtaaat 120
agcacacaca gtctacacac agtcacacgc taaaacgata atgcagccgt tacgtagtta 180
gcactacggt acaggttggt gctacctgga aatgtaatcg ttacatgtct tatttcccct 240
tttcgggttc ccgtttctta ttatacacac acacacgcgg ccatcgaaat agaactgttt 300
tgttttacct ttggaacggt acatttcgta ctgaggtaaa aaagggtattc tgtcgtatac 360
tggaagtttt ttccatgtgt atatgtacat attatcttct ttactcaacc taaatttaaa 420
tatagacctt ttaacgtaag gaatgtattt caataaactg cattgtaatt aatgcggttg 480
atgctgattt cataaatagt ttcataagaa ataagacttc aactattttc ctggtaacat 540
aagccaatat gtatcggttc gaatttcaat gggttcttct gctcttctcc aaaaaccagg 600
atcagcacgg cttggaatgc gaaagca 627
```

<210> 400

<211> 682

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (65)..(483)

<223> Area matching *Drosophila* EST AA264865.

<400> 400

```
gccccgatca agtcttaacg gcaagttgca gcaacaaaca ttttcattcg ttttcgcata 60
gtcgaagcgt acggttcata ggaggaacgg aacgaagcgg ggaacgcgac ggaaactagt 120
tgctgttttt ttgtccgtgt taaataattg acacaagaaa atttagctac acttaagcaa 180
agtcccgcaa aaatctatta aaaatcggtc gtcgttttgt gtgtgtgacc acgaaaaaag 240
tgccccgata ggaggatttt aataaattca attaagggtc cgtcccaacg atcgtttttc 300
attgtctgac gctcacgcgt gatgtacaaa tgaaaaagta aaaatttaaa taagatcaaaa 360
gaaagaaaga tcacagtaaa atttaaagtg ggattgactg cacaagaaaa agaaaagtgc 420
cttacctcct agccagaagt caaaagtga gcgaaaaaca gagtgggaga taacaattaa 480
cggttaagtt gtaaagctaa aactacacaa taaacatatc atgaaaaact ttataaaaca 540
```

taagaagggg ggcattttat tattttgggg tatcagcatt tacatcacct tggttcgaat 600  
caaactgatt ttaacatgca ttgggaccaa ctacaccgtt cgaatgtatc tcttatggaa 660  
atggtattgc tatattatcc at 682

<210> 401

<211> 668

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(246)

<223> Area matching *Drosophila* EST AA263693.

<400> 401

gtgcagtgcg tgtgttaatt aattttggtt gccatttcgc acattctgta tttattaatt 60  
ggcagtgcac agcttccggc ggaagagggc aactttccgt tcattttcga gcttccgttt 120  
gtcggccaat tagcagcagg tcgacaaaga aaaagcaaaa acaagcgtaa aggataagcc 180  
aacatgacgc actgggagga cttctacaac acacacctgc cgcccgcgga cttcgaggac 240  
aatcgctccc tgctcaagga gttctgcgaa cggcacaaca agctccagaa tcgaatcgtc 300  
ctcgtcacgg tgagctggga ttaatccaaa tccgaattag gattaggatt agcgctaaat 360  
aaccactgtg ctccgttaat taactggcca agctggtgaa agctttcatg gttgagccga 420  
gcgcctgggg cattaaaaac aaatgtgtaa agtgtggaag tgaataaatt ttagattggc 480  
tagaaciaag ttcgtaaatt ttaaacacat gcagggggcg accagcaatg cataaacaat 540  
taacattttg tgaatggaaa aaaccaaagt gtaaagtggg ttttttttta acatacttta 600  
aaaagcaaaa acaccttttt ttggtgggtt taaattttca tttcagaaat tatcttagtt 660  
aagtttca 668

<210> 402

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature



<222> (137)..(160)

<223> Area matching Drosophila EST AA698620.

<220>

<221> intron

<222> (161)..(378)

<223> Probable intron in gene represented by EST  
AA698620.

<220>

<221> misc\_feature

<222> (379)..(475)

<223> Area matching Drosophila EST AA698620.

<400> 402

```
cccggaatga taaactcaac atgcttgcta gtgtgaccaa cgtatctacg cacgatgcga 60
cccacctatc gatagcttct tcgccagtta ttgccctgcc tttctcatca ctaaaaacag 120
cggcatttta ttgtgcaaata tagaatttct taatataaac tgtaataaga actgctcact 180
atgtctttta tgaaccccggt ggatatgggtg gatgaggacg ccgccgacct gcagtttccc 240
aaaggtaacc aacgccctac accaaccgaa atgcaactta caagtgaac tggctgaaac 300
ctttggcttc gagtgcacca aaagtggcac tcctccacat ttttaccaca ctgaattgcc 360
tctttgcagt tgagccactg gggccacagg ttaagcggtt catccatgca catcaggatg 420
aacacaccag gaactccatg gttttgtata atccgcacac gttgcacagg tacttggagg 480
agatggagga aaagacgcgg gaccagatag ccagtgttcc atcggctaca aaggatgcca 540
atccggtgtg ccacatgtcg ctg 563
```

<210> 403

<211> 618

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(51)

<223> Area matching Drosophila EST AA391350 (inverted).

<400> 403

gtctggacac tgtatcacca acttttcggtt gcaactgcact tttttcgccc gcgacagcgg 60  
tagagatgta aaataacaat ttggcatcga ctaccgatga ttcttggcga tagttgtcga 120  
ttcgcttttt gctatcgaag ttaatcgatt catcggtcga tatctacact ctacaaaatc 180  
tccactcact tatgttagcc aatacaacaa ccaagtcgcg gcggtattca aaaaaaattt 240  
caaatatata aaaaaatcaa acaaatgatt tactataacc gtagcgaagc tttctcttag 300  
gtattatggt taatttcaaa tcgcaaccct taaatgagtt aaacactggt tggatcgcga 360  
tagtttacgt ttattttggt tgagaaatgt ctagaacacc aataaagtaa attcagtagc 420  
aaacaagttg gattagtaat attaaatc cacttgctgt tcgcatttat tgcttcttat 480  
ggctctcttg gacttaagag tatatctata taaataccag taatatgagt ataataacca 540  
tttcgggtat gaaaaagatc tacaatccaa tgccttcat ttacgtttgt aattgatatg 600  
agtattgcct cgattcat 618

<210> 404

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (100)..(499)

<223> Area matching *Drosophila* EST AA392183. This EST  
has sequence similarity to DNA J genes.

<400> 404

atttctacct atatatgcct ggagcataca caaatctggt ccccaatctg ttatttaca 60  
gtccccagat agtaattacg cactacttct tctgttcaca gtaaacagca aacaaaatgg 120  
ttaaggagac tggatattat gatatacttg gcgtgaagcc taatgccacg cccgacgagc 180  
tgaagaaggc ttaccgcaag ctggccctca agtaccatcc ggacaagaac cccaacgagg 240  
gcgagaaatt caaggccatc tcgcaggctt accgaagtgc tgtccgatgc ggacaagcga 300  
caggggtgtac gacgaaggcg gcgaggcggc catcaagaag ggcggcgcag attccggtga 360  
cttcgcgaat cctatgggac ttctttgaag aagttctttg gcgctggatt cggaggtagt 420  
ggcggttga cgcaggcgca gaaggcgtt caagggaccg tgggtcacca gatggtccgt 480  
acagctggag ggaagctgt 499

<210> 405

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (149)..(348)

<223> Area matching *Drosophila* EST AA696390. This EST  
has sequence similarity to Ubiquitin fusion  
protein genes.

<220>

<221> intron

<222> (349)..(411)

<223> Probable intron in gene represented by EST  
AA696390.

<220>

<221> misc\_feature

<222> (412)..(457)

<223> Area matching *Drosophila* EST AA696390.

<400> 405

gcttggtgccg caacccacaca cagtgtgtgcc acctgtgggc gaaaaagtta cgtctacatg 60  
gtgttcttgggt cacactgtccc ccgccgtgac aaacaaaata gaaaaaaaaat aaaacaaaag 120  
ataaaaatttt agcctccccc ctttgagaaa taaaggggtca tttgaggcag tttaaatacga 180  
aaagaatcca taggcacgga gagcccagca cacatagaat gttccacttc agcggcttca 240  
acatgatgtt cccggaggga cgcaattttc atgccaaacta ccaagtgtt ctccgtatcc 300  
catgttgcca ggaaacgagc gaacccgacg tggaaaaggc cggaagagg tgagttaccg 360  
aagtgtaggc ttggcctgaa attcatgtga acaacacatt ccatcccaca gttattatgc 420  
ctccctcggc gcttggacac gctcaccgc ttgaatggtc gattattcaa tggctgggtca 480  
agctgcccc

489

<210> 406

<211> 518

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(267)

<223> Area matching *Drosophila* EST AA802961 (inverted).

This EST forms 816bp contig with EST AA817584.

<400> 406

cgccacaca gctcatccac tgcacccctc gccagtaaa cactccgctg cgacggctgg 60  
cggttgctgg gacgtttttc ggcaccttcg acggcgctctt ctgttccaat cctcgactgc 120  
gtcgcgaacg gcgatccgtt tgttgcaact tctggcctga cacgctgccg attcgtttat 180  
ttaggcgttt ttttcacgct aaaacaccca agaaatgtga gcaaatacat gcctctggct 240  
tatcgatagt ccccccgca tatcgctcgg ccagcgcaac tgcggcatgc tcatcgataa 300  
taaccgcgtt aagctgagat atgccaaaaa tggcttaatt tatgtgattt attaattttt 360  
tattacggta acgagcaagg aaaattagtt tgcagggcgg ttcatttgat tataagccaa 420  
gttttttagta aaatattctt tttcttttga acacattaag agctggcaaa aaataactaga 480  
tggtcggaa tatgccagaa taccaacatc tagaaacc 518

<210> 407

<211> 565

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(259)

<223> Area matching *Drosophila* EST AA699045 (inverted).

<400> 407

ctatagccca tggccggctg acatcccctg atcttgctga ccttctgct cagcggattg 60  
taggtgctgc cattgtagtt gggcatgtcc acaaactggt ggatgaacct cacatctcca 120

gtgacctccc gtgccgtgga ctectggctc tgttcgttga gcagtcccag agcagcatcc 180  
gccagacgtt gacccaagat ctgggtgctt tcgaacatat ccttaccggg tccggaggca 240  
aagcaatctc cctcgccagt gggacaacgg gaggtcagta gatcacactc attgccggag 300  
atcgagcact tgggacccat tatattgggg gacacatcgc caaggttgga tgagcagaag 360  
gcaccacga acttgccctt tccgggcac ttgttcggat tgtactcctt ttccaggagc 420  
agggcggcat aaccacatt gtcgctggtc accagtctgg ttggtattgg tcatgggagg 480  
tggcatgcac cgcataccca gttgaaaagc gccaggaag gttggtttcc aaggtcgaca 540  
aatcgactg gggtaagtg cttaa 565

<210> 408

<211> 498

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(99)

<223> Area matching *Drosophila* EST AA952055. This EST  
forms a 1205bp contig with AA202358, AA202625 and  
AA951416. Sequence similarity to Human SIAH  
binding protein gene.

<400> 408

atcttgacaa aaatttttgc aagcgcataa aattaacaa attgtagagt tgtggacaac 60  
aaatcgccac tagaataact ggaaaaaagc gaaaatgggt agtactagac aaacgcgact 120  
catttgcctc gcagcagaga ctttttaact cgcaccaaac cgaagattgc gtctttcgtt 180  
ttcccgtaga atttgcgcat tttttcgga ctttcacagt ggcgttgtag cgaccgctct 240  
tgggcggcat aagggttaag gggcatgtgg gtggctacgg gtgggaggtt tccgcggagc 300  
accccgctgt gaccttgctt ccatttggga ctaccgacgt cacagctgcc agctccgggc 360  
gggtagatac acatcccgaa ttaacaccac gcgctccgc acctccgatt cgccgtctca 420  
tgggaagtgg aaatgggaag tacagccctt ttggtccac atgcggattt tacctggggg 480  
gtggaaaggg aaaagggt 498

<210> 409

<211> 601

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(601)

<223> Area matching *Drosophila* EST AA142266 (inverted).

<400> 409

aagcagacca agaaaaggaa taaagataag ggcgtcagaa tcaagactgc aacgaacggg 60  
aatgccctt tggctctggg aagaaagtaa acaatcggag gtgaaggcgt ttgcgagttg 120  
catttatcaa aacggattat tgtgcaatag agaaaggtgt cggacagggt gtgttttttaa 180  
tgacacttcc cctcgaaact gcaacttctt catgtcaaaa cataactcga cgaaagacag 240  
gacggatcaa ttcttacttg aagatttcac ttcttatagg gagatttgta agtcatatta 300  
atggagttag gcgtatgttc atatatcacc gggtataaga gttaggaagt ttgaaaaacc 360  
cgtgttatcg aactacaaga tatacgttag tattatatca ttttatttat ctagtttttaa 420  
ttctacagtt ttttaatcca cttttaatgc aatacagtaa aactattttt ggagttctac 480  
gtactgaccg gcaaattcaa catgaactaa acgcatagta caacttttct tactgtcgaa 540  
agactaagaa attaatgcga gctgctccgc tggccgcaac gaaggagaaa acgtaacaga 600  
g 601

<210> 410

<211> 628

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (52)..(534)

<223> Area matching *Drosophila* EST AA696974. This EST  
has sequence similarity to hypothetical proteins  
from yeast and *C. elegans*.

<400> 410

ggccagatgg aacatattgc tttcggggagc acaaggatcg ggtctactac gtctcggagc 60

ggatttttgaa gctgagcgag tgcttcggct acaagcagct ggtgtgctg ggcacctgct 120  
 tcggcaagtt ctccaagacc aacaaactga agttccatat cacggcgctc tactacttgg 180  
 cgccctacgc ccagtacaag gtgtgggtga agccctcctt cgagcagcag tttctctacg 240  
 gcaaccacat acccaaaacc ggactgggtc gcatcacgga gaacgccggc cagtaccagg 300  
 gccgtggtgg tttactccat gaacgacctg cctctgggct tcggcgctcct ggcgcgttcc 360  
 acaacggact gcaagaccgc ccgatcccat gaccaccgta tgctttcatc agtcggatat 420  
 cggcgaatat attcgcgccg aggacacgct ctttttagatc catagatgct aagttttaca 480  
 tgttttagtc aataaccatg tttaggtaaa taaataagta tgctgaaaaa cggataaact 540  
 gcttttgatt tatattttta tggttaatact gataataata ataattgata taaaattacc 600  
 tacatttcat aaattattaa aaaaaatt 628

<210> 411

<211> 1139

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (503)..(626)

<223> Area matching *Drosophila* EST AI532170. Forms a  
 1565bp EST contig with AI544333 and AI062662,  
 sequence similarity to MTF-1 gene.

<220>

<221> intron

<222> (627)..(733)

<223> Probable intron in gene represented by EST  
 AI532170.

<220>

<221> misc\_feature

<222> (734)..(1069)

<223> Area matching *Drosophila* EST AI532170.

<400> 411

gtcaaaacca tccatagtga tgtgattttt tgaaaatcta tcaaaatatt ctgaggtaaa 60  
 cttatgcgct tttgcgtcgc gtgaaaaagt taacgcaggc aaacagctga taagcgtag 120  
 gtgttttgca aactggcgga gtcagtggcg cctagcctag caatttgata agtgaatgaa 180  
 aatacacaca tgcgtaaat aaataatggt ttcaccttac gcagtaaata aaaaataatt 240  
 aaattgcgaa tattattaac ttttgatttt gtattgaatc tcagaacaat ttgtttctgg 300  
 ttctttaatc gacacctact cgatagttct gggtatcgcg ccgatcttat ctttttcaaa 360  
 actaattttt gtcctcttga ttataaaata caaaaatgct ttattaaagc gaaatattaa 420  
 aatattcaaa acgagtaaca gccacggata acaaccaacg ttttttctgc tttccaggcg 480  
 actacagctt taaatgcccc ggaagatgga tgccacaagg cattcctcac ttcctacagc 540  
 ctgaagatcc acgtccgagt ccacacgaag gtgaagccat acgaatgcga ggtgtccggc 600  
 tgcgataagg cgttcaacac gcgctacagg tgagtaatca tcttccactt cggaggactg 660  
 atagccaccg gaataaacca atggctgcgg gcccggccct attaattctgt aatcaacgtc 720  
 gcccgattca caaacagatt gcacgcccac cttcgtctgc acaatggcga gacgttcaac 780  
 tgtgagctgt gccagaagtg cttcaccacg ctgagcgacc tgaagaagca tatgcgcacg 840  
 cacacccagg agcggcccta caaatgtccg gaagatgact gcggcaaagc cttcaccgcc 900  
 tcgcatcacc tgaagacca ccgaaggaca cataccggcg aaaagccgta tccctgccag 960  
 gaggacagct gccaaaagtc gtttagcaca tcgcatagtt tgaaatccca caaaaagatt  
 1020  
 accagcgaca attgcaaac aaaggctcgca agaaaggcca ctaaagacca gcagaccaat  
 1080  
 gcagcgatca ggagcagaag gtcccagcag gaggagcaga ggaagaagga gttcattaa  
 1139

<210> 412

<211> 569

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (442)..(569)

<223> Area matching *Drosophila* EST AA567128.

<400> 412

ggttgtagcag ttcggggcgaa ctagttatga attgaaccgg ttcgcgcggt gctttttacc 60  
 agagttatca ggccatgccaa aaagcgcgcc tatcgaactg gtttatgtgg tacatataag 120



ggaccctaaa tttaaatttc tggcaattgg gatttcaaataaaaatcaaataattgaaatg 180  
 cactgtaaga atgtacactc tactagtcacat gtttaattgt aaataaatat ataaaaacat 240  
 atagtattat taatttgatc aaattagaaa gcagtcttag ggcccattat ataactgtga 300  
 gaaaataatt tccttatttt taatacattt cgcattgtgt tctgatgtat tatcatttta 360  
 taaattagta ttaatttaag tgcacgaaca acctattcgt ttattcagtg ggctactactg 420  
 ataacgataa gtccgatatc gataggagta ttgtttttat tttgtttaat gtaatatata 480  
 atacgaagta attgttttga tttcatgaga atgtcgaacg cgttggaacg ctgccaggag 540  
 cctactgtgg gccgatcacc gctaggaaa 569

<210> 413

<211> 574

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(79)

<223> Area matching *Drosophila* EST AA950480.

<400> 413

ccctggggaa ttggcagttc actttcgttg gtggctcgag tgcgacgtaa agtgcggcag 60  
 cgaagagcgc ttttccaggc acagtgcgcc actacttgcc tgcaagtcag ccacaacaat 120  
 ttctcggtaa ttgcgttgca aagtgcgtaa ttagagcttg ggggaaaaac tgcgttttcc 180  
 gcaataccag aacgtgcccc atttccacaa gagcgtacgc agatccgtga gttcagtgat 240  
 tcctctaagc tcaatgtggt aacgagagcc atggcgatga ctttgaaatg cggaaatgaa 300  
 agtacaaatt cggttgcgtg ctggggaaac ggctctgaaa attttacagc caataacaac 360  
 aaaggcaaaa caaacgcgta attgcagaaa tcagcttggt tacctacgga cgaaccagag 420  
 ccccataaag aagaggggca catgccccct acccgcgcac ccattatccc cctccgtcc 480  
 acaactatgg agcccaacag cttggctcgc aagccctctc tcgcgtctc tctctctctc 540  
 tctgctttgt ctgcctttt atggactaac tttt 574

<210> 414

<211> 360

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (2)..(360)

<223> Area matching Drosophila EST AA950161. This EST  
forms a 1217bp EST contig with AA950864 and  
AA950181.

<400> 414

cctccggcca agcgccataa ctccacaaaa ctcgatccgg aattatattg tgagtttgtg 60  
tgaatgtcta ggcttgatcg agtcgacaat atcggcagta gcgaacgact caagttctag 120  
ccagcacaaa gaccacattc tgcaaggaat ccgctagcga ggatcttgct gaaaccaagt 180  
ggaagtggag gagacgagga ctccaggcgc cgcgcacaaag aacacaaaca acaaacgacg 240  
agtgcgctca cagcgaacaa cgcattcaaa atggcgccca caaaagcaac aacgcgcgcg 300  
gccatcacia gcgggcatca tcagctgcag caggcagtga atcccatctt gggagccctt 360

<210> 415

<211> 649

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (30)..(194)

<223> Area matching Drosophila EST AA539625. This EST  
forms 882bp EST contig with AA202440 and AA390927.

<220>

<221> intron

<222> (195)..(290)

<223> Probable intron in gene represented by EST  
AA539625.

<220>

<221> misc\_feature

<222> (291)..(366)

<223> Area matching Drosophila EST AA539625.

<400> 415

agacgtgggtt ttcccaactt gcaatgcagc gaattaacgg atgtaatgcg acgcatagct 60  
tcccgatttc tggaaacaag caaacgaagt tgcagcccg aggttgatcc ttgcatgaca 120  
accgattgaa tgagagagat tgagacatca acgcgcagtt acgacatcgg gggattacag 180  
tctggtcaga tattggtgag tccgagattc agatgcgaat tgggtgatgg ggtgtctgtg 240  
gttactgcgc attacgttgg tcgatcccc ctaaacgac tgctttcaca gggcaagcta 300  
gcaaaaggaa aacaaacgcc atgtcgacag agcgaagctc gcattcagct gaaccagcgg 360  
at ttggcgct tttgttgac cgcataaca tcaacaaca caataataat aataagaata 420  
ataataataa taataacaac aacaacaaca acaataataa taatgacaat aacaattgcy 480  
gtcgcagcaa gaaccggtgg gaactcacag ggaaatatgc aactgctgaa gccccagct 540  
cattagaatg tgccccgcag caatctgaca gcaccaagca acaacaatt tactcgattt 600  
gccagcgggc gcagcgggca taactggatg atcatatgcy cggccttta 649

<210> 416

<211> 572

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(255)

<223> Area matching Drosophila EST AA951297.

<400> 416

gggtgggactc ccgatatttt gtggagcggg aggtgttttg atttccttag catttagcac 60  
aaaaaaatgc aactagtata aagtactgtt cactataaca atttttaacc accgatagcy 120  
agtgttcac tgtgtgtgcy agtaagagag atagagagca actagctcca gcatcatgag 180  
aatacaaca agcgccttgt tgttgttgc gctggccgtg acgtcgcaag gagatgccga 240  
gtccaattgg aatggtttgt tcttaatttc taactagaat gagttcatca gcagccatag 300  
aaaattatat tgcattcatg ttttcatatt ttctgatctt taagtgcatt ccactgccgt 360  
acttattaca caaatgcaca gagataaaaa ggggatgtga tgcggttggg tttttctta 420  
tcattcttga taagaaacta gaacatcctt ttctcgttca aaacatacaa aagtccgaaa 480

tgtaagtttc ccttactttt ttctggggta tgcgcagtac atatctcaaa gaatttgttt 540  
atgatccata taccaccgac ccattctctct tg 572

<210> 417

<211> 654

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (20)..(95)

<223> Area matching Drosophila EST AA948996. This EST  
forms 781bp EST contig with AA541068 and AA950730.

<220>

<221> intron

<222> (96)..(478)

<223> Probable intron in gene represented by EST  
AA948996.

<220>

<221> misc\_feature

<222> (479)..(654)

<223> Area matching Drosophila EST AA948996.

<400> 417

atccaaggtg cataaaacga caaagtaaga aactgtgagt gctgtggaca ttaaaccagc 60  
ttcgatttca agaagtcgca ctccctgaaa gcaagcaggt aatgtaaaac attcatcgcg 120  
tgcgatgcaa gggttatttt gaagtgcggg atcgcaacgt tcatatgcgt acaggaatcc 180  
tcgcacttgc atacatactt acattgcata ttctactgat gctaagggga tatttgaaat 240  
gcaaaaggtg tcacgagtgc atttcgtgtg ctttctgtct aaggattgcg gaaactcccg 300  
aacaactgtg gtttaagggg acacgggctc tgtttgccga atctgcgtat gtaccgcagt 360  
ggctgtgtct gtaggtatgt tcgtttgggg gtaagaacgc ttgagactgg gaggtcacat 420  
tttctgaac ttaccattt tgccttagcg tcaatcgcta acccctcgcc tttgctttca 480  
ggatcatcagg tccagacttg tcagtgattt gaaaaccgga aaaccctttt gcgatcatcg 540

taacgaaatg agtgccgtca ccagcagcga tacagccatc agcggcatgg ctcttggccg 600  
gagccagaca tctgccgtac tacgtgcgcg gcattgccgt ttggggaact ttgc 654

<210> 418

<211> 378

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(378)

<223> Area matching Drosophila EST AA941568.

<400> 418

ggccagaccg aaaaatagca tcgaaattcg agcgaacgtc gtgtataagt aaaacgaaag 60  
ttgtgtcgct ctgtgcgaaa gagagaggga gaaccaata tttttgcaag ccagaagtcg 120  
aaggtgaaat taaaatgcat tagccacca attgaagagg agtcaactac gaacaaaact 180  
cggatcttta agaatcagcg aaaaatcggt tgtgaacatc catacaacca caaatcggtt 240  
ttgcctgctc tcgtgtagtt cctgtgtatt ggtgcgcgcg ccctgtgtgt gtttgtgtgt 300  
gcgtgcgtgt aagcattgga atggattaac taccctaact attccaaacc aataataccg 360  
caacataatc gcaatagt 378

<210> 419

<211> 552

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (228)..(522)

<223> Area matching Drosophila EST AA801928.

<400> 419

gcacgtacat accaaaagaa gcgaggagcc agagagcgag agtggacagg ctaagagcag 60  
cgaagtgatc tgccactcgc tacttccgtt ctctcacttg taataaacga gtgcaaagag 120

agcagtagca gcagcagtag caacaacaac agcaatcgac gggcaaccac ttgaaagcaa 180  
 ctcgtttcga ttccatttag cagatacctt ttgtacgttg attaagatac cttggcacac 240  
 acagacgcac tacaaaagaa gagaaggcag ctaaaaactg cacttaaaaa acacataaaa 300  
 taataagaag tcaactcgat taattcagaa cagttctcca aatgaatgta caacaaaatc 360  
 cacttgacca aaaatgtctt gagtaaaagt gtcgcatacg cgtaaagcgt acgtataata 420  
 tagaaataga tatatgtatt cgtgtgtgtc cgccagccaa tacaaaagca gcacaaaaag 480  
 gtgggttaaaa ggcattttaa atcaacaat atttaaagt ctgaaattag tgtggcgtgt 540  
 gcaaagaaag at 552

<210> 420

<211> 172

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (14)..(98)

<223> Area matching *Drosophila* EST AA951147. This EST  
 forms a 695bp EST contig with AA695598 and  
 AA540269.

<400> 420

ctattgagca ccgacaacgt tgcgtgtata agacagttta cataaattat tatttacaat 60  
 tgcacagagc gttgatgttg tgcgttctaa gcgaaaaggt gaacttgacc ccggtgccga 120  
 tagaccgccg agctattggg tgtgaaattc gcgagcgagc cttgtggaat tc 172

<210> 421

<211> 411

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(279)

<223> Area matching *Drosophila* EST AA697191. This EST

forms a 1002bp EST contig with AA392404 and  
AA438791.

<400> 421

atcccaagca gtagcaagca agccatcaaa atcgtaacct tgggcgtgtg ttaatcaagt 60  
gatccgtaca tccccgcctc tccccctcc ttttatcatc atacatacca ccaccatttc 120  
tacatccaac gattttgatc tggattactc ggcttggttg attgttggtg ctgtttcgct 180  
ggcggtttctg tttccgtgca aacatctggc gagataaggg gcctatatag tttcgccaca 240  
gccacctcgc agggcccccc tctccgggtc ccgccagcaa cgacacgaca gaacaaccaa 300  
aacttggttg gaaaaaccgg tgcttgaacc gtaagttgga taacgtcatt cggtttcgag 360  
gggcaaaatt aagacttctg aattgggcca ttatattata cacttttcca a 411

<210> 422

<211> 689

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (650)..(689)

<223> Area matching *Drosophila* EST AI518422.

<400> 422

gtggaaacga tttctcacga aggtaagatc ggcttgaact tgaacgggga tttcgggtggc 60  
taaggcagcc acgcggtttt acagtcactg ggggtcgagg tctgtttgga tgaccccagg 120  
ctacctatgg gtcacactat tggagggata tatctggact caagcgttgc tcacagaggt 180  
cctatggcca ctaccgccac taccaattag tcccgccagt gtcctcatgt tccgcaacaa 240  
ctggggacgct caaagatccc gatgaaaacg cgttttttccg cctggcaaatt agttttttatt 300  
taactcgcac gcaatttgca ccttttcact actttatttt gacgtaacag tgcagaacag 360  
ctgctgcgaa cagctgttta gggttgcaac gtgcgcggtg acgcaaggca gccggctaaa 420  
acgtagcact agaagtgtgc aacgtaaggc gacaaagtct gcaaccttaa aacggtagtt 480  
atttacggat gctgacatta ttttaaaagt agttacacca tttttattgc tcttttttga 540  
attaacattt ttacatctat tttgtgctt acttacgttt ttctataaac atatcgatag 600  
cacaagctgt ttctctttgc gcatctctaa tcacgtttac gtaaatttca gaaggagcag 660  
caacaaggat gtctagaaat ttgggttttt 689

<210> 423

<211> 959

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (27)..(689)

<223> Area matching *Drosophila* EST AI535025.

<400> 423

ccctgcgcgt ttcgattcga ttggttcttg aaatggtaaa atgcggctgg gccgtcgaaa 60  
aaattgagaa aaataaatcg cgtcgagtgt gggacgcgaa cggaatcgct gtgaaaatac 120  
cgagttaaat gtgcgtgata gaaactttcc tccgaaaagg atctgcaatc gaaacggaag 180  
ggaaaacgca gagcaagaca tccttgccca cgcaggatag ctgtgtgaag aagacgcgac 240  
gataggccaa gagggagggg gagcacaaac aggataagca gtggcagaag aagaagcaga 300  
aggcggagcc gcatctgccc gcagtcaaaa caagagaggg aagtgcaca aaagcgagat 360  
taaagtgcac tcagctgggg gaaatgtgaa atgtgaacga tgttgcaacg tcgcgctgct 420  
tgcatcgcca agtaaaagca gagtcagaag aaaagcaaaa ccaaagcaaa gccagaacaa 480  
acaaaataca caaagtgaga gaggagagaa agagagcggc agtgtttggt gtatctgtgt 540  
gtagtgcgtt cgcgtgtgcg cttgtgtgtg tgcgtgttac tttgctcaca acaaattatc 600  
gtttaatttg cttcgatttt gcgacaacaa caagctgtgc gaaaggggat gtcctttcca 660  
ccaccaccac tatcaccacc ccctgctccc taaggtcata ggtcaccagc cgagaggtga 720  
gtaaatacaag ttgtttgaat tttgttacct aaaactcttt tgcacctaac gataacaaac 780  
tgatgagttg acctcgctga aagccgcgta ggaaacgaat gccaaattta accaaaataa 840  
taaaacacgt ttgccaacgc cagcagcggc gacacaacag caacaacca tgtccaatta 900  
aagttgcagc agggaaaaaa aagaaaaaaa atccggctgc cggctgctgc aattcagag 959

<210> 424

<211> 598

<212> DNA

<213> *Drosophila melanogaster*

<220>



<221> misc\_feature

<222> (8)..(536)

<223> Area matching Drosophila EST AA950826.

<400> 424

```
attcgaggca agcgtagcga tgcgcaaaga acaagcataa gcgaagaaga taaagatata 60
gattaaaatt totgctacaa aaataaatat atatgtaacg catattgtaa atgttctaag 120
ttaagtgcga taaatcaaata atttgtgtaa agtttaatat tttaatacgc gtcgaagtag 180
aacgagtgag gctacagaag agcacacact aaagtgggtg acttggcgag cgcaaataac 240
ggaaatcaaa ttcgaaataa acgctgcgca atagacgggtg gtgtacataa gagtttaaca 300
aaatccgaat cagaatcagt tgaaagtgtg atttttttga gcctttgtct ggtaagtga 360
gagaaagctt taagcggaat tacatctata tatatatata taaatatata aatacgaagc 420
cagcccgtag ccatttttga aaggggattt taaaaaacac acacacacac atatataac 480
acagctgcga acacatccac atataacccc aaataaaatc cgaagaaaag agcataaaaa 540
aaacgcaaaa caaaccaatt tcgcaacttt ttaagtgaac cttccaatca ggcacttt 598
```

<210> 425

<211> 517

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (48)..(150)

<223> Area matching Drosophila EST AA949934. This EST  
has sequence similarity to mammalian Casein kinase  
genes.

<400> 425

```
tttgcgccgg agctcacttg atttttgata gcttggcgcg gcagttgtca ttccgtctcc 60
tctccgccg tatcattgtt tttgcaatcg cagctctctc gcaaatctgc gctgcgggtg 120
tgcagtacat atacttgtga gaacttgtgg tgtgttatac gcgttaatcg ctttatcgct 180
gtgacgttga ataaattgtg tttgctccag tttccttttg aaataaattt caatgcagtg 240
cagccacggt ttttattcgc tttgctgtgt gtgtgtgtta aaagttggac aaaaaaatg 300
gcctggaaca taacagaaaa gagttgtggc tgtcaaactg ttgctaaaca cctcttatct 360
```

caatcttttt tgacttgaca gtctgccac aactggaaaa ttatctatcc tctcttctcg 420  
ctctgttggtg tatgtgtgtg ttttgtgtat cttctacttt tttgagtcag ctggctgtgc 480  
tttacttttt catctcctgc acagctttaa cgagttt 517

<210> 426

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (411)..(582)

<223> Area matching *Drosophila* EST AI109292.

<400> 426

actcaaacca aaatagttgc aacagttgcc attcgcagcg aatcgtccaa acagctgact 60  
ggaaccgtgg agcttacgtt ttgctttttt catcatagcc caaacagctg acgaatttta 120  
actttactaa agtcttaaat ttttaactaa gccagggatt ataaatattt ttctgatata 180  
tctgtaaaaa cttttttgaa aatcatttat tctgtaaata ttttcaaaat ctatctttta 240  
taaattaatc aattacaagc tctttttcct ctttcagcta attttttgct gtacctgcac 300  
cattggttca gaatactatg cgatctatcg ataacaacga tggcgagggt gaacaagttc 360  
aagttcaaac agctgattcg atttgttttt aattttcatg tgatataacg aaacccaaaac 420  
aagtgaagcg ggcgaaagaa cacatccaag atggaccagc acagcccaat gttgtggcga 480  
cctctgcttc tgctgcgcgg cctctacctc agtcaacgcc accagatgag ccactacgac 540  
gcactgggat caagccgtca gtgcacgcag aacgaagatc ag 582

<210> 427

<211> 709

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(279)

<223> Area matching *Drosophila* EST AA202259 (inverted).

This EST forms a 1693bp EST contig with AA391736  
and AA820861.

<400> 427

gttgtaggtg tttgtagttg ttgctgcgct aggaaacgtg tatttcttcc tgcgccatgc 60  
taaccctttc catataaacc tgatttaatc tttgattatt gtgctctcgc tgggggatta 120  
ttgctgccgt tcgttggtgc tggctttgct atttttgaaa attccactaa attatccggt 180  
gtgccgtccg ctgctctcc gccgttcttg tagttgttgc tattgtgcgt ttttgggcag 240  
gtaaaacagt tcatttgccct agggttgcca catcggtggg cggtccccag gaccacctgg 300  
aatgcacata aaatgttaag ttttattgcc ctttttacag ttctccaca ttacgactg 360  
ccattgagtc gtaaaacacg tgaacaggta gcgatctatt caaggccaca gctgtttagg 420  
aggttggtcaa ccctggcggg caggagattt caaaacttcc agtggatatg ttctaactca 480  
aggaattttt atagccgatt tgtttgaata aatgtacaat gtacataatg tctgcggcag 540  
acgctgttaa ttataaatac aactgcggcc gcaagggaag tcatcaattt aaaaagctgc 600  
tctgcattaa ttggtatcta atacctcttt tgctggtgag ctttggaat tttccgttc 660  
aatcaaaca ttatataaaa gtgttcttcg agggacttat gaaaccgac 709

<210> 428

<211> 666

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (131)..(647)

<223> Area matching *Drosophila* EST AA142065. This EST  
has sequence similarity to succinate semi aldehyde  
dehydrogenase genes.

<400> 428

ggatggcgat agtctgccca gaggtggaga aaaatcgatt actcccgat atcgatgtct 60  
ctatgatcgg tttcttgta atttaaagcg attgggttaa ggtcccaatt aatcgaaagg 120  
tgaggcgggc tattttaaaa aagggaatt atccattaac tttaggtaga ctttgtgcac 180  
atttattaat atagcggcgt gttattctac aattagacaa caataacca atcgattct 240  
agtgaagac agcgtatgaa agcagtggg gtgatccctc catcggaatt cagtcgtact 300

tgaggttgcc catgcaaag tacttgatgt ccacatagtc gtcaatgccg tgtttggaac 360  
 cctcccggtcc gacaccggac tccttgacgc caccaaagcg agcctctgct gcggagatga 420  
 tgccttcggtt gacgccgacc atgccaaact ccagtcgctt ggccacccgg aacacctgct 480  
 gcagattctc gctgtagaag taaccggcca ggctctcct ggtgtcggtt gccttcttta 540  
 ccgcttcttc ttctgtcgg aaccggtatg atggagacca ctggacaaa gacctcttcg 600  
 agtagagtgc gccgaagggtg gcacatctgt gacaattgtg ggtgcgtaga aaagggatcc 660  
 cttgtc 666

<210> 429

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (76)..(559)

<223> Area matching *Drosophila* EST AA536402.

<400> 429

cgctcgggta taaatgaaga gctatttctt tagcccagct cagtaggttt tttttgttgt 60  
 tccgtgcggg tgctcatttc gcgtaatt agtgtaaatt cccatagctc ctagtgttga 120  
 ccagattgtg aacgttgtgc cagacgtctg ttaattagca tatagcacia cgaatatata 180  
 taccaaaaac ccggcaaaat tacaactcat ctccgacgca gtagccagtt ctttgttact 240  
 gctgctcgcg caaataacgg taaatgtgga taacgggtgga taaatcactg ctgacctcga 300  
 cctagacaac aaatttgtac atagctatgt acattgtata aaccgaaagc gacaaaccga 360  
 tttcttggtg ccggctatgc attattgatt ttcaacatcc aattcgacag gagagcggtg 420  
 gacagggggg agtggagcgg agaaatcgag tgaatcagtg ccgcaacgta acggtaaccc 480  
 ccgatcccg ccacctaga ccagtcccat ccaaagtatg aaccgcccag aggaaggtgg 540  
 tgcgccccaa gaatccttc 559

<210> 430

<211> 599

<212> DNA

<213> *Drosophila melanogaster*

<400> 430

ctcgatgttc gacgacgctc agattcagat tcagtttctt ttcacctttc gtcggttgta 60  
gategctgcc agcggaagca acggatacca agtcccagac acacaggcac caaatgcctt 120  
ggaaaatatt ttgaaaaat tccaagtcac aatcgatagc gactaatgcy ttcgagccag 180  
attaattagc cagaggtgaa aagtgcattg cgcggctaca gatactgatt ttgttttaaa 240  
aatcgcacac ccaaaaccag ttaaaaaaaaa aaacacaagc gaaatatata ttttcgagtg 300  
ccccagtgcc agtgcaaaaa taataaataa agctatcgta aaataaatca aattttgtgc 360  
aacgcgagaa tacacaaaag atatattcga ataaatacaa ctaataatat cgtgtcgtcg 420  
ttgcgtcgcc cgttgacaaa agtgcaataa tcatatattt attacaacca attacatatt 480  
ggtaatcaaa agtaataaaa tcgcaaatca aggcgaaata tttgcatgta catagcataa 540  
gtgcggttg aaaaatccaa aattgcaaga gttacgaaaa ccaaacgaa aactggaaa 599

<210> 431

<211> 606

<212> DNA

<213> *Drosophila melanogaster*

<400> 431

gggcacacgt atgcatgtgt gtgtgtgtgt gtgtgatttg tgcacaggta gaggtgaacc 60  
gtatctgtgt gctgcgagt cccttaggta agcaaagaaa atgtgcccaa ctccggtgaa 120  
caggtagacc gctgctcaca tgccggttgt tgttcttgtt gctcttggtt ttgctgctgc 180  
tgtaaggcc gctcatgttg ctgttgtagc ctgcgatgtt gctagctgct gttattgttg 240  
tctcttctga tacagcttct gttagggatg ttgcttctgt tgcttcaagc tgttgatatt 300  
gttgcccatg ttgctactga tacaactgtt actcgattg gttgaatcac cactgttgct 360  
cccactgctg ctgtttcggt tgctacattg tagcttctgc taatgatgtt aactcttgct 420  
tatgttgcat ttgtatgtta tggtatgtta tggatgatgc atctacaaaa gtgctgctta 480  
tggtgcagtt gtctttgcta attgagatat tgtagcttat gctggtcatt atgttgctgt 540  
aacaacactg ctggtattaa agataatggg gtgcattaag gtaaggttct tctgcatggg 600  
ggtgtt 606

<210> 432

<211> 169

<212> DNA

<213> *Drosophila melanogaster*

<400> 432

gtctagacca cataaacgcg tatcgatggc gacgaaatgt gtacatcgca catgaacgaa 60  
cggggagagt gagtatgtac agtttaagag agcgaggcaa tatgaaatat aaacaaataa 120  
ttaactgaca tatccgtatg cttatcgcg c aacaaaccgc agcagcagc 169

<210> 433

<211> 585

<212> DNA

<213> *Drosophila melanogaster*

<400> 433

gtacacagca taacataatt tgctttctct cgcactccca ctcttacctg ctgagagcaa 60  
cagccctgct gtctcgctca ttgcactcg ccagttgcct tctcgctccc ccagccaccc 120  
actctcccgt tcggccgctt tcaccgctg catttgctgc gcgcctggta ttcggttcgg 180  
ccaaaccgcc gttcgcttgt atgcgagtgg attattgttt ttgtttcgaa cgcgagtaaa 240  
gtcgcgctgg cgtttccaaa ggttcccgac ttttcgactt gaactgaagg cccaaaacca 300  
gtttccactg cagccgagga gtttgggctt tagggtcttg gcttagcctt ctcatctcgc 360  
ctcttgttta cagcttaatt tgccctgcac accccgatgg ttccaccccc tttcatccac 420  
gtgccgcata gccatacagg ctgacttcca taaatgggac atgcggaaaag aactactatt 480  
atacaatata aattataaat ataaatacat acaatgtatt ttaatgttgt atagaatatc 540  
ttgatattaa agataagatg caaaaattaa aataataatt tataa 585

<210> 434

<211> 849

<212> DNA

<213> *Drosophila melanogaster*

<400> 434

actccggcgc tttctcgctc tcacacacaa tcaacgggtca tgcgttcgta tcgcttcggtt 60  
gtgtgtctaa aaatagacac aaatattgaa gttgattttt atacggccat cgtcagatac 120  
ccctccccct cctgttacca tcccttgggt cgtttgggtg gttcgttggt gctatcaaac 180  
atcgccatc agtggtgttg ttattgccat tatgttgctg ctgccttcat tataatgcgt 240  
tggttggtgt taaaaataaa ctctgctgcg cgtggcattt ttttttcta tttcaactct 300  
ctcacgcgct tttggagagt ggtgagaagt ggggagagcg ttgattaaac tcaatgaaat 360  
aaattagatt taattcatgt ttttgctct cttcaacagg tccagtacat tacactgagc 420

aaatgtgaag aaaattcaca tattgtattc agcgatagaa ttatttttat atttagttcc 480  
 gtctatctct tctacttct cacgtagaca agtttttaaa aaatttgccg agcattttgc 540  
 aatatttggt ttctgttttt ttctgcgccca atatttttag cacctcttca atttttctct 600  
 gtcgctgccca ttttttggtt gttttcctac ttaacgccac gagctgtttt tctcagataa 660  
 aattcatagt gttggatgga ggtgggggtg gggggggggg tggggcatcc tggtgagtgc 720  
 aacattgttg cctcgtttga agtggctgtt taaccactg atggcccaga aggctaaaag 780  
 tgcataatgg aaagatttat cttagactt gttatgactt ttaaaggcat tttcatagca 840  
 aacgaattc 849

<210> 435

<211> 585

<212> DNA

<213> *Drosophila melanogaster*

<400> 435

tccccacct ttaaatttgc gggcttttcg tttgttttgc cggccgtggt tattggtggt 60  
 gttgttgctc ctattcgacc atctctcttt gcctttaata cccttacgaa gagtaactca 120  
 aaagtaaata aataaataaa ttaactactc ttgaaacata tccgttctag tgaaaaaatt 180  
 aaaattaatt ttaattcaat tatgaatgct cagaattata atgaggaaat cttcttggtt 240  
 ttgtagaaca tagctttact agtattataa catttcgaat ttcaattaaa agagtactta 300  
 tagttcggca tggtgcttcg gtttttccgt ttattttgcc atatgtatat ttctcgctcg 360  
 cttttgcgat cattcggtgt tgagccgcgc tgcagttaac aacgatctga atgattccgc 420  
 tcccgaataa attagcgcgt gtgcctcgaa atattttaaa tcgctaacgt gcgtgtgtgt 480  
 gaataataat aataataata ataataataa taataataat aataaccata aaataggaaa 540  
 ggtacatttc caaagcaatt tacgctgccg cgggtataat tagaa 585

<210> 436

<211> 505

<212> DNA

<213> *Drosophila melanogaster*

<400> 436

acgcagacga cgaactcctc atgtgaccga gtaataaaat agcgacgttg cgcacaatgt 60  
 aaataaaaagt aaagtgtgaa ggcagctggt caaaggaggg gaaaaagaat aacaaaaagc 120  
 gaaaaagcaa accaaggcca cataacataa cataaaataa taataaaaat gccggcgcgt 180

ttaagcggct gatttctgtg cccttctatc cgccatctct gcattcttctt ttctgtttccc 240  
 ccttttatta tcttctctct cccccacaaa cacaaacaca cacacacaca cagcgcgcg 300  
 aaatttctat cgtcgcgtac tattttcgtc agtcagctgc tgctgagtcc cgttacttac 360  
 ttcagtggcc ctctcgcttc ttttgcctcc tccggtgctt cgttttcttt gagcacctcg 420  
 tgcaagctct catatgtttt tccgcgctct gctttccgcc gcttttcccc ccgttttaat 480  
 atgtattttg ataatactac cccaa 505

<210> 437

<211> 581

<212> DNA

<213> *Drosophila melanogaster*

<400> 437

gtataaactc gtgtggagtc gtagtcacag tacgttcaac gtaacgttca atgatctaaa 60  
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 agtccacaag tgtctacaaa tttccagttg gcaatgcctt tgctggatgt aaagtgggtg 180  
 cactcttate ggctaggtgg cgctctatct cgagagcgat agtcggggta ctacaaccga 240  
 accactgggt agacatatac ggtgctgcca acttttgtca agaaaaaat cagttaggtt 300  
 tgaaattttg caaaaaaaaa aaatggggaa taaatatata aattataatt tagcaaaaaa 360  
 tttcatcatg tggtagctgc ttaggttaag gtatatcaaa taatatggaa aggtaattta 420  
 ccacaaaccc taattgattg caccatggta taatggcatt agtgagctat accaaaacga 480  
 gcaactttcg aaatccatca gtactggtga aaacaacaaa ccgaaagaaa tgagtcaagt 540  
 actacgcatg ctttactggc ttcccatttt gctgctgctg c 581

<210> 438

<211> 637

<212> DNA

<213> *Drosophila melanogaster*

<400> 438

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 tacagttatt caaaattaaa atattttgta tcacaaacac ggagtaaate gattatttta 180  
 agattaattt taaaaatgtt gttttgcgcg catgttggtg aatttaattt cgcagctgaa 240  
 tgccttggtga gttctcttat tctctttage tcttctctt ctcttggtcg gtctcttgca 300



accatatttt ccttatttct cgtgtaaaat gaatatatgt tttttacagt ttctctaaat 360  
 taaaataatt totatcacat cattcgagta aatcaatttt ttttaaggta attttaaaat 420  
 tgttgcttgc ggcctcttta ttgaatttag tttcatagct gcttgccctt tactgggggg 480  
 ttggtttggg aaatttatca gctggtagcc gcgctggtaa aggtaacagc gcttgcgacg 540  
 gacattctct aacacagccg ggaaataaac atccagaata atttgagtgg gcttcacac 600  
 tggcaggcaa ataaccatca agaaaaaagg atttaaa 637

<210> 439

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<400> 439

gaaagagccc tatctctggt tgacttggtt ttgtttggta ttctttactt gatttcatac 60  
 ccgtcacacg aacattacgt aggttatatt ggttttgcgt aagagagaaa gatgtcatga 120  
 ttgatcatta aatcaatca gattaatgct cgctaataaa atgtaatcag caattatcaa 180  
 agtgaagaaa gtttaagcca agctctcgaa atcaagtcct taaaaattta gtggtattaa 240  
 aatgtgctac tcttcagttt ctaaattggct tttgtaaaaa ataactaatg cactttttta 300  
 cactcttgcc acattaagtt ttcagtgaca gaagaaagct gattctaaat tgtcagtaac 360  
 gagcgggtat cactttggtc taggctaccg acagaagcgt tcattcttgt tttttattat 420  
 tattattatt acgttttttt ttgcccctc aacacgtttt ctggttcttt ctttgggtgt 480  
 atgggtgtgt gcttgagcat gcgggcgcac ttgtgccacg tacacaaaaa cacaatcatg 540  
 cccacgagga aggtcatttg aag 563

<210> 440

<211> 662

<212> DNA

<213> *Drosophila melanogaster*

<400> 440

ctgccgcttt taccgctctc agctgtttgc tctctcgctc tcattttcgt tcgtcgagag 60  
 ctggtttggc gttcacctcg ttcatttttg cactaaacgc ggcaagatgt tgaagtcatt 120  
 ttgatttctt cgagtgtagc caaatcaaaa taaatcgta acagggtatc aggaagttaa 180  
 agcatgtaag ttactaaact caatataaca atgtgcagtt acgctatcac gtaaaaaacgc 240  
 aacaaactca acataacccc actttcgata gtaaaaaacta taactataaa gttatgagca 300

taaattaata ggtagcagtt aattttctct ttctcccat attcgcatth ttctgcacgc 360  
 acttttttcc cttgcacgaa tatttatcgt cgctttgctt tgtcttttcg ctacaatcgt 420  
 gtagttattg ttgcgttcgg aaagcgacga acgcttaata ctaccaacaa caagaacaat 480  
 aacaacggag tagatacaca ccaaaccgaa cacaaaaaaa agtaaaaaaa aaaaacaaaa 540  
 atgttggtct tgagttatga tgttcctatc atcctttgac tatggaacat ccataactcaa 600  
 agataacatt gctttaatgg cttcgtatac tttagagtta gaaaggactt caaatgaat 660  
 tc 662

<210> 441

<211> 496

<212> DNA

<213> *Drosophila melanogaster*

<400> 441

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 tgtgacacac ataaacggcc ggggaacctg atgcccattn natcgtatta tcgcattgcc 120  
 gaaacgttaa ggcataaaaa caagcgggtg taagacagtt tgccgttgta attggccaga 180  
 aagcaaattc tgtagctaga tagttagata gttagtgaac acttaactgt tgagataacc 240  
 tcgcattggt ctccgatcgt agtgcacttc cctgatgcgc aaactgtttt cattcgattt 300  
 ctcaatgtta caattttacaa tttacaatta gccagtgate gcttccttaa agctgccgat 360  
 gcttgatgat cgattaagcg ttttcacacc tttcccagtc acgtcgcatt cgcaggttat 420  
 ctgtatggat atgggtacat gcatatgaag catacgacat ggtgcccctt tccccgtgg 480  
 gttatttata aaaagt 496

<210> 442

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<400> 442

gtgacacgta tgtgtgtgcc gaaaaacagt tgttttcttc gctcgccaaa gaattttctac 60  
 caaagtttcc cccctcatat gcatttcac accatgtttg ttggcccaac tattatcgcc 120  
 ctattccaat tggagtcgaa attttaatcg ctctgcgctg attcatacac ctgccgctaa 180  
 ttggtcgctt ccattttaca cctgaatttc gctttgtttg aaatttaagt tttccctct 240  
 tcttcgtggc agcaatgcaa ttagctaaaa cagctctat ttatttatga ttggctcttg 300

aatttttcca tttcaatttt tacttagttt ttgcaaccag gtttttggcc aggcgcattg 360  
aaccaccttc actttacagt ggagattgcc tataaacgaa aacatttcat gacttcagaa 420  
gtactacatt tttttaattt ttggctttta ttatcaataa tttgcatata aaatagaaat 480  
tttcaatgaa aatgtgacta ttaggtagaa tttacttccg gttggaacaa tacctattgg 540  
atggctcaat ttgctaattg 559

<210> 443

<211> 397

<212> DNA

<213> *Drosophila melanogaster*

<400> 443

gtagagtcgt tttcaagtgg cgtttctttc tttcttttta atgtgctgct tcttgcttct 60  
gcctcttctt cttgcctttg gctatctgct ttgttttgaa atacgttcat gtattcagtg 120  
tctgtgcgag tgtgtgcgag atgatctcta ctttttcctt ctcttttttg ttctcgctga 180  
tttttgtatt atttttcgta cacgtaattc ccgtagatat cgaactcagc tgctttttgt 240  
tttgatacgc ggaattatca acctgctttc gttggcgctg ttaaaaaaca aaaacagtaa 300  
aaatccagtt tggcttactc gaaaattatg cgaatatctg ggatgtaaag agcttaaagc 360  
ctgaaaaaaaa tgaaactttt ccattaccca tgaattc 397

<210> 444

<211> 470

<212> DNA

<213> *Drosophila melanogaster*

<400> 444

atccggatta ctagccatgt cgatacagcc ataactgact gtaagtccgt atttgttcgt 60  
ataatcgtaa agccctcagg tactattaaa gctaccctgg aattgaattg ccacgtacat 120  
tgagacacct agggatcaag gtctagaata cataactgtt tacgtccttt ttgttctaga 180  
aatctctagt ttagtgaccg caaacattac ttttttgcag gaccatttta tgaacggtca 240  
cattaaaaaaaa tggctagtga taaccacaaa atggcgaaga tacagactgt caagtccgtg 300  
gggacaatcg ataaaggatc cgatgatttt tttttgcaaa attacaatcc ttgaaatgta 360  
cctttattag gtactatata tcgtatacac attgtaccaa taaagtacag caatatgatt 420  
aaactttttt ttttataaaa tacttggttt gccaaaggcg ttgcactttg 470

<210> 445

<211> 182

<212> DNA

<213> *Drosophila melanogaster*

<400> 445

ctctatgect cgtttgctga gacagcagca acagacagcg gaacagaact gaacagaaca 60  
caactgaacc gaactgaaca gaaaccaaca cacaacaaca taacacgaca aaacataaag 120  
aaaccgaaca caaaacccca gcagaaaagg caaaaaagct gaaaaagagt cgctgagaat 180  
tc 182

<210> 446

<211> 370

<212> DNA

<213> *Drosophila melanogaster*

<400> 446

attcagcgct tctctttggt gagagctttc agaatgaaga gaagtaatgt taagagaatg 60  
taagagagga ggtctgaaat catgtttgtt ggaabtatctc tgaagggcaa gtgttgcaaa 120  
ctgctgcaca tttctaaaac aaaaatataa aaataaagat ataaaatata taaaataaaa 180  
aataaaaaat ttctaaaata ataaaataat aatgaaatga ttttaattctt tacgaaactg 240  
ttgtcagcag tattattaca ttattattga taaagggttaa gtttcttcag catattatcc 300  
acctcactcg tagacatgga aaacacatgg ataattcctg ggaaatgccg gtgtcacgta 360  
gaagacatat 370

<210> 447

<211> 435

<212> DNA

<213> *Drosophila melanogaster*

<400> 447

gtcgaaacga acgaactctg gaacgctgtc gcagagggttc gatggagcag ttttgagcag 60  
tttgagcagt ttgagcggat ttcccagcaa cacaatgttg cgactcaaat cgtaatggtc 120  
gtgttgctag ccgaatgttg ggactcaaaa gataatggcc ttgctatagc tgggcggcaa 180  
ttttgtttcg gcccttatac acttttagagg cggcacgttt tcaacggggg ggcggggagc 240

tcagcaccta cctgatccca cggattccac aatgattgta cacacctcag tgggttccca 300  
 agctcgtcgg cggaatgacg tctcccttcg acggcattgc ctgcttctgg ctgtcactag 360  
 tctggattca actgggtatc atcaatgccg gcttgagtt cctcaaggat ttcgtacccc 420  
 ttcagctggg gccgg 435

<210> 448

<211> 235

<212> DNA

<213> *Drosophila melanogaster*

<400> 448

acgtgaacca accataaaac agcgggctat cgaactgggt ccagccgaac agtgctggat 60  
 aatgcaacat atatcgcaac gcgatgggtt taaatttaac gttatgattt ttatattaaa 120  
 aaataaatat ttttttacac cagttattat gccaaatctt ttaaattgtat acaaattagt 180  
 aatatttaag gaacagaaac cattgttaac tattttactt gtcaaagccg aattc 235

<210> 449

<211> 328

<212> DNA

<213> *Drosophila melanogaster*

<400> 449

tgtagacca ctggaagacg tacatatgcg aagacggggg caaaacaaac ggcggcgaac 60  
 agaggggagat acatgtatgt aaaaaaaaaa aaaggaaagg caaataatac tgtttatcaa 120  
 gtgatgaaaa gcatttaaaa tgtcgagtat gccagggtatt gtgtttaaat gcatgccctt 180  
 cgctgcattt cggttggaat gcacctgata ttggtaagga gaatgttcaa aagacataag 240  
 ctgaatgctg ttaataattt taaaaatatt taagcaataa atgcatatat tgcataatgg 300  
 cattaaaaca aaaggcaata cagaattc 328

<210> 450

<211> 110

<212> DNA

<213> *Drosophila melanogaster*

<400> 450

ggtcaaccgc tctgggcccc gttttaattg ttcgggctgt ctgacaaatt tcagtttcgg 60  
tttcagtgac tgtccttgcg gcaagctgaa gctgatttcc ttgcgaattc 110

<210> 451

<211> 472

<212> DNA

<213> *Drosophila melanogaster*

<400> 451

agccaggcga ccagccaaag cttccatttt cctcttcccc tttttcggcg agagagcgag 60  
cttttcgcgc tagcacagtg ggccaaaatg tattcatcct gccagctcac ttccagtcgg 120  
tcttcacgct caccgatggc actttcgaac ttcccgaac atgtggagtc tctttgatat 180  
cctgctctct taaggcaagc atttaatggc catctgttgg catccttacg aagccacaac 240  
tctttgcccc gctttgcaga actcaacact tgccaatagt gctattttgt accactcaaa 300  
agggtaaact acagcgttta ttcttttggg tggatattat attctccttt aagcaaacaat 360  
ttacacattc gttgtatggt ggtgctaaat tattaagtgg agatactgga atactctctt 420  
actaccatgc ggcacattta ttagctttaa tgggttggtt tctgacagtt tt 472

<210> 452

<211> 790

<212> DNA

<213> *Drosophila melanogaster*

<400> 452

atcacaacaa aatcaaacaa atgaacggca ctgacacagc ggcaacacca acggcaacag 60  
cagcagcagc agcagcaaca gcaacatcaa cgcagcggca gcaacatcac cgcaacagca 120  
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gtaacaggcg cccagatttt ccgagagagc tgaaaaagaa catttccaca tgcggagtgg 240  
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tcagagaggc tgggcgagcg aagagggttg ctggtgtggc cttaactagt ttcagccggg 420  
ccggtgtagt tgccttataa acgagcctaa aaatgcgaga taaagagcgc ttgcacgaa 480  
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ccggtgtcac ttccttattt agttgttcac gtttgtttgt tgttttgtgc tgttgggtgg 720  
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 cagcgaattc 790

<210> 453

<211> 404

<212> DNA

<213> *Drosophila melanogaster*

<400> 453

tatgagctca tccagcactg ccgacgtcac cccccccgc gttccattta ttattttcat 60  
 gacgcggcca agaaagacgc tggaagagcg aaacaagctt ttcgtgtttt ttctattcct 120  
 tttgttcogt ttgttttttg gggaggatta catcaagttg gagctgccac atagcgcaac 180  
 aaaatgccgg gacagtcagc tggtagcacc tgctgtatc gataaatcga tagttcctgt 240  
 tttaaagccc tgtcgacggg acgtaacaaa atattagacg tcagtggcag tggatttcga 300  
 ggattttaaa atgctttccg tcaatttctt caacatcatc ccaatgtgtc tgcgcgactt 360  
 ttggtatgac tcgtcaagcg cgccggcctt tatagtccgc caaa 404

<210> 454

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<400> 454

gcggcgcgga aagcagctgc tgctctctcg cgctcttttg ggccataaac atcttacctg 60  
 ttacctacca aaccaacttt ccaccgaaac atgcggcaaa tcgcatgatg caagacgcct 120  
 caaacatttc gctagccaaa gaagtttgag aagtttacga ttgtgtgcca aaaataaagc 180  
 acgtgcggtc gctaagaga gagtcgccgc aatctcttaa gttagtttct ctttcgcctt 240  
 agtcattgac cttttggttg ggtcctaaat atgtgcgcat tttgtcgaaa tcttttagcca 300  
 ctttgttgtc actgactaat cctatgtgcc aaaagacatt agctcaatga tttgttttagg 360  
 cctttaattg cacctgattt aacggctttg tgggacaaat actgcaagtg aaacttgcca 420  
 caaactattt gtgtgcacaa taattgtaac aaggttaaat gtcacattgt ggtaacacgg 480  
 aataaaaagc tttcgatagg agagatgacc gtaaactaaa tacatacaat aatatcgtcg 540  
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<210> 455

<211> 518

<212> DNA

<213> *Drosophila melanogaster*

<400> 455

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cacatacccg agtcgtaatc gaaaagaaaa tcgagaaaaac aaattggaat acttttcgaa 180
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gattgtatat tttttggtcg gtgcacctgc ggcagcctta aatcgcaatc ggaatgcaca 420
tttaaagcaa aatcgacttt taaatccggg ctcgTTaatt atcacgccta gctggcaaac 480
caaaactaac attcaagtcg agaaatccac gaatcatt 518
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<210> 456

<211> 324

<212> DNA

<213> *Drosophila melanogaster*

<400> 456

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ctagggatgt aagaatacat cgatgtatcg agaatcgatg taccgtgccc ataattttcg 60
atgttttttg ttgatatcga tgctttgctg aaccagctgt ttaattatac accgttcaca 120
caaccgcttt ttggttccat gtgaattatt taaatcgttt tagatttaaa taaaagtttt 180
tgtgtgtggt cttttttatt tcttttactc ctattttcag tcagtttctt cttattatca 240
tatatcatcg tatatttatt tatttgtata tgctgatact tatcattgaa tgaatcatat 300
cttaaagctt ataaatgaaa aaat 324
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<210> 457

<211> 325

<212> DNA

<213> *Drosophila melanogaster*

<400> 457



gtcgttatgg gttattatgt gatgtacaac gtgtaagtgt gcgtgcctca agcacttgac 60  
 ctcgccatca atgatcgag aaggtgggtc ggtaaattg gtgaccaga tgcagtggaa 120  
 gcaatcagga agagaaagga tttgtctccg gaacaaagca aatttttgat gacgtgccta 180  
 ttggcgaagt caaccgcga cgcaccac cactcaaag aaattggggc aatcaaggca 240  
 tatgtagtgc ccataacacg gttaccaatc acttatcacc ttcccgagct acagttttca 300  
 ttgcattgaa gttcctcggc agcat 325

<210> 458

<211> 524

<212> DNA

<213> *Drosophila melanogaster*

<400> 458

gtgcagagag aacaaaagag agtgcgagaa agagcgagag agacgtcgtg tttttgggta 60  
 cagctgttaa cgaaactccc acgtgccgc ctctgttgct gcgctgctac tgcgtgccg 120  
 gcacgtgtgt tttgttgac atttttgtgc ggcttccttc gatttttgtt gctgtcatcg 180  
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 ggatcacctt tttctaaact gaattgaatt attataagtc gctaaataaa cgatattttg 300  
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 ctcggtatca atcctatgta attgggtgtt accataaagc attttgggtc cttatgcata 420  
 acgcaaactc ataacttga atggaaagt taattactta ttattccaat actcgtcatg 480  
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<210> 459

<211> 571

<212> DNA

<213> *Drosophila melanogaster*

<400> 459

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 gagagagaga gagagaggag tccgcgagaa agcgccacga agtatgctct tgttttgtgc 120  
 tctcattttc accttttgcg ttgtctcatc ttaacttttc acttgtgttt gtgttgccag 180  
 gcgagctttt ttcttaagaa ggagaaagga gaaacgagaa ttaagcgaag gtaaagagat 240  
 ggaaaaggag aagggttttg taagaagaag aatttcgatt acaaattggct aatttgtgaa 300  
 ggaaattaac cttagtttta agaagtataa gtaggtttga tctaattata attattatc 360

tggtatttta ttttatcaaa ttatttcaat ggtaatgtga catgaccact gtgacattct 420  
 tataccatat acttttatat atttttcatt tttttttcac acttatatag attatgagag 480  
 ctgactatta ttttaaccat tgctggtgaa gccacaaaat tggcatggta actttcatct 540  
 tcataaccac attatccagc ttaattgtgc c 571

<210> 460

<211> 455

<212> DNA

<213> *Drosophila melanogaster*

<400> 460

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 tgtgtgttctt aggcgatact ttcttggcgc cagcttaaaa aatttaaate ttttaatttaa 120  
 aaaatttcca ggcaaatgca ctagttttta taggcaacta agcggaatct aaagccattt 180  
 aactgccaat ttgtatacca tatgtattgg actgcaatga atttagtagc aaataaacia 240  
 catatgtaag gttattaata caaaattgtt tacttttatat acctcgctaa tgcggaactt 300  
 tttttgggtc catgttgctt ccaaggtttt agggtcactt aaaatttact taaatgaaag 360  
 atttttcaca gtaatggggg agatttgctt tcagaaagcg tcgaactcct tcttttctaa 420  
 gggcttaaag aaatgtgtcc cgagaagggg cgatt 455

<210> 461

<211> 106

<212> DNA

<213> *Drosophila melanogaster*

<400> 461

ccttgaacca atctacaata tcttcacnat cataatgac atccctttta acgcatcacc 60  
 cgatttcaaa gcaaatacag aaataaactc aggcagatc ggtttg 106

<210> 462

<211> 51

<212> DNA

<213> *Drosophila melanogaster*

<400> 462

ctccagatac tttttgaaca ctgaagaaaa cgcgcagttg tgggtgaatt c

51

<210> 463

<211> 79

<212> DNA

<213> *Drosophila melanogaster*

<400> 463

cgtgggcggc accagaatac gagagagaga gcacttccag cgcattccagg cacatagttc 60  
cgtttagctca gttgaattc 79

<210> 464

<211> 470

<212> DNA

<213> *Drosophila melanogaster*

<400> 464

gctgtgtgcg cttcttttga attccctttg ttttcgtact gcctgtcggc cacttgagcg 60  
gcgtatgcta catgctatat gctaaatagg caaacacatt tttgtaacaa ttctcgaaag 120  
tcgtccggtg aatgtgtggc atctatagga gctgtctaag tgggccattg gccattcgt 180  
tatggggcgt tgaaagtgg ctgcactttc tgaagcagcg atgatgaatt gtttgaagca 240  
ctggcggtg gcagctgctg atggcctgtc ggtcaagatg aaaagatgag tggcaaagtc 300  
gattgaacca taacagatac tcgtagtcag ttgcgcgagc gggagtttct tcgggatcca 360  
ttaatggatt tgggactata aatacacttg cgccgtggta tctatctggg gaatcgtttg 420  
atatttccat ataaatagcc ctagcatcgc actattgaca ttttgcaccg 470

<210> 465

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<400> 465

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gaccggagg acgaaggctc tctcgaaatt atcttcaatg tgaagattct tctttctgaa 120  
tgttagctaa aatatgtttg gaaactggcc agtagagatt gcaatggctc tggtaagga 180

taccattagt agaacatcag cacagtagaa acctggagtt tctgttgga atttacgtgc 240  
 gttacaatgc tgacatagga catataagta tgtacatata taaatataca tcatggacag 300  
 ttttttacta ttttgtgaaa aaataaactt atcacacctg tgttcaaggg aaataattaa 360  
 tatatttatt ggtattgtag aaaggaaaat ttagtggtga aagaaatgcc aagtgggata 420  
 tccccaattt ggtaagtatg gtacatatat actggaatag taagggtag ggaactctaa 480  
 tccggatgtc caaagctttc cttaggg 507

<210> 466

<211> 260

<212> DNA

<213> *Drosophila melanogaster*

<400> 466

atctacacga tgcctaattg caagtgtgga aagtaaggga ctgttttagac aatgccataa 60  
 attaacctgc aaatcgtgac aaatcgggac atcggaaatc gaatatatct tgaaatcact 120  
 ggaaacattg aattgaaaca aaatatgcat aaatttaaca aaaaaaaaaa tgcgcaaggt 180  
 gcctatgccg gggggcatcc ttgatccaat gagaattact tttagaactt tacgaaatat 240  
 gaaatgaccc ttaattaatc 260

<210> 467

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<400> 467

gtcccacgga agctttaaca gtggagcctc gtgttttgct ctctcgctct caaactgttt 60  
 ctgcgattgc gtgtgtatac aaatgtggtg ctctcttttg ttggcgctct atttggaatt 120  
 gagatcattg ggtaaaaatc tgtagataa aatggtgacg gagcattaaa tgctgaagat 180  
 gattttatgc agtaactttt aaattaaaca gagttattac gttatgttct gaatgggggt 240  
 ttgaatgcgt tagatgtaaa ctgtgatgtg ttaataaaaa caaattccaa tgtgttttcc 300  
 ctaaaatatt tagtaatatt ttgaaaaatt cttcaatata tcttaaactc gtttttcgca 360  
 aattgcctat tgacgttcca ctgaaatatg ttttctctcg agtgagataa cttcccttaa 420  
 attcgtagta aaaatgtcga acattaacag aaattaatca tatgggtcat gaagttgatg 480  
 cttgcaagaa agtgcttatt taaagaattg tggaaggga ttgatggctt tggc 534

<210> 468

<211> 615

<212> DNA

<213> *Drosophila melanogaster*

<400> 468

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ctgcaaagta tgctacgaac aagaagtttg cttgaggata atcttaaaaa acattttatgt 60
tcatccttta aaatgtcaaa cgatttgagg actctagaga tttcgggaac accctgttat 120
gtatgttttc ttgatttgct taccttgctg caaaagaaca tgatgcgaaa acagactctg 180
attcaagcac ctggttgatg tgttgcaccc ttacacacac acacacactc acaagcacac 240
acacactggg aactgacaa agctgtccac ccacgcaaaa aagtccttgg acttcaacac 300
ctgagccctc tctgtttgat gatgttgttt tttgtgtgtt gttgcagaca agctgaatga 360
aaatgaaaag agcacaaaaca aagaaaagaa aaatcgaaag tttctacaaa gtctctgggc 420
actcaaacac actcgcacac acacacacac aatcttgac acttgcagga cacaatgtct 480
ttcaacgttt ttgtcacctg ttctggtgct gttttgccac atgtctgtct gtgatgttgc 540
gtactgtgct tcgctctaca agagattcca gtgacacatg acgaaacaga aaaccgaaca 600
cagcacgttt atacg 615
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<210> 469

<211> 27

<212> DNA

<213> *Drosophila melanogaster*

<400> 469

gttcgggttg agttagagca tgaattc

27

<210> 470

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<400> 470

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ggcgaacgca gtgcatgtga agagtaccgc tataaaagtt tcgccatcag ctctcccgt 60
cgctcaccgt gttatatgag tccaacaccc aaaaaaggga ataaagagag ccaagcagca 120
gcgtcttttg cagcgccagt gccgaaaaac gttgcaaaaa cgagcgaatg aaatcaaaca 180
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actcgcagtc gaaattgttg ttctgcactt gattgtatta attgtttttt tatggtattt 240  
gtttttttctt ccttgcgttt cgtgtgaatt tgtctggctt ttcctttccg gctctcactt 300  
gtttacgctg cgcgtgagcg agagagcggg gaagagtggc ccgagtgcgg gagaaaggaa 360  
aagggggaga gactgtgcca attgttgctg gtggaagcaa caagttactg atggtcgaag 420  
ggggtgtgct ctcaaagggc gccaaaatga gctgcattta aaatttcgga atattgctac 480  
cataaacgtg gcttccaatg ggcccgagtc ccattacggt catttcgtgc gtgcaacgaa 540  
accagtgtga a 551

<210> 471

<211> 465

<212> DNA

<213> *Drosophila melanogaster*

<400> 471

ggccgagcca cgacgacacg aagcgaaaca cgaatggcaa acgaagccga agttgcgagc 60  
gagagagaga gaatgggaga aaagtgcgaa agagagtgtg taacggagca actacacagc 120  
aagaaaataa atgtgtctag gctagagctt tggatgaat accaatgat aaaagattta 180  
tgcacaaaag gcacagactt taaaagataa ataaagcaaa attacaaagt tttaggtttt 240  
tgacccttaa ttggaactac ttttcccca gtgtgtgggc cggcagagag ggagagcaca 300  
aagcaaaatg caacggaagc aactcatcgt ggcacaatgg gcagactttg tccgagggct 360  
ctccaccggc acctcaccac actacacaac tgcgcccctt ccaccctcct cttcgacaag 420  
ccgaagtttt tgccgtgaca cttcattttt attttccgac cttgg 465

<210> 472

<211> 215

<212> DNA

<213> *Drosophila melanogaster*

<400> 472

ttttgagatc gaaacatatg tatcaatcga gcggccgtgc gtgctgctga agtcgaagaa 60  
aaaatcacgg gaaatcacgc cacttcggtt aaaacagccg gcaaaatata atgagttaat 120  
atgtgttttt ttccgttgtg tttggcggat aagaaaatcg cggcatgagg gatgctgaag 180  
tgattgagtg cggcgacta atgtgcagcg aattc 215

<210> 473

<211> 412

<212> DNA

<213> *Drosophila melanogaster*

<400> 473

gtggggaata ttaatagatt cacgtcggct atgaacagaa ataggtgccc aaatatatac 60  
gtattacatt ttaggcgaag atagcgtggg cttacgatgt tttccaaata tacatatata 120  
ttcccctata aatcttatct aaatcaccta ctctgcttcc attatatgct atcattcaat 180  
ctctaaaggt ttaatcctta cagctgataa gtacagttta attggaggcg taagtataca 240  
gtgcttactt gattagtgtt caaactaatc cctcttaggt taggtcatta actctcacta 300  
atccttcgac tatttaaaact accgcgatca aacacaaaca cgaagacctc aagtggtcga 360  
ggctgccggt ttggctatct ctggcacttc atgcacttca atctatgaca cg 412

<210> 474

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<400> 474

ggcgaatgct aaacaaaatg agagagcgga atgaaagctg tctcttgagg agcattttcc 60  
agcactgcta gagcttttca agagcaccac aagattttta agcggaaagc ttttcaaaga 120  
tgtaactgcc tttttagaaa cgtaaaacaa aacattctgc aggacgtaca aaatgtatgt 180  
atttaataag acaaagagtc tattatttat gatattctata atataaaaca aatgatgtta 240  
caatcaaatt aaaaatattt tattttacttt cgtttttatat tttaagccaa ataataataa 300  
aagtaattaa aatgtagata ttaaaataaa aatttaaate gattcgggtgc acacttttgg 360  
taaaatgtag aaaccttcat atggatttcc attaattcct ttcgatactt tttaacactg 420  
gctgatagct tacagccaaa ctgggttcaag caaggaaccg aacctcaaca cttttttaag 480  
ctcccacttg gtgactttga aatagtaaac atgggttttta tcagctaata tcagatogtg 540  
ccaatctatc aattaccca 559

<210> 475

<211> 474

<212> DNA

<213> *Drosophila melanogaster*

<400> 475

ggccactcgc tcgctgtctc tttctctctc cctcacggat actcgcgatt ttccgcgact 60  
ttgaaattcc gtatacgtcc gttccggttcg tcggtcgaag ctattctgag cgggtacggcg 120  
cttttgaaca catcggaata gttgaaaatt ttgagattta tttatagaga gaacggggcag 180  
tgttttgatc tctttgctga tttccaaagg tctctttgaa tataattaat caatgggtta 240  
atcagcccta tagtggattt cttattgaaa aataataatt aaaattcaat cactatgtaa 300  
ttaaatgtat ttttacaatt tatgagataa aaattgggtg tacaggttca taccatattt 360  
ctaactcata aattattatt cgaataaacg cacctcaaaa tagtttttga aaaagcccg 420  
taaaaacatt gacttcaatt cggctattac tattagccaa gtttacacca tggg 474

<210> 476

<211> 849

<212> DNA

<213> *Drosophila melanogaster*

<400> 476

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gtgtgtctaa aaatagacac aaatattgaa gttgattttt atacggccat cgtcagatac 120  
ccctccccct cctgttacca tcccttgggt cgtttgggtg gttcgttggt gctatcaaac 180  
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aaattagatt taattcatgt ttttgccctt cttcaacagg tccagtacat tacactgagc 420  
aaatgtgaag aaaattcaca tattgtattc agcgatagaa ttatttttat atttagttcc 480  
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aatatttggt tctgtttttt tttcgcgcca atatttttag cacctcttca atttttctct 600  
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aattcatagt gttggatgga ggtgggggtg gggggggggg tggggcatcc tgggtgagtgc 720  
aacattgttg cctcgtttga agtggctgtt taaccactg atggcccaga aggctaaaag 780  
tgcataatgg aaagatttat cttaagactt gttatgactt ttaaaggcat tttcatagca 840  
aacgaattc 849

<210> 477

<211> 157

<212> DNA



<213> Drosophila melanogaster

<400> 477

ctcaggccat tcaacttctt ctgcagtaag gaaatctcag cgggcggcag cttaagaacg 60  
ttcctttcga gccggatgtt tagctgctgg cgtatggcat caaatatctt gccggcctgg 120  
ttttgatagc tacgcagctt cttgcgtccc agaattc 157

<210> 478

<211> 94

<212> DNA

<213> Drosophila melanogaster

<400> 478

atacagaaca tgtaccagca gctctcacac accaccgcc cgcccccttg gcggtatcga 60  
tatataaata ttttctatgt gtgcgtctga attc 94

<210> 479

<211> 485

<212> DNA

<213> Drosophila melanogaster

<400> 479

gaatgaacat atctcaccca gtgaaaccgc tccaccttcg ctcagcgctg cgtcggcggc 60  
gactgcgcag tcggcgggca gcagcggcag tggggaaaaa agtgaattta tttcatgcac 120  
acttttttgg caaccagtt tgagccgaat ttttctgggc tgcccggctg tctggagttg 180  
ctagtgcacc cggatttctg gtggacaggg gcaggaagtg cagagttgctg tgggcgcatt 240  
agggtgtgta gggtgacagg ttttgatatg gatgccacaa atcggatcgt cacctttgtg 300  
cgacacttgt tgcttcgctt tggtatttta tattttatctt ttctttgaaa aatgacacaa 360  
accggtgtgc cttgttaaaa atgtgcgctt gcctttggaa ataaatgttt ccgccataga 420  
aaatgtattt gaaataattt ttgtgcacgc cattcgagac ttccataaat acaaagagga 480  
atggg 485

<210> 480

<211> 1145

<212> DNA

<213> *Drosophila melanogaster*

<400> 480

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tggtgaaata gttttgaaag ttttactaat aatctttata gttattaaga taattgagaa 120  
aagcgctaag gaaaacaatt cttaaaaaca aaatattaaa tgcgacccctt taagatttat 180  
ttaatatggt cccttcctat taactaagat tttttccata aataaataag ttgtagaaac 240  
agtaatgctg cattaccaca gtaaaattta aaactatttt caatgcttta tctcttaata 300  
gtttgaaaaa aaaactgcc aatagatctac tttacttact aactcaaaat gatttttctt 360  
atattttgat tacgttttagt atacctcagt aaaatcaaaa tagtgggtac tagaaaaaaa 420  
caacaacaaa accgctctct gacgtcggtg cgtctgtctg gcgtctcgca cacagccata 480  
caaaatacgt gcacatattg atgagagaga ttttctgcat tgctctttgg attcgtgttg 540  
ttgctgttgt aattgcaagt gatcgtaaac cggcgcata cactccggcg ctctctcgct 600  
ctcacacaca atcaacgggc atgcgttcgt atcgcttcgt tgtgtgtcta aaaatagaca 660  
caaataattga agttgatttt tatacggcca tcgtcagata cccctcccc ctctgtttac 720  
cgccccctgg gtcgtttggt gggttcgttg ttgctatcaa acatcgcta tcagtgttgt 780  
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agtggtgaga agcggggaga gcgggagaac gccagctctc tcatgcgttg attaaactca 960  
atgaaataaa ttagattaat tcatggtttt gcctctcttc aacatgccc agtacattac 1020  
actgagcaaa atgtattcaa cgatagaaat atttttatat ttaagttccg ctatctcttt 1080  
ctactctcac gtagacaagt tttaaaaaat tgcgcacatt tgcaaaattg gtttctggtt 1140  
ttttc 1145

<210> 481

<211> 232

<212> DNA

<213> *Drosophila melanogaster*

<400> 481

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aataaaacgt ggaatttgtg ggaaacactt ttataatact ttttgtatgt ataagagtta 120  
taataagcat aatgagaaca tggcataata cgagacttaa gccacatgat gtactatgta 180

catacataga aatgtgtgta tgtacctaca taacataatt ttaaacgaat tc

232

<210> 482

<211> 522

<212> DNA

<213> *Drosophila melanogaster*

<400> 482

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eggacgtttt gagcgcggtgt gccgtgccgc agataacgaa acattcgcag tgctatcacc 120  
agaattgaaa acagaatcgc atcaaataca ttatacttca cagttgaatg acgagaaatc 180  
agaaaaaaat attccccgc ctttctaaag aaatcaaaat cacaagttta taagtgccaa 240  
aacaaaaatc aataccgatc gcatacaatg cagcgcccca aaaagtgtc aaaactgtgc 300  
tgaacaaata ttatacaaaa aaataataaa taagcaaaac aaacaacaga aaatctatat 360  
ttaatctatt ctatatctat gtgtaatcga atcgaaatgg gcagtcgaac aaattgataa 420  
aatggcagct aaagccggag aagctacaaa taaatggatt aagcccagca gggtgagtta 480  
tcaaaagcga cgccgcatta cggtagcccc acaaatgaaa ta 522

<210> 483

<211> 325

<212> DNA

<213> *Drosophila melanogaster*

<400> 483

gtctaataa atcaccgcag cgcagagcaa catttaaaag ctttggccaa caaaaagcga 60  
attgcgtaca gttgtgcaac ggcgaacatt cgattcgatt cgattcgatt ggtttggatt 120  
ggattggatc ggattgtaat cgcaggcggg acagagggcc gcagcaaaag aatcggtcat 180  
aaaccgcaca tgtagttatc gagatatttc ggggaaatgc ctggcgccaa gtgtgggaaa 240  
tcaacggaaa catttgtgat tgaagcggg gtggatttga ccggtgctat agaaacgggg 300  
gttaaaacta atgattttta atttg 325

<210> 484

<211> 426

<212> DNA

<213> *Drosophila melanogaster*

<400> 484

ggtcaaccag agagagagag ggagcgggag agggagaggg agaggcagag gaagttttgc 60  
gaagagagcg agtgaggtgc acggaaaata attgattgat ctaatctatc ccatgaaaat 120  
ctggtataat tctactttta aatgagagct ttgttttaga gttcgaatcg attgttttat 180  
tgcttagggt tttggtaaga atatcatatt ttatgaggtt atgtggtaat ctoggcttaa 240  
gtggtgaagg cttcacatta aaatctctat tgatccgtta actatcttaa attactatct 300  
taatattttt tactttcata attacatata tttttataa attaccgttt cccaattgga 360  
aaattatttg gttggtatgt atgggccgcc cggggccggc gtgcaaatca ttttctgcat 420  
cattaa 426

<210> 485

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<400> 485

ggctggattt agagttcggg tcttcgggca tatatcgccg acggcagacg gactagacgc 60  
ccaacaactg acaccacccc ttcagtctgg cgattccacg ttcagtcgcc tggatattgc 120  
tacttttggt gttgtcgctc tgcttgctgt ttgtttttca cgtcttgccg caacgccagc 180  
gtcgactgcg gcgccccttg cggagcagag ctgattgtct ggctattttc tggctatcaa 240  
ttacaagcca ggtacaaatt ctcaatggaa aatgtttcca gaaagtatgc tattatttat 300  
tattatttct gctatcaaac gaaatatgta tgattgctac tgtaagatta atttgtggca 360  
taaatttagt ataagtacaa acaataatag agatctctct attaagcgga caacataagt 420  
cgtgtattta atactattag acttacgtcc aaagaagcta taagcgcac c actattgtgg 480  
caaatgaat ttgccttaga ggattattca gctagcacca caacact 527

<210> 486

<211> 504

<212> DNA

<213> *Drosophila melanogaster*

<400> 486

catccgattg tttacggccc tcagcggaga gcaactagtg ggtggccact tcaaactcggg 60  
gatgccggtt tagctattaa atagttatgt ttaacattta ccagtgggtca tttcagtcag 120

aaactactgg agtgtggcac agaaagtgtg aaagtatgca taacatatta aatataaatt 180  
 gtgaagccta cggtttacaa taaatacaat acctgccact ataaactata gccatttgtg 240  
 tatggatatct cagagagaga agacgcaata agatgagcaa cagaggtatg gaaactaaga 300  
 gcacaagaaa gagagacaca ccaccgtgat acggtttgtt gtggaacgca aaggggtatt 360  
 cgatcgtttg tggagcgc at tgcgtttgtt tgtggttcgc aattgtctta gcccgcgaga 420  
 atatttatta ttaatttatg gcattttatt atgtaccgc ttgttggtta ataagcaatg 480  
 tgtttactta agcttttgag tgta 504

<210> 487

<211> 584

<212> DNA

<213> *Drosophila melanogaster*

<400> 487

ctttgaacca ttgcttttgg ttcgcttatg aactgactgt attttttcaa cgtagtgtcg 60  
 tttttatttc gttgttgatt cgttctttgc tcagttcgtg cgcttatctt gacttttgct 120  
 ttgatgcgcc attcgcattg actggcgaga gcagcctagt gtgagtgtgc atttaaattg 180  
 ctccccaatg agagcatcat tttgtggccc tctttttgtt cagatcttcc ttttgctcct 240  
 cttcttcattg ctccccagcc catccgtcgt ttgttgttct tgctccgcct gtttttttcc 300  
 attcggtttt gaatttacac aaaacgtttg ccgttgcttc ttcattgctga aatagtatat 360  
 atgtatgtga atatattgta catatttctc tacacatcca tatgttttat ttgcaaaatt 420  
 tattaatagc gcagcgccac tccgcggctg tgttagtgcg ccagagtgcg aaagtaacag 480  
 taaaaaacta aatattaatt cgcgttgatt ccgattcgta ttgcaagttg ttcaaaaccg 540  
 agtgctagtg atatttgcaa aaaattaaca tattttccgc tggc 584

<210> 488

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<400> 488

gtgtgggtgt gagccgcctt tgccaggaaa actaacaaga aaaaattccc tggcggttaa 60  
 atttgcacaa aaaatgttga atcagttcga ttttcaatg aacactcacc cattaatata 120  
 ccattgtagg aggggggtata ttgatttccg tcagaagctt gcaacgggga agggaaacgt 180  
 ttgcgatcat ataaagtaca tatatatatt ttggataagt ataaactgcc aagacgattt 240

agccagggtct ctccttttat tcgtccgtcc gtatctaagc aagctagtca tgaagttggt 300  
aagttatctg gataagtcaa tcaaagtggt gtttctactg caggaagtat gtatataata 360  
agtatatcgg acatgtacat cggaatatta tgacaaaaaa gtactttcat tatatataat 420  
tcatttttagt tttttgacc 439

<210> 489

<211> 118

<212> DNA

<213> *Drosophila melanogaster*

<400> 489

gttacgatca agacctagag ccgagccaga aaaaggtata ctgcagagac agagaggagg 60  
gcacagtgac agagagcgaa taccggaaag aaacattcaa gcaataatca cggaattc 118

<210> 490

<211> 352

<212> DNA

<213> *Drosophila melanogaster*

<400> 490

atctgctcta aaatgagcgc ccctttcggg cgctcggact gcggccctgc ttgctctgtc 60  
gggtgtgcaga ctgtgctcag tcgatatttt tgaagttgct gtactttgcc gtcgcgtcgc 120  
agtagttgtc tcgctcgctc cgcagccatt ctgcttgccg cagcgtttat ttctgtacac 180  
tgcgactgcg atgtgcgctg ctacacacg tatacatgca tacagcatac agtggcagaa 240  
aacagtttgg cacgggttat aaatacgtat ttattagtaa aataaataag ttgctcagtt 300  
ctttagacga aactatggat tttattttta tattgaatag gatgagaatt cc 352

<210> 491

<211> 333

<212> DNA

<213> *Drosophila melanogaster*

<400> 491

ggccaaccaa gctggttgcc ccctatctg tgtgcctctg ctgttcgctg gtgttggtgc 60  
gctgtccgtg tattggtggc tctacagctg agcccgacac acttaccctg tttctgcctc 120

tttctgctgc tgcgcatgtg caagagagge tcttcggatg ctctatccaa atcgaaagta 180  
 actcagctat gtcactgaag taaacacatt gtattgtaca ttaacaatac cttatacttt 240  
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<210> 492

<211> 91

<212> DNA

<213> *Drosophila melanogaster*

<400> 492

tttcgtactt tgttttagcgc agtgtgacca gccgcaagtc gggatgaata acgtacaatg 60  
 tcgtacaaat accgaagaca atattgaatt c 91

<210> 493

<211> 426

<212> DNA

<213> *Drosophila melanogaster*

<400> 493

ggacagctgc atacaaatgt tttgctctgc tcttcccttg tgttgctatc tttttctctc 60  
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 gacattttga tgcacttccc actcaagctc acacatacac acacacataa aactacgctt 240  
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 attcgattta cttctacttc gaaaaaatag ccgagacaca gtaacttcaa aactgtgtcg 360  
 cactatcagc aactgctctc atgtatattt ttatcattaa tggatcattg gtttccgctt 420  
 aatttg 426

<210> 494

<211> 548

<212> DNA

<213> *Drosophila melanogaster*

<400> 494

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 atgtttatca tcgcaatcgc cacaaaagca aaagcaacgc aacagcagat gtttatgtgc 180  
 caacggtaga gtgtgcattt gtgtgtgtgt cagagagtat gtgtgtgaaa aggtgcatct 240  
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 tataagaaag aattaagtaa tatagtattg catagtagtt tatttaccta ttgaatgtat 420  
 aactttagaa aattattcgc gacagtcgac aaccctggaa tctgttattg cctcgtctgc 480  
 ttttatctac gcgcacacag gccaacagtc gacagaattt ctgtgctttc gtcgcagcga 540  
 gcatataa 548

<210> 495

<211> 120

<212> DNA

<213> *Drosophila melanogaster*

<400> 495

aacgcgtaca aaagcgcata aattgagagg cgagagttgg ctagcaacgc gcagggttgt 60  
 cggctatatg gggaaaaata acaaatacat ttccgtaatt atatggttcc gaaagaattc 120

<210> 496

<211> 408

<212> DNA

<213> *Drosophila melanogaster*

<400> 496

gccccaaactc tctcttttgg caagaaaaat cgatttcggt tttttgcage tctgggacgc 60  
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 taccactatt acccacactt tacttaaatt tctaaagcaa tcattgttat tacatgacag 180  
 attgttcaga tattccocta caagttattt acttgtttac ttattttctt gtattgaata 240  
 cgtataatta aatataatat actaattaaa aataaataac gaagacaaga gaaaatgtct 300  
 aaaatagaaa tgagcttaat ttaagtaaat aaattatata gccttatctc taggggcggt 360  
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<210> 497



<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<400> 497

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cattcaaact ttaacttcag ccttaacaag ccttaacagc acgtataact aaaaagacaa 180
tgacagtata atattagtaa ataaacagta aaatattgat taaaacatta atattaatta 240
attaattagt taatttatta ttaactttta aatatgaaat gctaggatgc accgaatgct 300
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ttgatattac tcatcatcat ctcatgctca tctcagttgg aaaataattt acgcttgtag 480
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gtcctaacta tttggttcc 559
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<210> 498

<211> 592

<212> DNA

<213> *Drosophila melanogaster*

<400> 498

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cattcctttc caggatatta aaccgcagc cgggacgggt gggttaacga gtattggcca 180
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aattcgaaaa actgctttta gattagctca caaaatcggg acaaagctag tgatattcta 300
ctggaattaa aaaattgatt ccatattcca tgtgaccttt aataaattgc aatttattat 360
tcaaaaggcc catccacctg ctacactttt aaaacaacca attatttacc caaatgatcc 420
gtcattacc ttataaattg atgaactcat attagacca ccagcgagcc gagtgaccaa 480
acaaattagt caattcgttt aataattggt ttggatacgt ctacaatggt gcatgggtat 540
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<210> 499

<211> 108

<212> DNA

<213> *Drosophila melanogaster*

<400> 499

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tacgtatgta tgttttatgg gggggatgga gcgagtgtat tagaattc 108

<210> 500

<211> 284

<212> DNA

<213> *Drosophila melanogaster*

<400> 500

gaccaggcgc totcgaaata ggcgccaaaa actaacgaag ctcgaccaga tgctgcaccc 60  
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aataacaaaa aggtgacgtc atggcggcag cacacggcat acaaacatac agtcgctatg 180  
gatgtgtctt actacagtcc aacttgctta ctaaaaccaa tggtcagtat agaaaaaggt 240  
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<210> 501

<211> 455

<212> DNA

<213> *Drosophila melanogaster*

<400> 501

gcctagatgc tagctatgta tgtgcttgat tactagtga aataactaact accggttttag 60  
atgcccggcc agattgtgtg cacaaaaaaa aaaaaaatga agaatggac gggcgatcga 120  
gtcagctagc gatcacttat tgcacacaga aaaatttggc ttaagatcgg gactatgac 180  
gtggatgcgg aagaaagttg aagatctaag cacatttaag tacgatattg cacgttctca 240  
tccggaaaga ttctttgcgt tgagaacatt caaatcttga accaagaatg gctttattcg 300  
cagtggtagg tggcttagct aggtgggctt ttcgcttgac cacgatccaa ttgccacag 360  
gaagcttaaa gatcagggcc cgatcaatac tcaaaccacc ggaccaggga agtcgtttaa 420  
aggcttcttc atggggaaag tcagttgcga gcatt 455

<210> 502

<211> 522

<212> DNA

<213> *Drosophila melanogaster*

<400> 502

agctagcgaa ttaatcaccg atgtttgcac ctgcctttc attttcgaat cgaaacatca 60  
tcgctgtatg agcgctcac gtcacctttt aaacttatcc caatgctaca gagactgaat 120  
ttgaataatt caaaccact caaacaagcg cgtagcaaa caagctatcc gctgcaatac 180  
cgcgatatcag atatgaatag taatcgagt accttgtctg tgtgcgcagt cctgtccgaa 240  
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cgccaacttc cttggcgtct atccctgtcg ccagatgggc tagcctggag gacgcccccg 360  
aatgggctct ccaactaacg ccttgtgcga ggtcaaaaca ctggaaatgg aacactaggc 420  
cacaagtacc aggacttttag ttaaatgggt tgctgacgaa aggtaacaat tgccaattca 480  
ggtgagtttc actcgcaagg aaagataagc tgaataacat aa 522

<210> 503

<211> 676

<212> DNA

<213> *Drosophila melanogaster*

<400> 503

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ctgccttttag cgattgcaag tagccgaacg catccggtga tcgtagacca cgatcaccgc 120  
tggaatgtgc cagcgttttt gccgcggttg cggcggtgc aacatgcggt gatgcagccg 180  
gtggtgcagc ggataccgtt atcagcaggt cgggtgtgggt cgatcagtc atactttctg 240  
gttgcggtt ctaattgcca tgtcctacta cttgtcgctt gattttgtta ccacccctc 300  
cctgtgcgtg tccttcgcgc tctgaatgct tgatgttcct aatcgcttga cctgtgggtg 360  
ttgcacgctc aatattgtac tggatatttg attacgttca gtttctgggg tggtttcttg 420  
gttaaatgaa tgccaatggt gatatttttg taaataacaa tcaacactgg actggtcaca 480  
ttataactga aaagaaaaat ataaccaag tttggatatc aaacgattaa tcaccaaaga 540  
actgagttat tacagcttaa gtaaaaccac ttgctaacac tttaagctaa acactatggt 600  
aaaaacattc ttctactaaa atataataaa aatattaagg ggaataatgg atggcaacct 660  
ttcattggct ttgagg 676

<210> 504

<211> 541

<212> DNA

<213> *Drosophila melanogaster*

<400> 504

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caaccgcacg accacgcgcg caccaaccct ctgcgtcaca caggcgccga accccatgta 120  
gtagagatgc gaccgtgagg cgattttctt cgcgcgagac gcccgacttt gaacatgcag 180  
tcaaccacgt tagcaccact ctaacttctg ctacgttttg gttgttttat tgtagttaac 240  
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ttcattgcac agaccattca attgcacatc tctagcagac aaccaaccag gtggcagcgc 360  
tttcgactca aatacaagtg gcaaccacgg tcgggcattt taataacgga aaagggatga 420  
aaagtccaga atagcgcgcg cgtttgggaa atggttaaat atcaaatgta ctaggaagtg 480  
tgggataata tgaacacgaa tggaaagcga ttgagtacct ttaagaactt agaataacca 540  
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<210> 505

<211> 59

<212> DNA

<213> *Drosophila melanogaster*

<400> 505

gaccacgcct aaattaggtc aaagctcagc atcgttttgc atctttccga aatgaattc 59

<210> 506

<211> 288

<212> DNA

<213> *Drosophila melanogaster*

<400> 506

ctctgaatta ccattgaaaa ttcattcgct tcattcattc tttgaacaca ttcatttagt 60  
ttatttcgat cggacgcctg taagtccgaa tacatacgaa gtgaacgcaa agagaacgcg 120  
accaactgaa tggcatgtat tctgaatacg cagtaaaacg aatcgatact ggagaatggg 180  
gttatgcac cctctagtac gtgtggcgt cgtttttcaa tttgttgctg ccggggaagg 240  
cacattaggc gctaccagct cctgcacacc gttatccagg gggaattc 288

<210> 507

<211> 234

<212> DNA

<213> *Drosophila melanogaster*

<400> 507

gcttggtccac tctaaattga aaaactgttg gtcacacaaa agtatagacc agatatcgat 60  
agacgccgat agattcgggtg aagtaaaatc gtgcaatttc ttttccaaag acttccacta 120  
gttaaaaaat agatacaaaa atgtccgaat tgcaggtgaa ctgaatctac gtcaaatacg 180  
cattcgatc ttaaagtctg attacctatt caaacttaac ctaaacagga attc 234

<210> 508

<211> 31

<212> DNA

<213> *Drosophila melanogaster*

<400> 508

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<210> 509

<211> 892

<212> DNA

<213> *Drosophila melanogaster*

<400> 509

tgttcggcat tgccgtttca cagaagcgat ccacaaaaag cttgcgctct gctcgccttt 60  
ctctctcaca gagattggga agggaatcac ttttgagatt gccatagtga cgatcatcg 120  
acatctactt atctactgat ctacttatga tctgaatact tatcgtatct ataccaatta 180  
aagtagttgc atacattaca tacctgtagc tctgtggagta aataattaaa tttatattaa 240  
gctccgttgt ccggttggtc gtccttggtg tcctaagagt tgggtgtggag aaattgcaat 300  
agtttatgag caattatagt atcacttact tcttttagct gagttactgg gggatatcaa 360  
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ttgatgnaat tgtgaaacaa aaataatgct taacaagaga gaacgctaata gatgatttta 480  
tgttcatttt aatggtamca gagtttcaat gtgtaattaa catactatat tatttttcca 540

gcctatctag gtacacttta taaatagaag tgattagcca cttgggctgt ggtggcgaac 600  
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 ctggagtttt ttcgatttcg taacgatgtg attcagctgg tcattcagat cttgctccgc 720  
 ctgtcaacac gtttgccgtt gaggactgga atcctcgcgg atttgtctta tttatggcca 780  
 ctggctgggt ctgctaatag ccataaaatc ttattaatca tatacatatg tcaagtgagc 840  
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<210> 510

<211> 53

<212> DNA

<213> *Drosophila melanogaster*

<400> 510

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<210> 511

<211> 197

<212> DNA

<213> *Drosophila melanogaster*

<400> 511

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 cgtaatatcg agtacacgat actttacttt tcccttcgtc cctttgaagc cctggcactt 120  
 ttagatttcc cgtgaaagtt caacgtatat cggattagt ctgcatactt ttagacggca 180  
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<210> 512

<211> 305

<212> DNA

<213> *Drosophila melanogaster*

<400> 512

tgccattcgc tcgtctctcg gctttatgag ccgaatgtga tgtacaaaca gtgagaaaac 60  
 tggttgtgtg tgtgtgattg cgccatcgct ctatgcctgt gtttctctct gagcagagca 120  
 catttcgttt gtttacagtt tttcgttttt gcgccatggg aaggctgtat tcggattctc 180

ttttaagcaat gaattttaaca aaaaatttagc tagccagtga agcatatctc ttttaattcta 240  
 ggctgtaaaa taatttttaa gaataccgat atgttttctt tgtaagagtt ggcaatctga 300  
 atata 305

<210> 513

<211> 387

<212> DNA

<213> *Drosophila melanogaster*

<400> 513

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 ttcgattttc acttggtttt ttaaaagcct tctcttatca gcaatcgggt ctttaatacgt 180  
 ttcaaatttt tctctaaaac gattggacat acatattaat gcacatatta gtgtttatatt 240  
 tgtcaaatta aaatttttga tgagagcaaa tctgtcttca agttttatca taaaaatgaa 300  
 attgatttat tctcttttta tttaaaaggc tcgtgtcctg aagcgcgcta gaaagttaa 360  
 gaaattataa gaattttact agaattc 387

<210> 514

<211> 530

<212> DNA

<213> *Drosophila melanogaster*

<400> 514

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 aagaggcaag ttcttttggg gtatttacga ctaagcaacc acattgggtt tggccagcgt 180  
 aatgagtttt tcgacatgca ctcgataaag tcgcagcgat aaggtcgcag agtgctgaat 240  
 cagtcgactt cccgcatggc aacagttgga actcgttttt agccactgga actggcgctt 300  
 gtgccacata aaccggacag ttgccgctga aagttgccgt taacaaagcc attgcaatgt 360  
 acagtcgagt caagtgggtca cgtgattaaa aacgagcaag agcagaaaat caaaagcaag 420  
 ataaacgggt ttcgttggcc aaaatgcgtc atcgccataa agccttgccg aagtcaatag 480  
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<210> 515

<211> 516

<212> DNA

<213> *Drosophila melanogaster*

<400> 515

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ttccgccagg accaattgcc ttcccttggc aggggaaatc gttgaaagcg gccccgcaat 120
tgcgctcctt ttcgactttt tagcaattac ggcgtagcgt aattggagag aggtgtaaat 180
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gattgcgata ccattcgatt cgattgtagg aaatgaaagc acttaaaatt atatagatag 360
atacttgtat cttctccagc agaagcgtgc ctttacttga tatgcgtgac aagcaaacac 420
cattaccctt taaatgtcag actgcaatga attttggatg tattaccgcg attctggcct 480
tttaaagtcg ctcgataagg caccgtctgg tcggcg 516
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<210> 516

<211> 583

<212> DNA

<213> *Drosophila melanogaster*

<400> 516

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gtaacgttga gttccgcgtc cgtgcgttct gccttccaat agaaagtctg ggtgtgaatt 120
taccaagatt ccagtgcgaa aatcaactca cattgctcgg tgatccgtgc ggcggtataa 180
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ctcgcgtca cccacacagt cacaaaagtc ggcgacgtcg acgaccaca cgctcacata 480
ggggacgtaa aatccgtgca tacgtgtgga gcgtgcatat ataaccatat tggccgattg 540
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<210> 517

<211> 437

<212> DNA



<213> Drosophila melanogaster

<400> 517

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tccgggggtgg ctgcccctgg ccccaagcgc cccggagaat cgctggcatc tgcaacggcc 180  
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tttcgtgccc gtttatgaca agcccggaca tacggtttgt tcattgccga ccggcatctt 360  
ttattctgtt acagtgcctt ttacctctcc gtccctccgc cccacccggg cggacagtct 420  
tccttcggca cttcctt 437

<210> 518

<211> 442

<212> DNA

<213> Drosophila melanogaster

<400> 518

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gaaacttaac cgtgtatgtg ttttccaatt ttgcgtgaac aaataaaaga gctcaagcat 180  
tttatcgttt gagtaatttt agataaaaat ttattaatat tttttaatgt tttcaatttg 240  
ccatagacaa cattttttcc aataaaattc ggtaataata ataacaccat gcctgcaatt 300  
tttatataaa tttttagtag cacgctctta gtttaatat taggtcaata aaataattat 360  
ccttattggg ttttttttta atttgcatat tggttggtga ccagctgtta agaagaagag 420  
agggagagag aaaaagagaa cc 442

<210> 519

<211> 536

<212> DNA

<213> Drosophila melanogaster

<400> 519

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ttaaacaag cagctgcatt tcaaaacttg ccaatgtaag tgaagtaact gctagaagct 180  
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 acgtatacga cgcgagaaca aaacgaactt gaatgttctg cggcaaggcg agcggataga 300  
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 acccactagc caccacccat tttggggggc acatttatta tcgcagacaa gctacttagt 420  
 gtaatcgcat ttgtatctgc aaccacgcga cctcgggctt tttgattgtg actccgecte 480  
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<210> 520

<211> 469

<212> DNA

<213> *Drosophila melanogaster*

<400> 520

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 cgtgcgcacg ctctttggag tctaccgct ctttcagtc ctctttccac tctctcgatc 180  
 ccagaggtgc ccaaaacata agttgaaact tatttaagta cggcttgaaa tatttaaatcg 240  
 aaaaggaagt aaaaaaatat aaataaataa ataataaaat aaatataata atatattaac 300  
 ttttaatat tttttttaat gagcgggctt aaaaacatta aatgggcaag attatataaa 360  
 tattcaagtt acgcgggttaa ttaaaaacat taatagaagg gtttttcttt ttgaaattaa 420  
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<210> 521

<211> 417

<212> DNA

<213> *Drosophila melanogaster*

<400> 521

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 attttaagtt ataaacatat atttctgtta tatttaaata gtattgttta tactcgactg 180  
 ttttaagtgt atatcagcga tttgtaccac tgtgccgtgc tccacttget cccgctccca 240  
 ctcaccgtgt gtgccgtgcc aaaacggaga tctccacctc ccgtctcget cgctctccct 300  
 ttctactact acgatgccgc gcccttctgt tttcattcaa aatttcatta aaggatgcac 360

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<210> 522

<211> 543

<212> DNA

<213> *Drosophila melanogaster*

<400> 522

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attatttatt agaaagtatt actatagtat tgataaaaac tcaagtaaca accaaatatt 180  
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tgtctcataa atgttcagag cgttccgctt cgctagttgg gcacaaactt agcgttgcca 480  
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<210> 523

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<400> 523

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atgagcctta gccgccttat gccgctccc ctgaattgac cgaattaaag ctctgggatt 180  
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aagaccagga gaaattgcca cagtcaaaac aattagacag acgggccaga ctctgtctt 300  
caacttggtt ccgcggcgga taaaagttgg tgtcttatgc tgggaaaagt aaaaagtgtc 360  
taattaaatg cttgtccaga ctggctttgg aaaatacaag gtgcttcaat gcaaacaaat 420  
ctgtacgaag ctgaaatacc cttagacat actattaaat ttaaattttt caagcttgta 480  
gcgcattttt caagctttcg aaatgaattc 510

<210> 524

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<400> 524

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ataaagtatc caatccaaga aaatgaggtt atgcgaatgt agtaattaga ttctaagttc 180  
tagtttttct ccgtgcataa tgagagttct tcctgtttcg ctctctctct cctctcttgc 240  
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tgggctgtgc tgccgcattg ctgctaactg cggctttcca cttttaaact caaaataata 480  
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<210> 525

<211> 91

<212> DNA

<213> *Drosophila melanogaster*

<400> 525

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agagagatgc taaatttagt tcaatgaatt c 91

<210> 526

<211> 417

<212> DNA

<213> *Drosophila melanogaster*

<400> 526

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ctctttttaat atatggaatt taataggaat taaaattggt attcacttaa ataaaattaa 300  
gtgctatttta ttgaaacaag ttaagtgggc tgtaaatggt tacaattggg gaattaaaaa 360  
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<210> 527

<211> 578

<212> DNA

<213> *Drosophila melanogaster*

<400> 527

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gtggagtatt gtgaggttgg ttgtaggttt gtgatttcgt ggatgtgac gttttgattt 180  
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caaattcagt gagaagtaaa caaactagtc tcgaacgcat tcgaataaca acttttccct 420  
atcaactagc attgatcttt gcacttgaac aaaacgccga aagcgacgtt gagcggcatt 480  
caaaagttaa attgacaggc ccccgagcc cctaaaatat tttttttaa ctagaactga 540  
gcccgcgccc ccattgcatt atctattaca aaaaaaaaa 578

<210> 528

<211> 169

<212> DNA

<213> *Drosophila melanogaster*

<400> 528

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gttggattcg aaacaagacg accatgatgc atacacaaga ctcaaagacg gagttttttt 120  
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<210> 529

<211> 348

<212> DNA

<213> *Drosophila melanogaster*

<400> 529

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tgcagacatt ttttaagatag ttttaagtcc ccatttttatt atacagcaac atggcacaat 180  
ttgtattaat atttgtttta ctatcgccgt cttaacagca ctgaaatttt ccagtgtgaa 240  
aactactgat attattaatg cttctagtgc tatcgatata atagcgaata caccacctt 300  
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<210> 530

<211> 463

<212> DNA

<213> *Drosophila melanogaster*

<400> 530

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acggaactaa gcagatttaa ccacaagtat caattagggg gaggtttact aatgattttt 180  
tttttttgaa tttgggtcaag gatttttaaag cgagaattat taattcaaaa acatcatttg 240  
gaaatttggt agaaacattt tggcacaaaa ttgaaagtat tcataacata agtgtgatta 300  
gtaaatttat tgaactaata attaaaacat acatatgtat atactatacg ggcataacag 360  
tgaaaagggt atccattcat tatttaccat cgggtgctctc ctgattgcta agtatattat 420  
agtcgggagc gtgccccttc ctacttggtc attgtttcct ttt 463

<210> 531

<211> 150

<212> DNA

<213> *Drosophila melanogaster*

<400> 531

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acagcagcaa catcagcgcc aacgattggt acacagcgcg aaaatcgggg gtgccttcaa 120  
agcaattcgt ttcacaggg aggtgaattc 150

<210> 532

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<400> 532

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actatgatat ttccactgcg tcatttgata ttgatgtat tgtgattcaa agcttgatc 180
aattgcctgt tcaattatgt atgttatatt ttttagtagg aggggtaaat ataatgaagc 240
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aattgtgcct catttcctac tcaaattttc tcttaagcta caagggatt gtaatgaaca 360
gaaaagctca aacattcttt cgttaaaaaa taaattacag gcctcataat ttaataccga 420
caattaatat ttatttaaa 439
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<210> 533

<211> 521

<212> DNA

<213> *Drosophila melanogaster*

<400> 533

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gtacccatca aacacacgaa aatattattg ttactgtgta acgctttaa attaatatt 180
ttttatttgc aaacataagt cgcaataaaa tctgtttaga aattaactta aattttaata 240
ataataaaaa ttggaatgaa taatatacta aagtaaggag tgcctaacia attagcaaag 300
aaaataaaaa atttaaatgt agcctaaata taaaaccat cggcacagtt agtacgctgc 360
aaaagtaatt tagcaacaac attcagatgc aaccagttcg ggtttcttgg cttcctcgct 420
ccattttcac gtgccttttg tttttgtgcy ataatcaca aagttttctg aaaacgaaac 480
cactgatagc gccacaaagt cccccaaca caaaccacca c 521
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<210> 534

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 534

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cctatggtac cctctaata gatttagggc caattggctg aactagccga tccgctccgt 180  
tcgctcgctc ataaatcact gcgaaactgag gactgtcgcc gtcgccgtcg acgtcgacac 240  
actatgacta atccccgctg gcacgcggcg gtggctccaa ctacaataac agtatgtaaa 300  
acagccacag ccgcagcagc agcgccgcac acaacaagaa acaacatcgg cgggggatgg 360  
aagacaacaa caagtgcgat cggaagacgg cagcttttca ggagcaaac atacaggta 420  
agatatgcag actaatccca tctaattgg aaacacacac tattttattcg gggttttttt 480  
attaatacca agctgaattg ttacatttaa c 511

<210> 535

<211> 461

<212> DNA

<213> *Drosophila melanogaster*

<400> 535

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tgtgcgtgtg tgcgcgggag gcagtgaaag cggtaagagc gcccgcgagg gagagggaga 180  
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aaaactgcaa cccttaacgg agttggggcga aacttgacct caagctgaga gagagagagt 300  
gagttagaga gtgagtgggg gtgggaaat agatgggtgt gagaggctta cacttaaaaa 360  
gagaggacgt aatgagtagc ctatttaagt ttatgcgaat aataagatat taccaaaaac 420  
agttatatag gggcaatatt ttaacatag tcctagtttt t 461

<210> 536

<211> 383

<212> DNA

<213> *Drosophila melanogaster*

<400> 536

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gcgctctctt tgctcttttt gagagcggcc aagtatctgt gcgctgggtg gcgtgcgaaa 180



agtatctgtg tgcgctggaa aaagtagcaa acgaggcggc acgacgacaa cacgaacggc 240  
aacaacggca ataattgatta tcattataag tgggctggcg ctccggctgt gtgtggcact 300  
caggggattg ggattggaat cggcatcgga atcggtatgc tacggtagat acccctcaac 360  
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<210> 537

<211> 544

<212> DNA

<213> *Drosophila melanogaster*

<400> 537

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gcttttcgat ccgattcaaa ctcatcttcg ttccgttaaa atgcaaataat cgtggataat 120  
tgagccgctt actttctggt ggctgctgca ctttgacggc ggggttatatc gtgggttata 180  
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gctgcagggt actgagcaga tgggagcggg gctgaaactc atataaaaat aaatagtaaa 300  
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gaggtactgt atcggtaaaa tttttgctaa ggaaataaaa ttacttggaataaacttgaa 480  
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tcca 544

<210> 538

<211> 530

<212> DNA

<213> *Drosophila melanogaster*

<400> 538

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aagatcaagg ttgttttggc gtgacaaata tttgaggtgt ggactaattt gatttgtatt 360  
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gtccgtatcg aattggtatt tgaatttatt tcctatttca tactatatac attttaaaca 480  
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<210> 539

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<400> 539

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gaacaacaaa gggggtcaca aggcgtaaat ttagttttaa ctatcccata tttcaatttg 420  
gctttcacia tcttatcgcg gccacgggtg taatctgata aaatcccagc cccagcaaaa 480  
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<210> 540

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<400> 540

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tcttctcttt tttgcgcact ttgcagaaaa aggtggcagc tgctcggtcg ccatttataa 180  
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caagcaaaat gaaacattca atatnnnna tgtttcaaag gttttctata ttttatattt 480  
ctatacatt accatctcag caaacggta attttccatc tacacgaata acacaacatt 540  
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<210> 541

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<400> 541

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tatttgccag tgtgggaaca cattaaatat ggtagctgg aaatcaaagg ttatctggat 480
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<210> 542

<211> 302

<212> DNA

<213> *Drosophila melanogaster*

<400> 542

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tttgttcggc aaagctttgt ttcggacacg ctgagtattt ccatcgcaac gggtgaccac 180
tgtggcagac cccccacaa aattcgtaac cgcaaccaa tctgcaaac catttgcaaa 240
ttaagcgca taacgatgtg tgggcagata gaagagaaat gtaggataaa tgggtgaagg 300
tg 302
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<210> 543

<211> 611

<212> DNA

<213> *Drosophila melanogaster*

<400> 543

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<210> 544

<211> 82

<212> DNA

<213> *Drosophila melanogaster*

<400> 544

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<210> 545

<211> 858

<212> DNA

<213> *Drosophila melanogaster*

<400> 545

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 atgtagacgt agacgatgat tatataacag ttttctgtga ttctcctcat tccgatcgaa 780  
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<210> 546

<211> 277

<212> DNA

<213> *Drosophila melanogaster*

<400> 546

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 gaagcgaaaa gagttcgatc cgagacaaaa aaaatgaatg ctgacaactt agtatttggg 180  
 gaatctggaa atgggatctg tttgattccc cgtttgttgt attccaagcc cgtttatgac 240  
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<210> 547

<211> 370

<212> DNA

<213> *Drosophila melanogaster*

<400> 547

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<210> 548

<211> 539

<212> DNA

<213> *Drosophila melanogaster*

<400> 548

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aatttttggc taattgttcg tcattgggca aaaatgaaat gctgaggaat ttgctttata 480  
aaaacactta aatttatagt tattagccac tgaatttgta ttgcagtcgt taagaattc 539

<210> 549

<211> 449

<212> DNA

<213> *Drosophila melanogaster*

<400> 549

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gttaataactt tacatttata tttaatcaag gtaagctaag atatttgaga tttatttagt 180  
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cacttggcac gttttaaagt attttgtacc gttacggata cggtcattatt ataaacaata 300  
aaatctcgat ggactcattt agccgtacaa aatataaaca aattaatacc aaaaagacat 360  
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<210> 550

<211> 85

<212> DNA

<213> *Drosophila melanogaster*

<400> 550

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<210> 551

<211> 485

<212> DNA

<213> *Drosophila melanogaster*

<400> 551

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<211> 314

<212> DNA

<213> *Drosophila melanogaster*

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ttaatagaca atcaagccaa acgatgcgtc tgaattaata aaagaaatac cataaaaaag 240  
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<210> 553

<211> 515

<212> DNA

<213> *Drosophila melanogaster*

<400> 553

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caattaaatt ttctaacgaa ttgatttaa tcgagtaaga aaagtaaata gtttaagcca 420  
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<210> 554

<211> 357

<212> DNA

<213> *Drosophila melanogaster*

<400> 554

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tcaacgcgga aagacaaaac cgagaatctg tgggtggaagt tttaaatacg tgttatttat 300  
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<210> 555

<211> 619

<212> DNA

<213> *Drosophila melanogaster*

<400> 555

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 ggctgccaga tgtgcgtgcg gtgcgttttg agcttcaaga tgttctggac gtccggggta 240  
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 attaaaagcc ttgaaacatg ccttaaatac gttaaaatag attataagaa ggaatggact 600  
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<210> 556

<211> 295

<212> DNA

<213> *Drosophila melanogaster*

<400> 556

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 gtattcagta tctctcggtt tccatcgatt cgtgcgcttg tgtgagactt ttagcggctg 240  
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<210> 557

<211> 203

<212> DNA

<213> *Drosophila melanogaster*

<400> 557

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 gggatcaata ttcgggtcaa cacaaaaatc caattggaac taattaaaat tataatattt 180  
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<210> 558

<211> 202

<212> DNA

<213> *Drosophila melanogaster*

<400> 558

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ttttactccc tgtgaatggc acgtctaacc gttgtcgata tcgcaaaagc atgctatggc 180  
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<210> 559

<211> 311

<212> DNA

<213> *Drosophila melanogaster*

<400> 559

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aactactaat tgctaccgtt ttaaattata cactaaaaaa ttgttttggt tttttgggat 240  
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aatttaataa a 311

<210> 560

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 560

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<210> 561

<211> 354

<212> DNA

<213> *Drosophila melanogaster*

<400> 561

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<210> 562

<211> 505

<212> DNA

<213> *Drosophila melanogaster*

<400> 562

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aaatacactt caaataatag agatttatat ttttatgcaa aaatatttat gctaaaaccc 360  
actatatcac aatattaaaa attagagata tactgatttt tatttcgagc taaatcatca 420  
taaataacaa ttaaatatgc atattttatt ataagcttgg gtcatagttc ttgaatttac 480  
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<210> 563

<211> 406

<212> DNA

<213> *Drosophila melanogaster*

<400> 563

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tggaatgtcc acttggtggtg cttttgtgtg ttgaaataaa ataatagtta tctgcgaata 180  
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tcagttagaa caaacaattg gctaaactac tccatggcca attaat 406

<210> 564

<211> 368

<212> DNA

<213> *Drosophila melanogaster*

<400> 564

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agaagggt 368

<210> 565

<211> 278

<212> DNA

<213> *Drosophila melanogaster*

<400> 565

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gagttcgaaa gtacgttttag catatgcagc aaccaactaa gagataaaat tcgaaatcaa 240  
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<210> 566

<211> 290

<212> DNA

<213> *Drosophila melanogaster*

<400> 566

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<210> 567

<211> 739

<212> DNA

<213> *Drosophila melanogaster*

<400> 567

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<210> 568

<211> 766

<212> DNA

<213> *Drosophila melanogaster*

<400> 568

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<213> *Drosophila melanogaster*

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<210> 570

<211> 484

<212> DNA

<213> *Drosophila melanogaster*

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<210> 571

<211> 497

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<213> *Drosophila melanogaster*

<400> 571

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<211> 373

<212> DNA

<213> *Drosophila melanogaster*

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<211> 1306

<212> DNA

<213> *Drosophila melanogaster*

<400> 573

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<212> DNA

<213> *Drosophila melanogaster*

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<210> 575

<211> 392

<212> DNA

<213> *Drosophila melanogaster*

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ttgtgtatgg tgtgcattca ctaattaaaa ccttttagtcg aaaaagcaaa taactcgaga 180  
agtggcccggt cgatcagagt gaaatattat ttaaaccggtt ggcagccacg ggggaattat 240  
tagtaatttt taagacgcga aacataaatt agtttcaaac aaaagacaaa gaaaactgga 300  
ttttcggaca gcacacgaaa atatttccga gctatccggc tataaatatg catgagcggg 360  
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<210> 576

<211> 375

<212> DNA

<213> *Drosophila melanogaster*

<400> 576

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atacgttata tgtatacgaa aaacgaagta ggggaaagcc tcaaactcga atacaaaaaa 180  
ccttgtaggc gaatttttgt gcgataatat aatgcaataa atatttaata tttaatgtga 240  
agattgcttt attactctta caaaatctaa caatttttaa caatcattat ccaatccact 300  
aaaatatact atccccctct caaaaaataa ccaaacgctc tccaatttat tcgaattaag 360  
ggtccaattt ttgga 375

<210> 577

<211> 322

<212> DNA

<213> *Drosophila melanogaster*

<400> 577

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taactataac atacaaaaaa aaaaagcaaa gaaaaatcaa atcaaatact actactcgaa 120  
acaacaaaat cgagcacaca ctcgaaaatt atatacaaat cgtaaggcaa ctaaaatata 180  
aagcaaacgg catgtggcaa caaagagatt tgtgcaaag aaaaattttt aagcaccaaa 240  
aaagtttgag caatttttta cgcaagccag gaaggaatcc gtatatattta taatcaattc 300  
aatcaaatc aaaatacata aa 322

<210> 578

<211> 262

<212> DNA

<213> *Drosophila melanogaster*

<400> 578

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gtgtgtataa ttgattctga tggcggttct tcggcctctt cctctctctc tcactcttct 60
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ggagcaaacg agagggggga tggcgacttc gcgactcggc tgcgctatct ttactctctc 180
ccactccac tttggcttgc atcttccct gcattgtgat gcactggctc tgcattttcc 240
aggggcggat ctggaggcta gt 262
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<210> 579

<211> 783

<212> DNA

<213> *Drosophila melanogaster*

<400> 579

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cgagtgttat tgtttgttt gccgtcgtcc tcgcatttcg tctttgtaa tttctcaaa 120
aagtatactg cgtcttctgt tcttcgtggc ataggtagt caaaaacata attaagtcac 180
gttgtgtgaa caattcaccg tgaaatttga ccagcaatta tattcccatg tgctatgcaa 240
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tgttgtgtat ttacattcta cgagcattta ttaaggcaca tttgataaga tataaacaaa 360
ttcaatcgta actcctctga aggttgtgtt tactgaactc gcgcgtgtcc taacactgat 420
caattggact agttgatttc aaaaaccatg agaactttac aaaatctgaa aacaaaaaaa 480
aaaataaaat aattccaaac ttaaataatta tattaaatct aggttttatt aactatatgt 540
acggttctaa attatatatg aacgaatcaa gccaccacca ttacacattt tgcaacacta 600
attgaccaga aaccagtgag aaaattgacg ctgctgatat aatttaaaag tttagttaag 660
gaaaaattaa atgttcttac tttggttttt tcaacatata ttatcataaa cttgtagctt 720
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ttc 783
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<210> 580

<211> 316

<212> DNA

<213> *Drosophila melanogaster*

<400> 580

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ttttaagcc ttctttaggg caggggtgtgt gtgttcgagt gcgtgtgtgt gtgtgtgtgt 120
gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt 180
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ttttctttgc actgtggcca taaaatgcct tcaatttctc aacttagatt cacattgtct 300
tattatctat ttgcat 316
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<210> 581

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 581

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gcgtactcac ttcagttggc atcggacgtt cgtcgtgcga gggatcgatc gcggttgtgg 120
gtagtgcgat atagtgaata catctcaaga tgccgaaaac agtggtagtt actcaccag 180
gaaaaccgat aaataacgag aaaagatttc gcttcgagct tctctatttc tgtgtgattc 240
ttctaattgt tgtgggttta gcagctggct atttcattgt gatgatgtgt gagtcattaa 300
agcgaatcgt agattgaata caatttaata accaataacc aattgttaac ctggttttagc 360
ctactccaca cattcgccga aacaagggcc tacacatact cgatcgagc gaaatggctg 420
ggggaaccac ccagtgggaa attaccgcac cttaagcttc cccgtctccc aatattatca 480
ttcatcacac ggcaaccgaa aggatgcgac a 511
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<210> 582

<211> 168

<212> DNA

<213> *Drosophila melanogaster*

<400> 582

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tctcggaatc tcacacaaca cagcgatcgt gcctctcttt ctggtcgtgt tccaccgtct 120  
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<210> 583

<211> 490

<212> DNA

<213> *Drosophila melanogaster*

<400> 583

gcctagatag cagggaaaac tagatagaga gtgatcttct cattacctgc atcgtgaatt 60  
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attattgggg catgtattag ttgaaaaccg atattgtcct ggataagact gttgttaaaa 180  
atagattttac ttttaaattt gtttagttgt gaagatcaca aacataatcg ggcgagttga 240  
taaaattaaa taccgaata atactcatga tcagtgcaga catatccaaa aattaaccat 300  
tatgtttatac ttttcgatta catttattta tcttgcagat cctaaggata tgcttaaaaa 360  
ttaaattgta aaaacaaaaa ttgtttttgt ttttccttat taataatcaa gttgacacaa 420  
caaacttttag ggctaaaggg aagttacatt ctatttaaca aaattgaaaa atattgaatt 480  
tttggcgcca 490

<210> 584

<211> 409

<212> DNA

<213> *Drosophila melanogaster*

<400> 584

ctctgctcgg taactgttcg tttgtacata caaacatttc acataaacat atataaatat 60  
atgtttaata tatatttata ggcaagtgtg ttaataccaa agtatataaa ttgcatatat 120  
cgccaaaacca taactcccc cegttttctgc atttctcttt tttcttgcag tgtaaagcca 180  
tttacatact tacattacat attaaattgt attttagttt taatccaata tggcagccat 240  
tttgtatcaa accattcttt caacttcccc cgtccccc ttgcctgcgc tgctgcctg 300  
tttttggtcc gccttttctt gagttcacct tcttaattca cctagatttt caaatatttt 360  
tcggtgatgt taatttttct ggccgctcgc cccttcgccc tctcttct 409

<210> 585

<211> 705

<212> DNA

<213> *Drosophila melanogaster*

<400> 585

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cgaccacagc cgtccagaaa gagacggcca cattgtgaag tatagagagg gatgtatagc 120  
acttggtaca gacttttctg ttgggcgggt tcttttctgc ccggttttcg cttttctggt 180  
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gtgactgact aaccgaccga gctagcaaac tgctgatctg gcaagaagat atccatattt 300  
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agctaaaagc gattgggtta ggcaataata tttgtaagtc gaatgtttag agatacgaga 420  
agcaagttca aattctcatt ttagccagga aagtaataca aattttataa aagtgggaag 480  
tctcttctat ctattcta atttaaaata gaaaacaata ttttttaaat aatcagatgt 540  
gttagatata aatataaata tagataagga tttatatatg tataatgcat taaaaattga 600  
tttcgaatat ctccacact ttccacaaa gactggccat ttcctttctc cttcctaact 660  
ttttgaattg ctgcggcgat ctccatttcc atatttgact actta 705

<210> 586

<211> 424

<212> DNA

<213> *Drosophila melanogaster*

<400> 586

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gctctcgctc gctcgcggtg gtggggcaag accttctgac gcgtttggtt ggtttgccac 180  
caccactgaa ccaccaccac cagtgcaccc agtataccca ccaccaccac cactgaactg 240  
aaacagagtg gctgctctct cactcaacga agcacactca ctcactcatc caatccaact 300  
agaaccggtt tgctcttatt agctcgctgt tgggcgcac tggttagatac tttaccgtt 360  
aaggctcttt atcgccggac ttttcggtt cgggggtctc aacttttttg ccaatttggt 420  
taaa 424

<210> 587

<211> 230

<212> DNA

<213> Drosophila melanogaster

<400> 587

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tatatcattt ctatcttgggt ttccgggtagt taggtaggta ggtgggtgatc aagtgtgtgt 120  
gtcagagtga aagagggtttt caccttgatg cctgatgccg ttacacacgg cgtatgggag 180  
atatattgat tatgagacgc gacttacgca tctctttcat tcgatctatt 230

<210> 588

<211> 480

<212> DNA

<213> Drosophila melanogaster

<400> 588

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actaagagag agagagagag agagagagag atctcaagct tggcttgacg ctacgtcatc 120  
aaacaagttt ttacgattac ataaagtcgc gttccgctgt cagcaaactt gctctcggtt 180  
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gcgcctgcgc acctagaaaa atatggattt ttattgcaac acctaaagcca agcaccatat 360  
ttaattggaa atcgatattt agagcaaata atccatattt aagttgatgg actggatttc 420  
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<210> 589

<211> 294

<212> DNA

<213> Drosophila melanogaster

<400> 589

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cttccgattg gacgtcgcaa atgcaattgg agagttctgt ctctgttctg atcagagttt 120  
ccgctccggc cgcgtgtgct agtgtgtgtt tttgtgtgtg ccgtaaaca gtttagcaat 180  
gcgtttcaaa tccgcgccga ttgtttcgct tattgtcatg ctcgatttaa ccgcttagag 240  
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<210> 590

<211> 460

<212> DNA

<213> *Drosophila melanogaster*

<400> 590

ggctgcacgg catacggctc cgggacgtct ggaatgaata ccaacttcac tcagttcctt 60  
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caaaaagcca ggccaaaatc tcaaagccac ggctcagtga aacagttatc agaaattttc 180  
gaaaaatcgc gtaaaaagtt ttcgaaaaaa aaaataataa ttaaaaacat aagcaagcaa 240  
ccgatttcaa gtggcaaaaa taacaaatta gaaaaaaaaa acgcaaaca aacacagcac 300  
atTTTTtggg ttaagtgcc catagttcct gttagcagca gcaacacaca ccaaccactt 360  
ggattactat aaacaacagt attatcactt aaaactagca caaaaattgc aaaattttct 420  
tcaacaaaat tcaatcgttt tttaaactac aacaaaactg 460

<210> 591

<211> 485

<212> DNA

<213> *Drosophila melanogaster*

<400> 591

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gtttgcctcg ctttttgcac ttctgcgtcc gttcgaaatt tttattttgg atttaacgcg 120  
agctaccgct ctatatatac cactatatat aatatccgtc tatatgtgct accatatcga 180  
aatcggttct atttatcggc acacacaaat aatcacattc ggatggccaa cgtaatttga 240  
catcggccaa taaataaact aataaagtac aaaaaaagggt gtacaagttt gaaaaacgct 300  
gagctcatta tttctgccta attagcatac aaatcgtaga gagaggctct aagtcggctg 360  
taaagtgtta taaacaaaat aaaaatatgt ttcttccatt gggaaaaatg agtggttgatt 420  
gctaatacgt aattccttag caatttatag tgcaataaac ataaatcgtg accagtgaca 480  
tagtt 485

<210> 592

<211> 300

<212> DNA

<213> *Drosophila melanogaster*



<400> 592

gtatcgcctt ttaaagtgcc aaaaatggag agagaccgaa gagagagaga gagagagcga 60  
gagagagaga gagatgatgt ggtcctcata atatggtcac atcctgcatt caagtggcga 120  
gaaatgattt taaatatttg tggctcatgc attttaattg gcatttgcaa acgtgtgtgg 180  
cctacaaatt gaagtacttt ctatacggat taaaataaet attttgtgtc attgcgttgg 240  
cgtgtaaatt aatttaaatg agcttcgctg gggattttat aatcaacatg aatcgaattc 300

<210> 593

<211> 184

<212> DNA

<213> *Drosophila melanogaster*

<400> 593

cgctggatcg tatagtgggt agagatgggg aaaacatcga tgggtctgag gggatcgata 60  
tatcgattgc gtttttgact actgtcgatg attgcaggcg ttagtgcctt ttggccgggt 120  
gtgctttcac cctctctagg tttacccggt cgctgttaac cgttacaggc gctcttttta 180  
tttt 184

<210> 594

<211> 866

<212> DNA

<213> *Drosophila melanogaster*

<400> 594

ggtctggcga actgaaaaca gccaaaactt ttcgcctgcg ccgacgtcga cgtcggcagc 60  
gcagctgttt ggagctgttg gggctctgtt agggccccac gctgttaggg ctctgttagt 120  
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 cgtgctaaat agtttctata agttgctttg tgtgtttacc aagtgatttt tgcgattaag 780  
 gggttatctct taggttatgc atctgctgtc tgtcgggtgca actgacttta caatatagtc 840  
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<210> 595

<211> 352

<212> DNA

<213> *Drosophila melanogaster*

<400> 595

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 gttaaattga agaattctaa aaaatacttt tcagtttaaat tttaaattaaa taacctatct 180  
 aaagaccaca atcaggcatg ttccggtaat agtaatatct tttcgattac gatttggcaa 240  
 aatcttttga cttcggtttt aggtgctcgg gttttcgtcg aatttttgcg atcggaatgt 300  
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<210> 596

<211> 846

<212> DNA

<213> *Drosophila melanogaster*

<400> 596

gggttagtga gtgagagccg ccgaaaacaa ttaaactaaa tttttgtgat atttgaccgg 60  
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 cacacagccg aatgcaatga cgcactcact cttaaataa aatatacgag ataaactttt 600

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<210> 597

<211> 443

<212> DNA

<213> *Drosophila melanogaster*

<400> 597

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 ctcttgccctt cttataacct tttatagggt atcatggcaa tttaatgttt ttacgccaac 360  
 tacgataata gctttttattc agtcttagac taaattgggt tacccttgat atctaacata 420  
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<210> 598

<211> 402

<212> DNA

<213> *Drosophila melanogaster*

<400> 598

tttcggacta ttgagtgatt tccctctctt cggggaaatt cgagatggag agtaaagcga 60  
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 gggttttatg gctacaccaa gacacttaat tgggaaaaag cttcaataaa atgttgcatt 180  
 aagccattgt agctacgaga tcttaagccg agcaattgta atttgagaca ttttatttca 240  
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 tacggggaaa ttaagttata tatattccca tattgggaaa tataattagg ctttaggtta 360  
 ttatctttct tttatagtta aagactttgt taattagcaa ta 402

<210> 599

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<400> 599

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atccactgta catggcgata aggcagtttt ttgaaaaccc cctccaaatt gaagttcaca 180  
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taaaaatgat ggaaaaacat atctatgcat gtgctgggtg tgcgtgctg tgtgtgtgtg 300  
ttngttnng taaacaaatg tgtgttgga tgggaaaaac aagagagggg agcaaagccg 360  
gggcggccaa taaagccaga gtgcgaggcg caagcaacaa caagcacacg cgggtgcagtg 420  
ggaaacacgt tttccgcttt ttgttgtggt ttttcatgcc cttatcaccc gttatgcgaa 480  
atgctgcgtt aaccgaaaaa cccaattacg aat 513

<210> 600

<211> 600

<212> DNA

<213> *Drosophila melanogaster*

<400> 600

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aataagccat caaagtcagc attatttgca gtgtttgccg accacttccc cgataagcca 180  
tacatataga gttacgtaac tggagatcgg cgactcgagt ggccgggctt tggctttata 240  
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aatttataga gcgatccata aatcataatc gactgggtatt tattgtgcgc tattcgcaac 480  
tactcgagcc cagcttttag ggtttccggt ccagctggaa gatctttgtg gggacgcaag 540  
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<210> 601

<211> 571

<212> DNA

<213> *Drosophila melanogaster*

<400> 601

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tgtttggctt tttggcaaag ttgaaaatgt tccgttaaca gttaaatttg cacttttata 420
ccgctgggcc aaaaggaaaa agaaacctg ccccttgata ctgccacca agtttgttgt 480
tgtgtgtgaa tgtgttgggt ggggtggaaa atgccgtgtg tgtgtgtgtg tgtgaaatag 540
gcgcccctcg cccccacaac caaaacaaaa t 571
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<210> 602

<211> 475

<212> DNA

<213> *Drosophila melanogaster*

<400> 602

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cgcgaagagg cgcacaaaaa ggaagtaact aaaaataaca aacatctcgt ttgggttgt 120
aaggtggaat gaactcagaa cccgcgatgg agaagatgcc gaaaaggaga cgccgaggag 180
acaaaccaga caccagaga tccatgcccc aaaactgatt gaactacagt gatcacttgg 240
ttagaggcac cctaatacatt aacacgcctg gcacacacga ttgaaaatga agtcaccact 300
ttaaaataac atatatactc atttaaactc tcccatttac cccaatgtgt tctaaatacc 360
tacagtctct gttaatacat gtttaccata aatcccgcca gattctcgga attaaagtgc 420
tttgccaata tttttttgaa ccatttaaaa agatattaac ccaactgtta tgggc 475
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<210> 603

<211> 371

<212> DNA

<213> *Drosophila melanogaster*

<400> 603

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gtagaagcgg taagatcctt gcacgaaatt gataaacagc attgcatcag caattagggt 180  
tcggtgttgt ttaagttctg ggaatcgaac aagataacca caatatttac ttatttatcc 240  
aactttttgc tctctctcac gttgttcaat aataatctcc acccgctcaa cagcaggtaa 300  
atacgtccaa agttctacaa ctttctactg atgaaattca ctttaacacg gaaaccggta 360  
tgtttttgc a 371

<210> 604

<211> 488

<212> DNA

<213> *Drosophila melanogaster*

<400> 604

aaccagacca ttgcctatcc gcgctcatcc accgactgct tcatcatgtg cattggcatt 60  
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atgcccgcgg tcttttggac agaggttcgg gagcactatc tggcattgaa gcgtctgggt 180  
catctcctgg atgcggcaat agctccactg gtactcctgg cctttggcaa taacatgtcc 240  
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gcttagatat attatgtata tttttttttt agaaatatag gtgttggtgact ttctggtgat 360  
gtttggcttt ttggtactcc ttaggattcg ctgtagttcg cactttactc actattttcg 420  
tggttcttcc cataaacgaa tacaacgaaa gatgtcacag cctgcgggga tgtgcctcca 480  
gagcttgg 488

<210> 605

<211> 500

<212> DNA

<213> *Drosophila melanogaster*

<400> 605

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gtttaataaa taaaatgtat ttttaatcgt taatttttta ccaaggaaag ttttttaatt 180  
taatttttct gtttacgata cgcactctaa tttgcagcat ttttgactaa aaaaaactta 240

aaaccttatt tcatagtgc aaaatgattc atcgcagtat ctgtaatctg tatctttctt 300  
 ttcacttctt gagattaacc attattaata atcacataat ataaaccact ttttaattcaa 360  
 gtaagttgtc agttcctgca ccccgattt taaatgttaa cgcataagcc cggggcatta 420  
 aaaacaggtt tggcagggct tgcgcggtc cattgcaaaa aaaattcccc gccacagagt 480  
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<210> 606

<211> 387

<212> DNA

<213> *Drosophila melanogaster*

<400> 606

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 attcatttca tccgaaactc aaatcgtttt cgagacttat caaagcacgt taaaattgat 180  
 ctaaattgggt atacaaattt cacacatata tttttgttta gaaaactgca tttaaaacgt 240  
 gtaaagttgc agcatatttg tttctctgtg tggagcgcgg taggtgcgag ataaggtgat 300  
 tcgaaagcac gttcaccact cgcacgggggt ctgttttttc ttccagcaac ctctagaaga 360  
 aatccccact agaataatac tagtttt 387

<210> 607

<211> 322

<212> DNA

<213> *Drosophila melanogaster*

<400> 607

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 ctccggcggt tcgcccactt cgaccattt cgctggcccg atcggccgat ggcttggcat 180  
 gaattagcac cttttttgga ctttcttttt gtccggtctt gacgcatttt taatgaattt 240  
 accatggcca aataactttt actaggctgc gtgtctacgg gttattcgaa tccaactcac 300  
 ttctaaggcc ctgccacttt ga 322

<210> 608

<211> 590

<212> DNA

<213> *Drosophila melanogaster*

<400> 608

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ggccaggcca aaaatacagt ggtcgtcgag taaataagcc accgattcag aatttccatt 60
tgtcaataaa gccagcaac aacaaccag tatagcccat atatcactgg gtctggaaca 120
tacataaata tttttatata gtttatggat ccccagctc agctgtgtgg aggtgtaaga 180
aacaaaaagg cgaaacgcga aataaaaaac agtaaccaat ttcgcaaaa gctcgccaag 240
ctgacagaac ggcaaaattg gaagagagta aagagcgaaa cgctgacgtc gagcagcttg 300
ttttaacttt tgtttaaaat ttaaattgct aatgaattga tgatgtcttc tggttctaag 360
aacatactaa gggggaaaaa gacgtgttat agggatatgg caatagaggg gagcaactta 420
taattaagag cttagcttgg cagtaaagcc ccacatgaag aaaaaatttc ttaaaaagt 480
taactttttt ttttaaatac aagaaacagt ttatcttacg cttacttgaa ataaatctaa 540
atttttgaac tttttttgac tcctttacaa tgagaaacat gactaccctt 590
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<210> 609

<211> 416

<212> DNA

<213> *Drosophila melanogaster*

<400> 609

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ggtaaagggtg tgcgactttg tctttgcctc tctctctcgc acaccgctc ttctgtatgg 60
ctgtgtatgt gtgtgtgtgc tgcagcaggc gggctttttg tttttttttt togcgacctg 120
ttgttgctcg cttgataatg gcaggctttg ttgttgctgc tgctgctgct gctatcagct 180
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gctggggtag ttgttgcccc tatagagagc acaccaacaa aagttacagt tgtttgtaaa 300
ttgttgctta ttggtataaa tgttggtgta attatcacta ttgttgcggt tacttctact 360
aaagttgctc ttgttgaaag ttctcgtcgg tgtaccgttt ggcgttggtg taacta 416
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<210> 610

<211> 504

<212> DNA

<213> *Drosophila melanogaster*

<400> 610



gccacgctc tcccacagtt accaaccgtc atccacctcc ctcttttctt ctctctctct 60  
 ctctatgtca tttatgagag ccaggccgaa cgaagagccg aagtttctgc tgccaaggca 120  
 aaagctaaag ccgcacttaa acaagaatgg ataataaaat gggttaaaaat tctgataaaa 180  
 attgatcagg tagaaatatt ctaagttata tgaaacttgt tcataaattt aggacattat 240  
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 tgccggattt ctagttctgt cgtggctgct gcttttgtcg ctgcctctgc ttctgtcgct 360  
 gcctctgctg gcggaaaact cctgggtccaa aggagccaa aacaaccgtc gacggatgac 420  
 gacttttccg actaacaacg gacgcgcatt ttcccaccgt ttccgaggcaa gagcgcattg 480  
 aaatttgtgc gacgccagcg caag 504

<210> 611

<211> 879

<212> DNA

<213> *Drosophila melanogaster*

<400> 611

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 aaggaaacga catcaaagat gggctaagcg cgttttcaaa gtataccgca taaaatattt 120  
 ttagagggca aacattttga acatttaaac attttactac attagaatgc ataaattgat 180  
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 agaagacact ttccaagaag aattaatctt cattttctaac agcgacttcg aagagcttga 540  
 aagcgaaata aagattgaga acttctgtag ttatggcaaa gatttggagc cagttaaagg 600  
 cgtcccgtcg aagctgaaga cgtgtaaatc caaaatagca aagaagcgcc ccttgcgaaa 660  
 gcaaacagat acgtttaagt gtacccaatg caaaagacg tttacaagaa aggaaaacct 720  
 cgaatcacac ttgcgacttc acgcagaaga acgtccgttc gagtgttccc actgctccaa 780  
 gagctttgga cgcaggacgc attacaagcg acacttgctc aaacacgaaa agcgacctca 840  
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<210> 612

<211> 443

<212> DNA

<213> Drosophila melanogaster

<400> 612

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eggagcattg atttgctgtc ttgattttg cttatgacct gaggtgctct cttacatata 120  
tataaacgcc atcatccagg cagacagtag gcgagtgtaa gcgagagaga aagagcatgc 180  
gacacacata cgcacacaca ttgacacctg gcgcaggagt cgcggcttgc ggcactttca 240  
aataaattaa aaaatagcaa caaaaccaac agggagagag gcgaatagag cagtaagcct 300  
ttccccagct tctctgctca gtagtaacat tagtaagagc aacaaaaaca gggacaagag 360  
agcaaaaata catgcctacc ttaacccaat taaaatacca tattatttaa caaaagaaat 420  
tgtgttattt gcaagcaacc cca 443

<210> 613

<211> 231

<212> DNA

<213> Drosophila melanogaster

<400> 613

ctgctgccga ttctgagttc tcgattctca gttcgattct cagacgttgg cgaaccgaga 60  
accggtgacg tagtacgttg ccgtccgcca ttattacaac gtcggctgcc acacgcaaaa 120  
ttggacatac cagctaacca aaaataacca acgccaactg cagctcggat gcgaagtgtg 180  
cttgccaaaa gtcaaacgat aacgaaaata acgcaggacc ataaaattcc c 231

<210> 614

<211> 473

<212> DNA

<213> Drosophila melanogaster

<400> 614

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cgctctactt tctccgctcc tctctccact caataatgtg ccaactgttg agtttccttc 180  
cgcttccgaa tgcgagcgcg aaagagagag agcgagagcg agagaggggtg tgagacagag 240  
acggggcgag cgggagtatg tgggcgttgg gcggcaaagg gttgagggaa gttgagaacg 300  
atacggccac tcgctcgctt gctcgtcttc gctctctctc tctccctccc tccctctctc 360

cctctcgtct tctcgccggc atcgaaggct gcttacaggt ttttatagta cttcggttt 420  
gccgaccaca gccaaatttg ccggcgaatg gttggcttct gcgttggttc cgg 473

<210> 615

<211> 188

<212> DNA

<213> *Drosophila melanogaster*

<400> 615

gtctagtcac tgtctgtctc acttgacaaa gtgccgtgtg gtgggggggtg cggtttggca 60  
tggataaaga gagatccgca tactcttggt gtagttgttg ttgttggtgc tttgccggct 120  
ggcttgcaat taacgctgac gtcgacttcc acacacccct taacccttgt gtgccggcga 180  
atgcagtt 188

<210> 616

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<400> 616

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gggggtttcga gaagtgaatg taagttgatt gtcgtaagcc ggctttgacg tcgttttgag 120  
accggagatc ggagaccagg ggcccagat ttgagatttg agaccggag ccgcatagga 180  
aaggaaaaca agtttcttcc gacgctatgg gctgcgtcga cgtcagcgtt gcggcaacat 240  
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gaatgcacga tggaatagga cgggggggtg tacccegtc tgcaaccaga cccgactttg 360  
gctgctgccg cttggtaaca ttcgctccgt tgatcttgtc aacttgacca agttatttga 420  
actatgcaca tgttgcaga 439

<210> 617

<211> 144

<212> DNA

<213> *Drosophila melanogaster*

<400> 617

tgtggtaaga gagtatgagc gtcgaacaga aagacaattt aagagagcgc agatcgact 60  
tatgagtaca gtcgtgggca agaaaaagtt aaacaacatc cgaacagtcg gaatctcaga 120  
tagtgctcag acacctaagt atac 144

<210> 618

<211> 410

<212> DNA

<213> *Drosophila melanogaster*

<400> 618

gtctgggact ggttgtttat gctggtgtta ttttcattgc aaacaaatga tgaggaacac 60  
gcaaacgcac tcagacggtc ctctgtctgc tgggccacag gaaaagaggc cccggggtct 120  
caaattgaaa tcacaatgag ttgaggactt ctgaagtcgc actggcaggc acataaattt 180  
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tttttatgtg gcccaggagg cagtgcagcag tgcacataaa aataaatgga aaagcgcaag 300  
aacattctgc ctgctcgtga ttaaaaatat attttgaaat tctgctaaaa tcgattgcat 360  
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<210> 619

<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<400> 619

ggcggacgga ggcggtgacg cgactgagat ggcgccgataa tcgcgctacg cgtgcgtagg 60  
cccggcagag gcggtaacgg tggcagaagc ggcggcagag gcagcgacag agcgccagcg 120  
actggctgga atatttcatt ttcacgacta gcagtaaaac ctaccctacc tgtgaacagc 180  
tattccaaac attaattcct attttcaact gttatttaag tgaaatatat ggcataatgca 240  
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tatacacgga atttgaagca attttataaa ttaaagcaaa atcacatttt tatgttttaga 420  
taatgaaaag gtatttttact gatctgagtg aaacattatt aatattattc aatatcaact 480  
aagttttcac tgtattacca tttgtcacia aatttcatta cactttgcta a 531

<210> 620

<211> 583

<212> DNA

<213> *Drosophila melanogaster*

<400> 620

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cagttgcttt cttctaaaat tcttttcgca gcttcttctt cccgtgtgac actcgattgc 180
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aatgcttcgc aggattctac aatctaagat atttacttca aattgagaat tttattctc 360
agtcaaacat attcgtagcc attggtttgg aatttaagct tattatgaaa tttatattta 420
gctatgttga ttaaataaac tgtttgcaat tattcgcttt taattttcga atgttattta 480
atagctacta caccaattct tgataactag acttatgaat taatgaataa caagttgaaa 540
tctttttata tttttaaatt gtccatggtg ttgaatattt tga 583
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<210> 621

<211> 462

<212> DNA

<213> *Drosophila melanogaster*

<400> 621

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tacaagaaaa acaccacac gtacatttat gttacaatcg tacacgaata cgcttagaaa 120
atgcacaat gaagtttcat gctctcactc tcacatacta ttttttctt agcgatttgg 180
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ttacatttcc gatttctagt cattcttgtg gacaattatc aaaatagaac cttgcaagcc 300
tttgtaaaca aacaaaattg tggttctacg ctttttaatg attcattttc gatttaacag 360
cctggcaatg acaagattta acagcagtac ggtaccgaag ggataaagcg acgtcagatg 420
ttgggaaact aactgaaatg gaatttctta ttgcttacat tt 462
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<210> 622

<211> 145

<212> DNA

<213> *Drosophila melanogaster*

<400> 622

gttcgaattg acagtgggtg ttggtgaact agatcgcgga ctcgaagttc gggaaactttt 60  
tagtgtgttaa gcttgccagt aatgaattga agtatttaaat aactttattt tgaatgaagg 120  
gtttgaacat aaaaaatatc ttcgg 145

<210> 623

<211> 518

<212> DNA

<213> *Drosophila melanogaster*

<400> 623

ggctggcgat tggtgtcgct gctaactggg atactggaat aaatcataat gcattttacgc 60  
accgttgctc ctcaattttc gagtctgtgt gcatgtgtgc atgtgggtgt tgtgtgtgcg 120  
tggtgtgtgt aacctttggc aaaggaaaaa tcaatagcaa cagacgtaga catttgtttg 180  
ccgctgttta tgtgcagccc tcgcattgtc cttcgcccc aaaacaaaga gccacccttg 240  
cagagatggc caaatcccaa aaaagaaaca agtgaatggt ggtctgcata cagactataa 300  
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taactcgtca gcatgctggg tctgggtcgt tgccctctttt ttttcgatt ctgattccgt 420  
ttcttctcgc tgctctggct ccccgagaga aaaagctgct ccagaaattt gtctcaccca 480  
tctgctaccg gcattccaat ccgccatttc cattgccc 518

<210> 624

<211> 249

<212> DNA

<213> *Drosophila melanogaster*

<400> 624

gtctgtcgtc tgctgtaatt tttttttttt tattgctttt gttcctttgc cttacgtttt 60  
agtttcattt ttggcttggc caaaccttga accgtacacg ctcagtttat tggccgcttt 120  
tttactacga ataccgttca ttcgcttcgc ttggcttcga ctgactttcc gatgatgacg 180  
ccggcgaacg ttgattatga agatcatcat cgccgttctg tgggttatcc gagggtaggt 240  
atatatttt 249

<210> 625

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<400> 625

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ctgagcaccg agctggcagt tgggtagaaa tcagagtgcg ccagcagcgc gaccgagatg 120  
acccactttt cgggtattcgc actgagaccc aactgctact acccacagaa agtggacaac 180  
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cgtggaagag gaaaacaggc gacctgaaaa agcagcagca gcagcaagca agaagcagaa 360  
gcacaagcag caaaaaaggt tcgcaaccgc ttcaaaagcc ccgaaatac caaatattac 420  
caaaagttag cccaaaagaa aaggataaat cctgttgctt cccaaaaacg aaaaccgcag 480  
ttttaagcca aaagtgtcca aatccctggg taaataacta ttttgcccag ctga 534

<210> 626

<211> 557

<212> DNA

<213> *Drosophila melanogaster*

<400> 626

ggctcaataa atataccatt tactcggtga gtgaatcggc attcccgtta ctctgtagcgt 60  
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cgtatctgca tcctagtata atcgggtgacg agtgagtctt cttgccgaaa atatctcatt 180  
tgtagcgctt gcattccata ttgccgggtgt gaaacctatc acccaattct gctctggttt 240  
cgttgcattt ggtgagggca tgaataaaaat aatttgtttt taagtgcgc ttagaagcat 300  
tcctcgctaa attgcgcaat tgtctgagcg tcccaaatta gaaaatgcat gataagctgc 360  
cttcagacat agtaatttaa tagcacacat gccacatgt tgagatctca aggcgtagat 420  
taaattttcc gaccggacag ccgcagcctg gttctgcgtg agttcaacaa tctctaaatg 480  
gtcgttgcaa tgtaatgtgc tgcaggcact gcgaatcggc cctttccctg gcgcaagcac 540  
atttttttga atgactt 557

<210> 627

<211> 397

<212> DNA

<213> *Drosophila melanogaster*

<400> 627

ggttgaggca tcaaaattga ttttaaatgat gccttcgttt cggatcgctt atcggacatg 60  
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ggaagggagt gagctggggg ggttttgccc aacaattttt catttctccg gccaagacat 180  
gtgcatgtat gtatgtccgg agtatttgga ttccgggtgag caatgagtga cgaaagatgc 240  
cctgtcgagg tcaccagctg tgcgtgtact ttccacggcc acagttttgg agtgtcgaag 300  
cactgttttc atattaggtg gggccttcct catgtggcag gtgcagcagg tgctcgctg 360  
cctttcacta aacaaaagcc gaagagccaa ctgagtt 397

<210> 628

<211> 408

<212> DNA

<213> *Drosophila melanogaster*

<400> 628

gcgtggccga tgtattttac gatgtttttt tcgtaacgat taaatatgga acttctgggt 60  
aattacagct aatcttcaat caatatattt catttgttaa ttaccaatg gaataaaacg 120  
atgtcgctt ctcacctcca tctcgttct ttggcggatg cttcgactat gagctactaa 180  
tttctcgga tgaggcaacc gcaaatggaa gagcgtcctg ttgcacatgc attaaccatg 240  
gcatcacgac attatgctaa cttacacaca cactcagtgc tgcaccgat acgagaatgt 300  
ccatacatat gtacatacat actatgcaca tatacaggca caggagctc atcaagtctt 360  
ccggtttgtc gaggatgttc acattgttta tgctccggaa taaatgaa 408

<210> 629

<211> 566

<212> DNA

<213> *Drosophila melanogaster*

<400> 629

gtctgttgcg tcatcgatgt ctgtcccttg agctctcttt gtttagcact tctctctctc 60  
tggtttttaa ttttttttaa tttttgcccg caaacgctca actgtcacia caggcgacgc 120  
caagaaaaat gatggggcag cgggggctgc ggtgggtgat ttgcaaaact attgggttgg 180  
gggatagtgg gtggtgttgg ggggtgctagt ttgccagtgg gcgtcattta tcgtatgatg 240



cgcatttccg gcgcactca acagactaca gccatataaa caccaagcaa acatcaataa 300  
 tcacaacaga tacgggtogat tttctgttac ttaactaaa ttacatatat acaattttgt 360  
 aaaattactt aaacattggt tattacacaa taaaatagaa aaataatggt tataaaacct 420  
 tactcaaata acttacaaat ttataaccaa atttccataa caaaatacac aatagattaa 480  
 actgtaaaaa tataatttga ataattctca aacatttcat tacaagaatt tttaatttta 540  
 taatccttaa acagggtttg aaacta 566

<210> 630

<211> 570

<212> DNA

<213> *Drosophila melanogaster*

<400> 630

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 agccgaaggg tatgatgttc cagaagagca cttagtttca tatctttgta caatatataa 180  
 tatgattata gtaaagtga acaaattaaa aaaatatatt tgtggagaat gtggaaatgc 240  
 cgaaatcaaa atatattcca ttataaaaaa atacaataaa tatcacagct gtatttgacc 300  
 aaaagagcaa aactaaaagc ttatttttcc agttttcgcc atttttattg accttgattt 360  
 cgactaataa ctttagcatg caaaaataat aaataattac aataataatt aacaataatt 420  
 acaattttag ttattaaaat tgtgcaattt aagtttatta gttaaaaacc tctctcgaat 480  
 gatgttcttt tgctttctaa atactgttga taagctataa ataagtgtga atagctatta 540  
 ataatgtcgt ggctatatta aattatataa 570

<210> 631

<211> 579

<212> DNA

<213> *Drosophila melanogaster*

<400> 631

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 aatcgcggtga tcgagatttt gttggttaatt tatgggccga acctggtgga atttgcaagt 180  
 cagatttata aagcaaacat gcctgaagtt gattaaaggt ttggaatcta catttctatc 240  
 ttogaatgcc atttaaagca gatgactctg ttcattctatt gtctggcttt ctaatgtggt 300

ttacaaacag cggatataca aaatttaaga gagcttccct tacacatttc tcttgagctc 360  
tctttgccac atttatattg tttatgaaat gttatcggag gtcggcgggc gacgaacaag 420  
aagccagacg cccagttcac agaaatgttg ttttatatat cccgaaaaat agaatcacgt 480  
tcacctattc ctgataacat cgccagatcg ttcaccaggg cgttttgaat aatgaacgct 540  
tgcgacacct gagattacce tactattact aggctaata 579

<210> 632

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 632

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ggacaaggga cttgtccggt atttcattga gacagcccag aaagtgcctc taagtccttc 180  
cgtccgatcg tccttttccct attttcccaa cctgtaggta gttgagcaaa gtaacgtatt 240  
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atgcattaat gccgcatttc gggaaatctc ggcaggctct tttcagctcc ttccgatcgc 360  
atgtgtttgt cattgtttgt ctttcccggg tcgaaggacc tgctctgttg aagccttgaa 420  
aaattttcca ccccgggaga agcacgttca gatagggatc ttccgaattt tgggtttttg 480  
gctcgggtta cgcattttac tggaattcgt c 511

<210> 633

<211> 505

<212> DNA

<213> *Drosophila melanogaster*

<400> 633

accgggtcca cgagaagggtg tgtccgctcg ttoggctcgt tgggctgcag atggaacgca 60  
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ttcgggtgcat tgccagcagt tgcagatcga ggctaggtag ctccaaacag agtgcacata 180  
ctccattcta aatgcaattg ttcaattgtt ctttattttt tatgcaagtt tttctaggga 240  
tggaattgta catattcgat aagatcagtg ctaccagact gcttaaaaca gctgtatata 300  
tacttggtat cgattaggcg ctaaataatta caattttaat cggacattaa attcatgggt 360  
tttcataagg gaatactagt ttattactta ctgttctagc gttatccttg gtttatttat 420

tatgaaatac tttttattgg gaattaagtt gatttaaatt atactttatt aaatttgtat 480  
attccttattg gaaatcggca taatt 505

<210> 634

<211> 262

<212> DNA

<213> *Drosophila melanogaster*

<400> 634

ccatgggtag tttgaagtac tacgcggtaa aagccgaaaa tcggaaaatc cagagggcaa 60  
gaacatacaa aactgcaagg caacgaacgc actaacacag cgacatccag acagacacgc 120  
actcgcacgc acacacatcc acaccgaga ggtttgcagt tttggtatct cggatttcag 180  
cagttgttac catcgttttg tagtaactac catgaccact gggaaagctt tcccctttcc 240  
cccctgggcc ggggaaggag gt 262

<210> 635

<211> 210

<212> DNA

<213> *Drosophila melanogaster*

<400> 635

tgccgagggt aagccgaaga gccagggtat gcgtgctcac tttccagagt tgtattaggg 60  
ttgcagtagc tgccctgtga aagaggataa aatttgaatt ttaatgcaa cagagaacgg 120  
ataaataatg aaatcgtctt atttactttt ggcacccttt tgaagcgtcc ccttttatat 180  
tttgaccag ttttgacat aaacagttat 210

<210> 636

<211> 317

<212> DNA

<213> *Drosophila melanogaster*

<400> 636

gtcggaaacc aaaagatgct gccgcaagtg tgaccagatt cggaaatgta aaaaaacaga 60  
accgtattac cgccaataat tataacgac ttgtttagaa agaaaaataa aataattaat 120  
taattaaata cgataattta tggaggtggt cgattttcaa gtcattcaac atttcttata 180

tgatcaacat gaactacagc cegttcatta aatatgggta aaatataaac tccacattcc 240  
ttttacaaca attactttgc atattttattg ataatttacc tactgaaaca caacactatc 300  
taatcgtoct tcaagcc 317

<210> 637

<211> 170

<212> DNA

<213> *Drosophila melanogaster*

<400> 637

ggtataacct aagggaaatc cgactctgct tcagaactaa taacagatca agtcctaaca 60  
taaaaacgat caaaaccgat tgattatctt tgcacactcc attataacat ggctcttttt 120  
agacataaat atcggtgact tcagaattag ctctgtattg gactttcata 170

<210> 638

<211> 433

<212> DNA

<213> *Drosophila melanogaster*

<400> 638

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tgaggagagag agggacgaca caaagagcgt atcaacattc aattgcattt ttaacttggt 120  
ttcgtctctgg aatttttgat tttctcgcgt ttttcgattg ctttttggtta gcaacaatta 180  
atttacaggg ttcgtatttt tctctttctc tcttgggggg cggtttccac aagggaaaac 240  
tcgacgtttc cattgttttt ctccaatgcg ggtgctgtta tcgtcctctc tctcgtcgt 300  
taattaagga tttttgtgtt tgaattcacg cccactaaaa cacgacccat ttaaatacac 360  
taactttccc ctttgaaatc gtatattatt attattaccc gagccttagc atacaaatta 420  
ttaatgtatt gca 433

<210> 639

<211> 606

<212> DNA

<213> *Drosophila melanogaster*

<400> 639

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 agcgctgcag cagcagaaga gagctccacc gcgcgcttct ctctctctct ctctctgcct 120  
 ctctttttgt agaattggaa ttgcagaatt gaagagtctt ctcttaactg gcatatgtac 180  
 taacttagaa aacgattcac aacatatgaa taattgaaaa caaaagtacg aaagttatct 240  
 ttaaggaaga tgaaatacaa agataaacgt gaaatttaag ttgcttagat tcactcacc 300  
 tttcttcctc tcggatcacc tcggcgatcc ctgcttgat ctccaagtca tcggcgagcg 360  
 aaggatcccc cgctgaacc cactccgcct gcacctctc ctccaactcc cccgcgcgcc 420  
 actccaccac cgctgggtg gtgcgggagg tggaggcgga aggcgtggct tggcggaagg 480  
 acctgggtccc aggcactca gttcatggca gcggccatgg cggctgctgg gccgagggga 540  
 aaacgggaat ctccacaggc gatgccgggt ggtgggctga tccggcggtc tggaagggat 600  
 gtgggc 606

<210> 640

<211> 375

<212> DNA

<213> *Drosophila melanogaster*

<400> 640

gggcaacggg attcgcgttg tccaccacga cctgctccgc tcttggtctc tcgctcgctc 60  
 ccctgttgct gttgctatct ccctccagtgc cgcctgcact ttgcatgcga atgctttgtt 120  
 gattcttttt cttgctttat tttctgcact ggtggtggtg catcgagagt gccggcagag 180  
 aggcaaaaga tctaagagat tgagaaatgc aatggggatt gagatgagag actggtgctc 240  
 caaggaacaa caaattcgga atacgaaata cggaatttat tgccatgtct cctgctttga 300  
 gtttattttg gcccgctgcg agtaaagtgg caggggcagg tggagaaggg gttgggttag 360  
 ccaggggggt gatgg 375

<210> 641

<211> 435

<212> DNA

<213> *Drosophila melanogaster*

<400> 641

ctctcgactt tctctcaccg ctctctttgg cggctctctc ttgcgcagca gcaccagcag 60  
 ttaacgggtgc atgttgaaaa gttctcacac aaacgtcgtg aaaatcgaaa tcgataagta 120  
 agcaacgaat tttagctgcc cagaaaaaga ccacaaattt cagtgaaaac ccagcgataa 180

gaatcccaaa aagtactaat ccagctgaaa aacaaccatc ttaaccggcc atgtccaaaa 240  
aaagtgttag ccaagtgttt tgaataacgt agttggtgta aatgcttaaa aaaaataagc 300  
tagtccgggg cccagagaaa atcgatacga tcccccaaa aaaagggggg ctgctgctg 360  
ggctgcccga gtgaaaattt ccagcttaaa aatagtacta gatttgagct tgaaagaaaa 420  
cccttgaatt tcctt 435

<210> 642

<211> 790

<212> DNA

<213> *Drosophila melanogaster*

<400> 642

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tcaccaagc gctctccctc tcccgcgagg gcgctcttac cgctttcact gcctcccgcg 120  
cacacacgca cacacaccag gccgtgcgac acacatagac atgggcagga gcagataaac 180  
gccatgtttt tcaaategct gccaggcgca ttcctttcca ttttggtcca ctttgctgcc 240  
aacgatacga atacgatccg cccataaccc catacccact tggctcgctc tcagtctcct 300  
ccactctcag ccactctctc cactctcacc gctctctcac tctcgcttgg ccgtgtttcc 360  
gacttcaccg actttgactc gctactccgg ctccgaatct gaatccggcg atatgctcgt 420  
ctcctctatg ccgtacgttg tttccctgt tttgectgtt ttccctatcg ttgtcgtcat 480  
cccgttcag ggaaagtga gtgaaaagt aaatgccacg aatgccggtt gccagttgcc 540  
atccacgcac gcctcccgcc tttgttggtg ttgtcatggc tccgcatttt cggccacttc 600  
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tcaatgccat tctgcagact gccatttttt agcataccca ttacaattta ttttaatttt 720  
tttaaattac ataatatata tttatataaa cattttgagc aaaaaattc agtttaagaa 780  
atgcgaattc 790

<210> 643

<211> 565

<212> DNA

<213> *Drosophila melanogaster*

<400> 643

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agattccac attttggcga agccaagaaa agcggcgagt actcgcgatt ttcccacgcc 120

aatccaatta acattgatta gttgattttg cgctcgctgt cctggaggaa atttgcattt 180  
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aagtctctct cactttgtcc tgcagagggt tttgctctcc tgcctctctt gatttatcgc 300  
acttgacgca gcgcagtgcc ttcggctgga atcacacacc ctgtgttttg ctttgctcgt 360  
tgctgaaac tttttggccc taatggaatt tacacgagtt cttaacactt tccccaaag 420  
tttcgaatgg tttttttggg ctcaggacgc cattttgtgg ccgagcgact aaaaattaaa 480  
acaataaatt aaggacatcg agcaggaggc caaaaaatgt gttgcatact ttggggcaat 540  
aaaaggggga tttcattatg aatgc 565

<210> 644

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 644

gtttggtgac agaaaacaac atggctgaca cgaaaagtgt gacctatagt cgtgcagcag 60  
aaaaaatca ctccgaagac cacgggcacc ctgtaagcaa aatatgaagg ggcttctgaa 120  
atgcgattta gttaattggt aaaaacaatt ctaattcgtt agtcactata tgacgtttat 180  
ttaaacaat aaagtaacca aacattttatt aaccttttaa attttaatat aatctatggt 240  
atatgttgat attgcaagat tgtgctggag tattgaacaa tttctgcac aacaagtctt 300  
aaatgtgcaa gtgctacaaa aaattttttc ctgttaattt aattgttact gctaatttaa 360  
gtagttacc atattagttg ggaattgctt atgttatatt atccgaagtc aagtggagcg 420  
caaatgataa tcttatcagt tgcgcacatcg cgcctatgcg tatgatgcc agtgtgacac 480  
ttggtggtat ttaattagca aacggaagaa a 511

<210> 645

<211> 558

<212> DNA

<213> *Drosophila melanogaster*

<400> 645

ctccggccca aagcggaat gaatggatcg gatcgaatag accgatgacg ataggttcgc 60  
ggcagagcga acaagtgcag aatcggaag gagcgtgttg tctatgtgct taatgcaata 120  
ctttttctgg aactgtggg aaaaagacat acccttacca tattttttatt attgattgga 180  
atattcttca taaaacatct ttatactggt tatgaccagt cttatttgaa aatagcgctt 240

aagcgtagag tatctgctct cgtatagtta taaaagtgat caatatattt gtctagctac 300  
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 atctaaactg ctgccgaagt atgtatggat gttacataaa ggacaccaaa ttacacctgc 480  
 ctaagtttta ataaaaaggg tagttcaagt atcttaccac tggcatactt tcgcgttctt 540  
 tcatgaagat gaattggg 558

<210> 646

<211> 572

<212> DNA

<213> *Drosophila melanogaster*

<400> 646

catcatgtgc cagacaactg ctctggtgca ctgtgtgtgt gcgagtggcg tcggccagtg 60  
 ttgcaagcgc cgtccagatg gacttaaaat tctaattggc gtggcagcga ctcgagcaaa 120  
 acgcgcgctt tcatacttgt attagcacac ttgcacttta ttctagcttc aatattgctg 180  
 cgttaagttg atoctatatc ctacacctac atttgaaaag tattcttaca ctttaactctg 240  
 aaggaatggg agatttccga cctgtataga aattttggat aatattcttg aacgcgcctc 300  
 aaaagtcaat ataacgtttt attatttgta aacttggtca agctgtatta tggaactttc 360  
 catcgattat tctgtgatgc agatgcgata gaagactatc aattctgaca ccacgtcttc 420  
 gaggtgctaa gagatagatt gagaatcagt ttgaatatag tataacatat ctgtagggta 480  
 ctatatatcc tcttaataac taaacacaca aggcaggagt ggactctttg attattgtac 540  
 tttccggggtc agcttagcat tcgactgact tc 572

<210> 647

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<400> 647.

gcatgaagta agaagcgccg agaaaacata gcgacggtct agtgaaaagt ggcaagcaaa 60  
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 caccaacaca ctagagcaag tgcgtgtaca tagagggttt gtgtgggggca catatgtgcc 180  
 cgcacgatgt cgatactggc tcacattggt agtattttaa aagcgacgaa cggccccgagc 240  
 tcgaaagcac gactgaaaac cttaaattgat taagcgaatt tgttctatca agctaattca 300



attgtctggc cagttgactg aatgatccac tgcaagcgca gcctttatgt aatcggaatc 360  
 agtgaaaaaa gcgaaacacg gcggccgcca aaggaatacg actccaggac ccgagtcaaa 420  
 tcgaatttgt ttgtggcgcc tatttacgtt aaagtaaaaa tcttggtgct tggggcaccc 480  
 gcttctcgaa cccttccac tcaaagg 507

<210> 648

<211> 26

<212> DNA

<213> Drosophila melanogaster

<400> 648

gccatgacga ttcgaatgtc gaattc

26

<210> 649

<211> 412

<212> DNA

<213> Drosophila melanogaster

<400> 649

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 cgatcgctga aagataggcg tcacacattc ctatcgatta tacttagcaa agactcgac 120  
 cgtaatgcac agtgaggcga aatgttttct tttacttata gtatagttat acaattaata 180  
 ataattttta taatttttga actaaatcat aagcgccgcg ggggtgttctt ttattcgctc 240  
 tcaggcacgt catccaatac aaattttctaa ctacaggttt ttaaaccctc tatataaatt 300  
 ttttgaaaag gttccttagc cagcactgag gtactacact ggccagggga ctttcgttac 360  
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<210> 650

<211> 492

<212> DNA

<213> Drosophila melanogaster

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 caacagaagc gatcgaaggg gctaagcagc agaattctgag aacgttttta ggcgcgcgta 120

taaacaaaaa gcagatcaca ggagggaaaaa tgtataaata gcgcccccaa gtoccaaagcg 180  
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 gtattttatt tttaaatttt tgcagtcggt gatgttggtg tttttgtttt tgtttgggtg 300  
 aagtcattgc gttgacaata tcaaggccag cccacctacc aaacctaatg tcctttgcac 360  
 agtaagaaaa agggattttt tataattatc cataaaacga aaggtcacga aaaaaatatt 420  
 gaaaagagct atcctttaca tcctataatg ctaaagctaa aggtgaattt agggttttta 480  
 gngcgacttt aa 492

<210> 651

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<400> 651

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 gaccaacaaa aggcgaaaac aacaacagca aatacaaact gtttgccctt gttctttttt 120  
 ttattttttg cacaaccgca tttcgggttt gcagcaaaat taagaaaaaa tctctagtgc 180  
 acttttaaga aagaaaattc cgtttaattt tagcatttta tgttttagcaa ttttaatatata 240  
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 attatcaagt cacgattata gttatgtagg ttcattcaacc tggacaaaaa tttgcccaatt 360  
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 atttttagaa gtaaataaccg gggttaaatg tttcgtggaa aactagaaat ttaccccaca 480  
 tcattggcta taattttatt atagcgggtg tatattttta atagagcttt atttaatgct 540  
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<210> 652

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<400> 652

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 agatgcgacg ttaagtttgc caagtttagac tcgtatatca gcaactagtt ggtaaact 180  
 catcaciaag ttgatttgaa aatattttaa gctgtaagtt tgttcattgc gcatacgccg 240

tggttaacatg tggttaggtac acccacatta cgcattcgca cggtttgctc atagagctgg 300  
 ggctttgata gataagaatc gggcccgaaa caatgtcatt agtccagtta acgtggcctg 360  
 actaaacaag ctaatttccc agttaccaa tgctggcaat tttcggtcag ttattttgaa 420  
 tggagtccaa tcatccgagc attaaacaat gtggcctctg caaagtttaa ctttattttc 480  
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<210> 653

<211> 446

<212> DNA

<213> *Drosophila melanogaster*

<400> 653

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 accgatatct tatgcgactg atgtgtgctt tgcattatct ttattaaagc ttttgtccgc 120  
 catatttgaa tttaaaaaat agagggaag cttgcaatta aaatgtttga ctgaagcagt 180  
 ctgttccatt tttcaataat gccttattta ttcgacgttt tttttccaat acacttgaaa 240  
 gatatcggac agttttgcat tttggtatct taaacaagat tacaacagag cgaacttttt 300  
 atgagcggag ttactagaat ttaaactctg caagcatcgt ttttcgggaa taaaaataaa 360  
 tgttttctaa gaaagttatt cggcataaca taattgggta agcccaattg attcttttct 420  
 attggtcttg gtaatagtgt aaaaag 446

<210> 654

<211> 403

<212> DNA

<213> *Drosophila melanogaster*

<400> 654

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 atcaaccgga agttgcagcg cagttaatgc tggtgttcgc cttaccagg cgccgcagtt 120  
 ggcggtctga cgatttgtgt gccaacagca aagatcttac atagtttcaa aatgtttatt 180  
 tgttttagttt ctaatctgta ttttaataatt aaaaaaagg ttaaagaatt tgtgctttat 240  
 tttattagta gaaagggttt tggtttctgt aaatttttaa tttttcatat tttcgtacga 300  
 tcgccgagct ccaactcgcat atatattatg tgcccggtgg acccccttaa tacattctct 360  
 gttcaataaa tattattacc tattgccta ttttggttac aca 403

<210> 655

<211> 525

<212> DNA

<213> *Drosophila melanogaster*

<400> 655

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ggccagcccc cgcgcccc ttttgc tgccttgctc gcatggacaa aatcaacaca 60
agttcacaca catacaggca cacggatgtg aactcacaat gacaaccact tcgtcaccag 120
caaataaaaa agtgctggcc tttaatcaat tgcgttttat gtaattccac tacattcgta 180
cgttacgaaa acaagcacta ttcattattac acggtataca ttattacttc atatcgagtc 240
caaattgcta ggcaggaaag gtcttaaat tttacgcttt atggggagtt taccttgggg 300
ttcgacctga caaagaagtg tgggccgcgg cgagactgtg agaaattacc aagtgggtgt 360
ctgttatctt aatcccaa atcttagaaa catttggtat actagaattt ggagatttaa 420
gcatattata aaatatattt atttatattt actaaaaatg cttcttaata ttcgaaaaca 480
ggttttttta tagccaaagt aaaggactgg gattttttta taaag 525
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<210> 656

<211> 589

<212> DNA

<213> *Drosophila melanogaster*

<400> 656

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cacaggcgaa tgtcggaatg ataacagtca gtgagagagg ggggaaacac gacctcctcc 60
tctctcgttg aaggattgca aaaagcgaga gggagaggaa gacagataaa agatagaaaa 120
aatcaaccta cgagatagct cgaccaaaaa taaaagacaa accaacacga agcgaagaaa 180
aagcagcgag acgaaatgag agcgaaaatg aaaacacaca caaaaatggc aaaaacgaag 240
agcagccaag caagcagcgg aagaatgtgg aacatacatt tttgtcgtca agacggcgga 300
aaagagtggg cttgagaatt gagaattggg gaagaatggc cggtttgggg gaataccttt 360
cggctttgat tgtgtgcgtt gcgcgaccgc cctccccgtc catacaagta cgatagtgtt 420
gtgttggtgc gttgttgctt gaaggttgcc agttttat ttttggcg ccatctcgct 480
ttggccatt gattttgcac tgcttgctg ccttctcact cgccacttg ccacaccagc 540
acttgtttcc cttttcaaca attctacat cttgaaaccc tataaatcc 589
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<210> 657

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<400> 657

ctcctgtgac gctgogtcat cataatcagc gtttgtcgat tcatcaaaga aaccgccgcc 60  
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atcgagagag tgccccctct ccttcacact tccctcatgg gtttctatg taaatcattt 180  
aaagggaaat tgttgacaaa ctttaacgag ttgattggag ggggaggggt gaggctaact 240  
gcttgtgggt tttcccggcg taaccctcat tcccccaacc cactcgcca ctttggcagc 300  
tgtcaattag agcttacagg gagaaaaaat gaaaaccga agcttcatta tggtaagttg 360  
gcccttccac aaggtcttcc gcccacacag gctgttggga aaatgagatt aggggtgggtg 420  
gggggtaaag tggggggacc cagcttttat gggcctggta attgatgcc aagctgccaa 480  
ccatatgctg atggaatggg ggccgttggc cgctgcagaa agaaaggg 528

<210> 658

<211> 776

<212> DNA

<213> *Drosophila melanogaster*

<400> 658

ggtaggagat acgaatcgga tttgaagtgc tctaactgat ttgaaattcg tatttggatt 60  
ggaatgcttt taatgcgtgt gcgacgcttc tgcgtgcgtc tgaatactta caattttatt 120  
tattttattta tgttgaactc gcggttggg tttgtttata tggacatctg gcggtggcct 180  
cgccattaat atttatcagc tgctgcacct ttcccggctt tgcagctctg ttgccttct 240  
ccatggcgct gcataaatcg cagcaacttt ggcccgacac gcccctcgaa cgcccgatt 300  
ttctctgaac tgccttggct cacaagttcc aggtacaatc aagtttttcg cttttattat 360  
ggggagtata atatatttta tacggttct atctgcgcc gtcttctcgc tccctttcca 420  
ccttttctac caatttatgg cggccatttt ggagaggtgg tgtctttgaa attttagttt 480  
attgcaaagt ctcataaata tttcaagagc aagtttttgc gtcttcatct cgttcccgt 540  
cgatttataa acctggccaa tttatattag tctgcgagga agcagggcat tttatgaggg 600  
gttgaaagag aaatgtatca tgaggttcat ggactttgat gtgccagtct gtcacctgag 660  
tcccactgct cagtgatgaa aaagttcttt tgagtgttt atgtatgttc cataaacacg 720  
attgttcatt gacttggcgg tgaggcattt atagaccag tcaatacggc gaattc 776

<210> 659

<211> 756

<212> DNA

<213> *Drosophila melanogaster*

<400> 659

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gtttcatcca aaattccgca ccccgccactt gcccttgat catcaatgct gctttaaaaa 60
caacatactc aattggattg gatgatgtgg atggagaaaa ataaggggcg gtcattgtac 120
catacaatgc tataatttta tatattcgcc caaagttggg actacgcaat acacagtatt 180
cgtctacgct taaattaagc gatgactaca tacatatagc atccaaaata taccagttta 240
gcagattcga aggtcatttt atgtgtcatc ctaccatcaa tagagagctt tataatgttc 300
taaataaatt taattgtttt cgagaggaaa aatgctatta tattattgtg aatcctataa 360
acgagtagtt tgctaaaaca agtaaaacac agtttaaaat ataatttctt aacagtattt 420
tttaccgtgc attcgcataa acagatgacg cgtcagtttt ctgggggtata tacacataca 480
catacagtac tccattttgct atatacgatt acaatgtgtg taacgtactt cctcttttac 540
gcacacactc ataatccggc ccaaccacc accaccacca tcgtcatcgg aggcaccacc 600
aattccggac tatggagcat tagcttcttt gtggaacatc cgtgccacgg aagtgggcct 660
catgccgtgg ttttcaactc gcagaaaagg acagaaaata agtcgaaagg caacacatta 720
ccattgccat agaacggact tgaaatgcgt tgagga 756
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<210> 660

<211> 630

<212> DNA

<213> *Drosophila melanogaster*

<400> 660

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cgccgaccag actctcggac aaccacgtga gatctagcgg atgcggttgc gtcctcacia 60
tcgggtcaacg agagcgtcgc actattatta ctttatgac actgcgcgtc tcgctctatg 120
gtgcgttaat atgcctcggg gaggcctctg acattctacc catcactcgg cgtaaaagac 180
ttctgtgttg ccaattgtgg tccgaaatag aattccagtt tcgaacatga caggcgggtg 240
gaacaaattg actgaatata gtagataaat agcatatata ttagctcttt attaggtaca 300
cgggtcttgcg gcgtgaaacg tgaacatgaa acctgaaacg tttacacgag caccaataaa 360
gaacataact agccgattaa ctaaattatt agtagcgccg agaaggccct tgactcgatt 420
gatgagaagc gcgtagaaga accatcgaac tctcgagcgc atcaactcaa cgctcaatgg 480
catacgtgta ataaattcag agctctacaa attattggat aattaaaact gttctattgc 540
gtgctaaata gacataccat aaatcacaaa tttgtgcgat atgcatatcc caaatgtcaa 600
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cttgcttcgt ggtgtgaagc cataaatata

630

<210> 661

<211> 162

<212> DNA

<213> *Drosophila melanogaster*

<400> 661

ctctggtgtg tgtggggtaa catttatgtt tgttgttttt gatatgttct agctttggcc 60  
aagttaaatt aaaaaaaga acaacaagaa gtggagttgt acacaggaaa aaatgatatc 120  
aagtgccttt tcttctaata tatgtttatc ttttgaaaaa gc 162

<210> 662

<211> 509

<212> DNA

<213> *Drosophila melanogaster*

<400> 662

accacttac ctgctgctct ggtccgcgga tcaaatgttc gtggcaactc gtaaagattg 60  
gttcactgtg tgtagctagt ggtacacaat gaaaatgcaa tcgaagtagg caataaatc 120  
gatgagtaca tatacatgtt tcttgcagct ttagcatact actttattac tttgtgttaa 180  
aggtacaaag tataaattca cttagcagga cttagataag gagttagata atccatattt 240  
ccggtgtatt tgggctgcta ccgattctgt gtgtttttat tgctgatttt gtcgtttcat 300  
cgtgtatttt cggttatagt gctctgcacg ctggagatcg agtagtcac aggctgtcgc 360  
taaaactggtt tcggactgca ttctttgggc cacgttattg gcgctgcgct agctgctgct 420  
gctgctgctt ctgctagttt gagcaggctc agcgcaagtc gcctggctga aagcgaaatg 480  
atcatatgcg gtgcaatttc tatgaattc 509

<210> 663

<211> 182

<212> DNA

<213> *Drosophila melanogaster*

<400> 663

ctctgcctga ttagcagtag cagcgtctag tttctcgtg tattattgtt tctgctctcc 60

gcgcgctccc gttgectctc ctcacagcag ccgccttcga acgcccgcgc tgcctgcttt 120  
 attttcgcgc cgctgctgat aaaataaaga acaatattaa tttaagttaa aaatacgaat 180  
 tc 182

<210> 664

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<400> 664

ggacaagcaa agcgacaaga gcgagagaag aaccagttgt cgtggcacgt cgaccacatt 60  
 ccacgcgaaa gaggtagatc tcttatttca ttcacatttc aacgttcgaa ccgtgtgttt 120  
 gtgtgtgtct cctgcagtga cgccggtgaa gacgtcgaat gagcagaggt ggtggcaccg 180  
 actgcatgtg gaggccgagt ttggagatct ctggatgctt ggcgcttggc atgcgacacc 240  
 cgaaaagacg aaataagaag ggaataaggg cacaaaactt aaatacggtc aaatacccac 300  
 atatgcatat gttttatata gagttatata gcatataacc atatatagtg gatccatttc 360  
 atgaatgcat aaccaatctt catatacaaa tattacctat cagtaacctt aaactgtcat 420  
 agtttaagat ggtttacata actgatacat aaaacaaaact ttgcatggaa accagagaag 480  
 aacagaggtg gcgccaatg cagggcccgga gagagagcag agccgcag 528

<210> 665

<211> 633

<212> DNA

<213> *Drosophila melanogaster*

<400> 665

atacagacga tcgcgcacgc cggttggaat tcgaaagctt catctgtact gagaagataa 60  
 aagaagtttg agaagttctt agttaaatat tttatgattt tctgaaaggc ttttcctttg 120  
 taattacttt cagagcccta taaactataa ataccactca atgtggtacc cccacacca 180  
 ggaactagca actttcatag atcgaaaatg cccgcaaacc cgactgtcaa aacaggcaaa 240  
 caaattgtgc aaataagtcg gggaaatggt atttatgccc gtaagatttt ccgtgattaa 300  
 ataactaagg tccaggccag tcgcctcgcc gcttggttgc agaatacag cagttgcaac 360  
 ttagccgagc tccaaatgtg tcagcatcgg ttgcatatta atggcccga ggtgtgcatg 420  
 ccaattgtca tgcgctgaaa tgcttgtaac aacgtcgatt gcttttggcc aagtcagtcg 480  
 tctatatata cccagcacca gccccacccc cagccagaaa gcaaatcaac ttcacatcac 540



tttcaaatcg agcaaagcca aagtcaaatc caactgaacc tctgctcttc cactttttct 600  
cttttaataca aaaagaagtc gatgcttctg act 633

<210> 666

<211> 460

<212> DNA

<213> *Drosophila melanogaster*

<400> 666

gtacactctt tcattgccgg ccaaaaaaat ccatcatatc cgaataatta tataactaaaa 60  
tataactacaa acgaattatt cgtgaatatt aaacctatct acgcagaacc aaaactacag 120  
taacaaaata tcatttgttt ttagagaaat gtttaaattt ttcctatctt catcacagaaa 180  
taaagtataa ttgttagaat taaattttat tttctgtatt taaatcttat gctgaagtat 240  
tagcaaaggc tcacaccaag gttgctatct gtgctaacaa tttaccaagc actccaacca 300  
attgaactaa aaatgtaaaa ctatttcttt ttaaatctta acattaaatg gtcttacaac 360  
aaaaaaatat gtggaacata accgtgaatt ggtttaatat aaaatttata ttttaataag 420  
gtggaataag gcaagatgtc aagcccttta agtgccaggg 460

<210> 667

<211> 443

<212> DNA

<213> *Drosophila melanogaster*

<400> 667

actgcggacg tcaaactggc gagccagggc gcaggcgttg gttcatttgg cactttgtct 60  
ggtactctcc cacatcggca tcttgcaatc tctttggctc agcatccttg taagctgttg 120  
tcggagcaat ctgggcatgg ggcaactgaa aggaaagcaa ctttcccatt caggagcgcg 180  
caagccgcag gaatcgcgag cgcagacaat tcagttcggc tttaacgtaa tggacggaag 240  
gtttgaatat cgcttctcgc cccagttgta cagataaagt cccactgcac gcaatagggc 300  
acttggaag atacaataga acgccgacca gtgggtgtgta tattaagggt tggaatgctt 360  
accaatgggg aattaagtgg caaaaatatt gcaactacga cctaaacgca agggcagtta 420  
ataacttcgc cagcttttgg cca 443

<210> 668

<211> 524

<212> DNA

<213> *Drosophila melanogaster*

<400> 668

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actgagagca tatttgtgca ccagagggct gcataacaac attctctttg tccattcggt 60
atacttcgta ttcagaatac atgtcattca gttgggtccg ttctttttgc gttcacttcg 120
tatatatctg gcgatcgaaa tgaactaact gaatgtgttc aaagaatgaa tgaagccaat 180
gaattttcaa tagtaattca gagtgcttaa aattcttcat gttgtcattg agtaaaatga 240
gttcggacag cgcgaaggta agtcgaagtt tgtgttttat tatgtttatt tgtattatta 300
tgtacactag tcggcatact tttgcgtgcg tcttataccg tgtgcgtctt atttaacaat 360
attgtaaaat aaaatatata aattatttgt tataatgccg taggggcctt attttgggta 420
tggatagtct tttggtcata gatatcatta ttctgaccaa gattggaact tttcaaggta 480
ttgcttctcg tattcaattc tagctggtct tacgtacgag atat 524
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<210> 669

<211> 537

<212> DNA

<213> *Drosophila melanogaster*

<400> 669

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cgcgagacgaa tcgcgagcc agagaagcgg taaattcgaa ataaccgttt ggaaagagca 60
acatgatgag gttctttatt cgtttttagt aaaatggtag aaagtgaata tgtgatttaa 120
ttgataacca gcatgggcgc cgtcagtgtt aattgcgttc cgaattgctc tttcgaaaac 180
gcagacacaa atgcacacac acaaagtagc ggcaccaca cgatcgcaat ggcaaaagtg 240
ctgcagtgat aaaacaaatg cacagccata aaggcaaagt cggaaaagtt tcacaatgca 300
ctggcgcccc atgcataaaa atgtacaatt tggcgctctt tgcacttgct accgtcggtg 360
gaaaagcaaa aaaacctacc aaccaacaac aataggaaca taaactgaaa caaaaagaaa 420
accatttttg cttcgcgctt tttgtttttg tttggaccgc cgctcacgca ctttcgcgct 480
cacacgcaca aactttttgc atttggtttc ttcaccggtt gcattatcac aacaact 537
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<210> 670

<211> 459

<212> DNA

<213> *Drosophila melanogaster*

<400> 670

gctgggcaca accgatctcg tttttttttt agttctcata tttttttgtg ggtgtagaaa 60  
agtttacgaa gtgcacacaa taacactccg taaatcggtt ataagttttt tgggccgtgt 120  
gattaccagg taaacacaca ctaaagttaa gacctaatg gctgataaga tagctttcaa 180  
ttggcaagat cgccttttca attaaccatt ttatcttggg aatgacagta ttatccgtta 240  
tgaaatttta tctacttcac atgaagccta atatcatgtt taaatgtctt cattcaattc 300  
atcagcttat ttacaatga ttaactgata aagatattat aaattaataa tcttgtttcc 360  
aaaccacgt ggggatgtaa gcaaaccag ttccgagcga aaccaattt tacctgggtt 420  
ctattccggt ttttgggcca tattcttcgt attggcaaa 459

<210> 671

<211> 371

<212> DNA

<213> *Drosophila melanogaster*

<400> 671

cctctgccac aacctgccta tctctcttct tctctctctc tctctctctc tatgtgtgtt 60  
tctctggact atctcctctt ctcgaaactt tctctctctt tcttcacaca cctacaccaa 120  
aaaaacacat acacacaact ggactggacc tggccaaatt gaatgaccta cattcaaaaa 180  
tacaacaaaa tacactgcaa aaaattattg tacctgacca cacattgaaa ccatgtaagc 240  
ggtaggccag cgctttggaa acgagatgct atagtcacgg gaccgtccac cagatatgcg 300  
cagcgggtaca tcacgcgcac gcaccatata agctaagagt tttggacaag tcactgaaat 360  
gtacagaaaa c 371

<210> 672

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<400> 672

ttctggccag gccaaaacaa tcaatgcgga gagcagacag tcgaagagag agagcgagcg 60  
aaaaataact aaggggaggg ctgccacctt ttcttttcat tgtcttcggt tcattaatac 120  
cccaaaaata tctcgtgcgt tgtgttaacc ttagacagac agctgtattt atttttaagt 180  
agacaattat tttatttggt gcttggagga aaagtgttgg taataaagct aacgcgacaa 240  
ccctgaattg ctctggcaac toccagctgt ttgcttactc tccatggagg caaacacttt 300

gttacagtgc tgcaaactaa gctatttcca agccaaatct ggcaactcat aaaagaaggt 360  
 ttttgcaa at ttcaaaatta ttattgtaat aacttttagaa aattagcatt ggtcagctga 420  
 agaaattaaa attaaaccta tatgcctagt tttgggggta aaaaggtatg gttaatttta 480  
 attttacctg caaagggatt tattacaaag gttaaccctt agttatttat tcgctaaaag 540  
 tgttgccaac g 551

<210> 673

<211> 382

<212> DNA

<213> *Drosophila melanogaster*

<400> 673

gtgccaggtg agaaaagtgg agaagtgttg gaaaatactc acgaagctcc gtgagctctc 60  
 aaaattagac ttttagcaaa ctgtacaaaa cagcaggggtt gtcacacgt gtcacaatat 120  
 agtgtcagaa gaatcaaaag ttgtagcaaa caaatccga cgaatatttt atcactatcg 180  
 ctaacaaggc gttcgatatt gtgttggtgc ttgcaataa tctcttctaa taatatcaca 240  
 cattgttgc agtgggtcaat agccgaattt tcgaagtcac ttgattcata ttactcgta 300  
 aaaacctgtg acgccgctgc tatttctatg attagtcaaa gcaactaaga atactacgaa 360  
 tattttacatt ctgatcgaat tc 382

<210> 674

<211> 515

<212> DNA

<213> *Drosophila melanogaster*

<400> 674

gagtggccac aactgaaagc aaatgtagtg agagggttga gagagagttg catcgaagag 60  
 aagaggagcg agagagctct tcggtatatt taattcataa aaattgagat acaatcgtag 120  
 tcgcgcccat tgtttttctt ctttgggcat cgccgacaaa gaatttacta aagattttta 180  
 aaagcattta atatgatttt aaattagatt tatctgttta tattgtttgt aaaaaaggaa 240  
 gactaattac caaatttatt acataaatta ttgcaagttt agacttttat atagacatca 300  
 tctcttcgat agtctgctag acttactgaa ttagtaata aagtaaactg caccataaaa 360  
 gagtagcttg aaaataaaga gattcttctc aaactcttta agtctatggt cgaaaaggaa 420  
 tctctggatt ctgcattaaa cacgaacaaa atgcatgaac tccttaaaag tcccgaatta 480  
 agtggagaga gaaacctggc ttaaaagaga agaaa 515

<210> 675

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<400> 675

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gcccggactt tacttacttt ccgttaaacy ccatcgattt gtttgacgga aaccggttc 60
cattgtgcca ttaaataatta atttaacttt gtggtcagtc cacccatccg taataatgaa 120
tgtcggtttc ataggactag ataatagaca attggagttg taaaaacttt cataaattgt 180
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taaacctgga aagatttgct gtatacggat tattcatcta ccagtatca cgtaaccag 360
tatttttgaa agccccttag aaatggtttg ttggattggg ggataagaag aaaccagaaa 420
cacagtcagt atcttttttag ccaggaaaca tgacgcgagc cagcaaagcc gcagaaataa 480
gaagccagaa cttgacagcc accgaggaaa ata 513
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<210> 676

<211> 549

<212> DNA

<213> *Drosophila melanogaster*

<400> 676

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acctgtagca taagcatcgt atgatacatt caccgcttca gtcaatcaca gttttgttcc 60
caatacaaac atgcgcatcg cggccaccaa agtcaaacac tgctggcggtt ttacttataa 120
acagaaactt ttggtccttc gatgccggtc ggccgcatat ctcttttgat tttcgataat 180
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catgcggagt gtgatttaac agaggagcaa aatttttcgt gcgtataatt atgccatcaa 300
gtttttgatt tgtccaagca ttaagtagtt cgttttgccg acctgcaaga caattatatg 360
ccttccatga ggaacaagat tggggaaaac cctgacgacg actttgctcc atatgaggag 420
aaacattact ctacatggtc attctaccgt agaattacgg caagggtag accaaatgga 480
ccccgaccgg tattcaactc aaataccgc agagaaccag gtgggttgag cgaattaact 540
ttccaactt 549
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<210> 677

<211> 339

<212> DNA

<213> *Drosophila melanogaster*

<400> 677

ggccgcggtg agaaaacacg gacggcacac agttgcataa ctttgagggtt atgtgtgcgc 60  
ccagtggaat ttactaatta aatgcgagaa attgtgaatt atcgctcagc atctgtgcgt 120  
agaatttagt gagttctttt atttgcagtt tcaaaggcta tcccttcatt gtataacacc 180  
tgcttttcagg tctgtggtgt gtgtctttga ggtagaacc ggcgaaagct ttccagtagg 240  
gcgttgaaaa atgagagggg tgcggggtaa tacaaattga caataattga cattgtttat 300  
aaaactatag ttggtaatat cgggccacca acaactatg 339

<210> 678

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<400> 678

tgctggcgt gcttcttctt cttctctctc cactcagtca attgctgttg ctgacgttgt 60  
cggaaaaatg tgtcttggtg cctttttgct ggctgataaa taagctaaaa tatgtactta 120  
cccactatth atgctagaga agtgtttggg attgtattta ttggcaatag attataaaaa 180  
atatcgctth aactggcgtt attccccgta ctaatagtac tatcgatatg gactactacg 240  
acttacatag atatgtcatc ttggtactaa agattttctg atggctattg ttattcaata 300  
ttatacaggc caaatagata gattgagtat tggtattaca gatgttttga acatagggtct 360  
gcctgggtta cattgtttat caaaatttaa taaggaaagg atcaaagaat atgggtcaca 420  
ttattatgta attaaaaagt tctcaactca aaaccagggtg cataggattt caactatgct 480  
atgcaatagc taacgtataa aatgccagcc tatggcctat ttggcgactg ctttggtagt 540  
agtatcgcta gtgggcatgt tttccaggcg ctctgcgcc aa 582

<210> 679

<211> 323

<212> DNA

<213> *Drosophila melanogaster*

<400> 679

cccaggccag cagcaaccca gggagcatcg atcaacagaa cgtgaacatc cagaaggccc 60  
 aggtttccgc aatcatgagc ttctccttga tggcccgatc agatggcgac gagaacaaga 120  
 cgaacaacgt ctactacatg cgacgttttc tctcagcccg actattttaat cacatggtgg 180  
 gtactgagcg cgtgtcgtcc gaggatacga tattggccat gatgcgaacc cattacaacg 240  
 tggaacatca gatccccgaa acagagcccc cgttgaagct gcacaaacag atcgactttc 300  
 ccgctgacct acgcctcgaa ttc 323

<210> 680

<211> 521

<212> DNA

<213> *Drosophila melanogaster*

<400> 680

acacaaacgt acatacgtat cgtaagctca cagtaacttg tgcaaaaacc acaacctata 60  
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 tggacgggaa gaattatggt caaacaggtc actgatacgc gatggaacca cagaaacata 180  
 caaatctcag atcagtctac acaaactggt gtaaaactac aacttagata tgatcaaaca 240  
 agaaacaccc ttacattggt gatatacag acgaccatat cggccatttg gtagctgtgt 300  
 tgtaatcttt cgaccgctgt agtgagtcga ttgccttcac agagtcaaata ataataaat 360  
 tttcacagcg acgtacatat gagtctgtta gtatgtcatg aatgtggaag ataacatatt 420  
 aagaaaatta aaacgaatca acacattaat ccaatgtata ccttccatct tataatatca 480  
 aatgaaatat gggtcacaca atacatatat ttatccaagt a 521

<210> 681

<211> 722

<212> DNA

<213> *Drosophila melanogaster*

<400> 681

gcccacgaca ttcgacgtcg aacacacagc gctgtcactt tggttcgacg cgttcgttcg 60  
 agttggcact gaacatctga ttggatcccc aggtgaagtg tgcgaggcaa cggcacgatg 120  
 ctgctcgttt ggcgcccgtg agcgacgctt gcggttagagg agcacagata tagggctccg 180  
 agcacgaaat tcaccttcgc gcgcttttca caatcttttc ggtattttaat ttaaaccatcg 240  
 taagccgtgc ggtattttta attagctaaa gtttagtaac gaaacttaac agcaagctaa 300  
 cttcaattag gaaatatctt tatattctcg taaatgattt cagttccaca aagtgtttcg 360

atttcaaaaa taatttgcac aatattgatt ataattaaaa gattatgtat tttctttttt 420  
 aatattttgt ttttatgcct taacacacaa tttttacagt aattatcttc ctatgatgtg 480  
 acgtcacgtc ataccatac acacacgttc tccattcgtg gacaccaaca caagcgaaga 540  
 gtacattcac gtttttcatt caaacattac tcgaacagcc ttcttagttc gacgccactc 600  
 tgcgaaaaag tgcgaaatac agagaaaatt gccctaggcg cctattttta acttggttatt 660  
 gccgcagaaa tgtattccaa attaaaaggg ggattccatc aaaaattaag tcggtaaaaat 720  
 tg 722

<210> 682

<211> 860

<212> DNA

<213> *Drosophila melanogaster*

<400> 682

ccagaaacag aaactgagtt tcttgctaaa actcagttgg aagccgaagc gagttcgtgt 60  
 atccgatgga tactttcgtc ggtggtggat tttctgcggg gggtgactgc gtgttgacgc 120  
 aacattgccg cgactgttgc aacatgttgc ggcagcagag agagggtgcc ccaaatttcg 180  
 gtttgcattc ccgagcataa aaacgtgcaa ttgatccag gattcttcaa cctgtaggat 240  
 attcaatctt tggaaacttc gaaagtcttt ttcttatcag taaatttagt tttgcagcac 300  
 gctttgcatg ctcaaagatt taaatcgact caatttatta aatgtgatat ttatataatt 360  
 ttactactat ttattaaata aatgttaaat aaatgtgtta tctgtgcacg gggccaacac 420  
 ctgtaatcgg aattagtttg cgaatctaaa gatggtggaa cattatccct tacgggtaaa 480  
 acttgaacat aaaattgcta acttataaat ttacatgtgg tgtattcatt tgtaaatatt 540  
 aataaataat attccatata gcctagtttt tgtgtccac caataataat tcattttctg 600  
 ttgaacgcct tggtttgaaa actaaataaa caaacaaaca tattatttgg cataattaag 660  
 cgatagtcta aatcaacgca atttatgttc agaaacataa tatgctaaaa agttcactgt 720  
 caaaacaaaa aatggtagta caccattaaa accgacaaaa ggaccgtttc catgttatga 780  
 tgaggtttca agtgtcaaga ctgttaaggg aatagtttca attcgaagcc ttagggatga 840  
 atcatttcca tggggaacct 860

<210> 683

<211> 570

<212> DNA

<213> *Drosophila melanogaster*



<400> 683

agctgtactt cagtagacat ttttgttcga aactgggttt caagtacgac gcttacgtcg 60  
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gctgttgcaa ctttcgtctt attttgtttt gttttatttt taatgtgatt tatgcatgtt 180  
cctcaatgtg tgagtgtgca aaaatacttg aacgaaatta ttgcagcttc tttttttcgt 240  
acatttattt ttgtggattt tattgttggt gttgtcgcga gcgttgacag tcgcagcctt 300  
cgatttattt ttaatgttta tgtctgtccg attgtttatg atttttgttg ggttttttgc 360  
ttacttaatt ggcgattaga taaatgccaa aaacgcaacg aagccgatga caatggaata 420  
gatcgactg agtactaaat ccccgccatc ctactcaaa ggcctctcca tgctgttctg 480  
cctccgtgac tgcataaatt tagtttgagc aaacgcgata gataagatag caagcaaaca 540  
gaccgcagca atcgaccgaa ccgtcagatc 570

<210> 684

<211> 485

<212> DNA

<213> *Drosophila melanogaster*

<400> 684

caccaggata ataatcactc tcaactgaga gcaactgaga gaggaagct ctaatgggaa 60  
aagctctcgc cagctgaagg gaatttctc atttcgctta cttttcaatc agaaagagtt 120  
tattccttctg gcttgatgga cgcaacgttt aattcgcgct tgttctgtaa aacaaagaaa 180  
accaaaaaag taattttcaa tcgcatgaaa ctcatgttta ttgaactccg tttgttttcc 240  
aatttgttta accccaattc cgacgctcgt tgtgtgtttt tgtaacgaat gcagtgaata 300  
tcaagtgaat acgtacaacc agaccttggt cacatatata ttatatggtg gtaaccaaac 360  
agtgttcttc tatttggtgc ctaaaaaacg aaggatacct cgtggcttaa atcatcagct 420  
ctaggtaaaa tacatctctc gaaatcgtgg ttgttgcat ggcgtttttg tgtaacatcc 480  
cgagt 485

<210> 685

<211> 22

<212> DNA

<213> *Drosophila melanogaster*

<400> 685

ctccggccac acggatgaat tc

<210> 686

<211> 378

<212> DNA

<213> *Drosophila melanogaster*

<400> 686

gcttgaggcta taattattta acgttgccct gtcactgtct gctcctcttt ccgctcctgt 60  
tccctcccca ctgaatcctt ttgccacctc ctgcgcactc ctgtttctgc ttccttcttt 120  
agtttagagc tcgcgcgcgc tcttgtaata atattttaaa ttaattacaa caaacatgca 180  
tttgcttctc tgcgctgggtg tttgtgcccc tgtttatctg tgtgtgtgtg tgtgtcagtg 240  
ggggtgggtg tgggtgtgtg caaccctcg acgcgactgc ttgtgtgtgt gcgtgtgggg 300  
cgtgcttttg tgctgctgcc tgttttgtat gaaaagtga ttaaggcgaa ttagcgcgc 360  
gtcgggctca cgttccaa 378

<210> 687

<211> 504

<212> DNA

<213> *Drosophila melanogaster*

<400> 687

ctccaacgat taactttaca tcttttgtat gcacgtcgtg cgcttcgac ttgtttattc 60  
ctctctcttt ttatttgtct atctctgccc ctttccacgt gtgtgtatag tgcttttttg 120  
acagttgaat gaacccaagc atttattaaa aaaaagaaaa acaaaactaa ataaaagcta 180  
tcacatacaa taacaaacag aaagagcatg caagataaac gaaaaaagct acagttgagg 240  
ataatgctgt agttgtactt ggatacagtt gggaaaagca gatggagaca agaaaatgat 300  
taaccattt gtttgagaca ttctattgta atttagtaaa ataaatattc agcattactg 360  
atactgcatt tttccccaga ttgatcccca caatattatt cttttaattg ggccgtttcc 420  
ctaaaatgta tttaaaatgt ttagcttgc tttgaaatgg agtttaacct gtgtattata 480  
ttatacagtt gttcatttga attc 504

<210> 688

<211> 427

<212> DNA

<213> *Drosophila melanogaster*

<400> 688

aatgagtgag tgccgtacga taggtgggcg gtgagcaatt gcacaggaag tgcccaacag 60  
agaaagagag agagagggac agcgagagag attgctacag agcgggagag agcctggcaa 120  
agtgtgagag aaagcaggca ggtgagagaa gatagtgcct acagtgggtg gatggaatat 180  
tgagttacct ggtgattttt ttagccttga tattatttta aataatctag ctaacaataa 240  
ataagctgca atattgaatg tctatttatg ataataaaca aatctctttc ctttttccga 300  
gggattactg taaccgacat agaagatggt ataaaatcat cttttctcac catttttctt 360  
tttctctcaa ttcgctctct atttttctct cggtggcggc gcccaaaaca gctgcttggt 420  
gtttatt 427

<210> 689

<211> 157

<212> DNA

<213> *Drosophila melanogaster*

<400> 689

gtctgcactt tcatggcgga aactcgaaag cgaaacaatg ccataaatac aacaaacaca 60  
cacacacaca ctcacggtcg ccgaaactaa aatagataaa caaattcggga aaggaacaag 120  
gaaaaacttt tacagaatgc gagtgcagag ggaattc 157

<210> 690

<211> 408

<212> DNA

<213> *Drosophila melanogaster*

<400> 690

gggtgaacca ttaattcaaa tttgcagcgg ttttggtgag cgggagaaga gaggggaatt 60  
gagaagagaa agactgtaag cgatttacta tgatctctat aaaatatacg tatacttgga 120  
gtttgagcaa tttaagactc caattatatt cgatatttgt taatatatct ttaaaatgtc 180  
ggtttctcat gcattttaag gaaagagaaa aacgaaagag acaagagcaa caagtttcga 240  
aagctttttt accagatggt aatgcctcgt tctcactgcc agtggttgta aatcaaaaaa 300  
agcgccaata ttgatgttcc tctctctctt catattgtc gctctttccc acccttttgt 360  
ttaggggtggg caggcggcaa acaagtttac tttgctctgc tttttgtg - 408

<210> 691

<211> 455

<212> DNA

<213> *Drosophila melanogaster*

<400> 691

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cgacaactaa tggatgagct ttgctccgc tgctctgcct cctctcatg cgctcttcg 60
ctctttcgct ctcttttttg ttgttggcga ttggcgaaat tcagtttgga atttcgtttc 120
gaagcaaagt gcaatatgca gagcgagtgg agtggaatgc atcacacgta cgcactcaca 180
gatacattcc catgtattgc aggcaccccg aagttaacag atacatatta attgcacttg 240
ctccattaag aaatcacaaac ttttcgattt gatggtcgaa acataaaatt gtttttactt 300
gttatgttcc acttttgact tcttaaaccg cgccaatttt gtaaattaag agttattctg 360
aacggaagca aaagctggat ttccaaaaaa tcagaaacca attgatcgat ctttcattta 420
gaagcaatta cagcgttact tttccaaatt gaaat 455
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<210> 692

<211> 686

<212> DNA

<213> *Drosophila melanogaster*

<400> 692

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aaccagaagc agaagaagaa gaagaagtgg tgtggtgcgg cgtgttggtc gggcgggggg 60
gagtgttaaca gggagagaga gtgaaaggag agagagcggc agaaaggcag ggaacgaggg 120
cagcaacagc cgctgagata caaatacaaa tttcatgacg ggcaagccgg cgttgttcat 180
gcattttaccg ctagttcatt ctatgcctct ctcattcgct gtgcctgtgt gagttggttt 240
ttcttcattt gacgtactca aagcactcat acacacaaac acacacaagc agtggaaacac 300
tcaaaacagc aacagcgcaa atagaagtag aaaccgggaa agtgagacaa gtcgactttg 360
agatacctgg taaagtgtg cctacttcag gcgtttaaac accatatcgc tatttagaaa 420
aacgttattt cacattatc agaaaaaaaa tggttatatta agtaatggga ataaatttag 480
gaaaccttta gagttaaaaa tgtcattccc cttatgtcga tacaatgcag tatacccgctc 540
tgctctatta taccgggtat aaaaaccacg ccaccaaaagc gaatgagaaa aattacttca 600
accaacggaa ctacactgaa ccaaaagaac agcgaaagga agacgaacag gcttgtttgg 660
gcacggccaa gtgatgaatg gaatgg 686
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<210> 693

<211> 927

<212> DNA

<213> *Drosophila melanogaster*

<400> 693

ttggagccca tctaataattt ctaacacatt tgatattccg aacgggtgcc gcaaacgcca 60  
gttccgttgg cgcacgcgtc atgggagccg cagatccgaa tcgcttaaatt tagcccgcca 120  
gtcgcgcgct tggagcgtgc tgaggcgctt gggaaagatg gtgactcaat tggattttcc 180  
gagaacggcg gacaaaaaac cgcattcttta agtcgcacac tgcaagtaat cgccatgtaa 240  
acggcatctg acgcaagtgc tgccatgaat ggatctacct ttgtgtgctt atgtttatgg 300  
cccaaagtgg atggtcgttc gccatggaaa aacgggaact tcttagcaga atgcatttta 360  
cttggggccat atctactcat agcatagcct ttcccccgaa ttatgcacca atgactgagt 420  
tgaggccatt tcgtagaaac atcagctgca ctgttgattc ataagaattt ctttatcaat 480  
tagtacgtaa taaaatgcaa tgaagggggg ctgtgtaagt agataactaa attgcatgat 540  
gatgcaattt tgtattattg taatgcccat acatatctgt tctaaacaat ctaaaattct 600  
cagaaatcaa ttaaatcctc aactgaacaa accatttcaa tatattacga ttgcatcaaa 660  
cttgttttaa tctacttgca tacttttagg gatctattaa gcttgtgggt catatattta 720  
ggaggtttcc aaattgtatt tttatgagcc taagttaatg tatataattt cagcttccac 780  
tatectaaaa tggttaattt gaaatccatt taagcagtaa aatttttaag ttagcaccgc 840  
gcttaactaa cttcattaat tactttcagc gaacgggtta aaggtaccac ttaattagta 900  
aacatggatc atccgttggc tggaaaa 927

<210> 694

<211> 355

<212> DNA

<213> *Drosophila melanogaster*

<400> 694

tgtgagactg ttgcctctct cgcgtctct cattggctct ccccttttg ccgcatcatt 60  
ctgacagtaa ttgtgtggc tctgcttcac accacattc gccagggccg cgagaatcat 120  
gaggagcata cgaaaatcgc tcagccggga ttttccatgc ggttttagagc ggttttatgg 180  
acttttcaca cttccgattg tttgtcattg cttttgcgct ggtcaaggag atattttggg 240  
atgtgtgaaa ttccgtgacg gataacggaa gtgtggaatt acttaaaaag tcaagggtgca 300  
aattggcatt attaaaacga aattaagtca agggagttgc atgtgaaatg aattc 355

<210> 695

<211> 201

<212> DNA

<213> *Drosophila melanogaster*

<400> 695

ctccgcgctt tctgcatttt cctctgccac cgccgatgtc tctgtcgacg tctctgccga 60  
cgcagagaat ccctcctcgt gttttggttt ttatttacca tacgcgcact ttttcatcca 120  
ttcccattct cagcgtgcac tgataaaaat aaatataccg aaaaatccca ctttctcata 180  
ttaatatattt ctttcgaatt c 201

<210> 696

<211> 114

<212> DNA

<213> *Drosophila melanogaster*

<400> 696

gtctgtcagc tttgtgtcgc ttcattggcgc cttgactcgc cggcgggcttt atttgccata 60  
ataatgtgta tagtagtcga tggcacactg ggcaacaggt ttacagaaga attc 114

<210> 697

<211> 696

<212> DNA

<213> *Drosophila melanogaster*

<400> 697

aatcaatcgc aaggggtgcc caaaaacaaa caaaagtacg aaaatagagt gccgcagacc 60  
acaaacaaat cacctgcgcc agtgtgtgtg agtgtgtcag tgtgcgaaac aggcaagctc 120  
ccaggcgggc tcccaccac aatcagtcgg ggaacacgtg ctccaaaata tcaacaaaag 180  
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cagtggtcgc ttttgttata attgtgagac ttgaaaacga tcgccgtaaa attcacattt 420  
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gttattatga gaaaaacata aaagattata ggacattatt tttttaaaaa tgttgcaaaa 540

atgatttaaa gtttgcgatt tccttggttaa atacatgaaa gcgtatacag gtattactat 600  
 taccaaatta taacgattta atatgcatat ccttattatt aatggctctt gaaataccct 660  
 aatgtaaaac tatttaagca atgaatacat tattaat 696

<210> 698

<211> 786

<212> DNA

<213> *Drosophila melanogaster*

<400> 698

tcttggccaa acaacgcgag cagctgatgt cgcattggtg gaaaatgagg gtggcgcgag 60  
 tggaagttgc catatcgctg cgatcacaag cagcaaatat ggaagattaa gcggaaaacg 120  
 aaagacaaaa taattacaat caaacaaccg aattataaaa agaaaatggg ttgtcctccg 180  
 agttcgttta aatatgctta tctacgtatc aattaaaaaa accgtagaaa gaaattcacg 240  
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 gtgtacacac ttttcttgtc gatgtttgaa gcgccattga aatgatcatt tgaatgtttt 360  
 caaattacca catcattaca ataaattaaa ttgcttatta ttgattttt actgggaaat 420  
 ccgtgcaaat ggaattacaa ttcagctgga atcgtcaaac ttacaacata aacttattgt 480  
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 tcagcagctg gacggcgtag cgcagcgtgg agctgggtcc aatctcgctg agacgtgtaa 660  
 atgcgtttctc ctccagctgc agtccctcgg tctgggcgag caacttgatt atctgctcca 720  
 tgtcggcagt ggagtagagt agtgtgcgga tgatcagcaa acgatcgagc agatctagcg 780  
 gaattc 786

<210> 699

<211> 574

<212> DNA

<213> *Drosophila melanogaster*

<400> 699

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 aatgcataaa atacttgtag gcaaataata tccgaaacta ttataaaatc tatgctcaag 180  
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ctaacgagca aaggtgtaac catgccacaa aattgaacgt caaaaaaagg caattatatt 300  
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gacacacaac ttctatctgc agtcatttca cactttatcc caccacacca cacaagtaat 420  
attcaagttc ctttgaccgc agtcttgaac ttttcccttc acctcccaca aattaggcag 480  
cttgaaagcc aaaaggcgtt gattgatttg aataaggttt cagtaaggcc cgagaaaagg 540  
tgcaatgat ggaaaaagtg acgcccgaag gttt 574

<210> 700

<211> 621

<212> DNA

<213> *Drosophila melanogaster*

<400> 700

ggcaggggtgt ggttggtccgc cagagccgag agagaatcgg cgagagagtg aaaggaaaga 60  
gagggcgctg ttgttgtaga gagattttcg gcttcacgca tcgcaacgca acgctctgca 120  
aaaaggggtgg agtccatttt tcaattccaa tgatccacaa aaaaggcagc ctgtctgcca 180  
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cccttgacaca agaagttcca gagagagaga gcgagagcgg gagaattgca ctggaaccga 480  
gtgagcaaca acaaagggcc gtccactggt gtgttggtta aatgccata ttgccgggtt 540  
attaattaaa acaaaggcag ctataaaacg taaaaaatc aaaaacgaga acaaaaaact 600  
tcattttctt ccacatacac a 621

<210> 701

<211> 366

<212> DNA

<213> *Drosophila melanogaster*

<400> 701

gtctgtactg actgtaccca tattattttgc gcgccaagct atcaagttat caagccgtca 60  
acttttatct gccaacgacg gagaggcctc tttggcgaac taacttaatc tacaacggag 120  
catacaaaca cacatatgta catatataga tttgtatata tacggttaca gggtacgttt 180  
acgggggcatt cgaagtacaa ttacgggttg tggacacacg gtcgtagaag cagctaagca 240



aactgaaagc tgaggcccct cgagaacatt tggcgatagt cacattctat atacatacat 300  
 atatacaatt ggacagctgg atttagataa ggacctaatt aaatgccatt atggttccaa 360  
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<210> 702

<211> 469

<212> DNA

<213> *Drosophila melanogaster*

<400> 702

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 atagcttttg cctcagattt tgctgtagct tcaggtagac atacagctgg ccatggctgc 180  
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 gttgacctgg gtcgcgccgc gtaaacattt tcaaatttgc caaacatatt tataaaatcg 420  
 acccatgggtt atggttcccc ataatcgaat cgatctcgca cgagaattc 469

<210> 703

<211> 963

<212> DNA

<213> *Drosophila melanogaster*

<400> 703

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 ttacgaagac aggaacaata aataaatagc agttaataa atagtagaaa atgccatata 120  
 aaatatatgg gaattgactt taaattacat ttttgagttt tcaaaataaa aactaaattt 180  
 taaatactta aattataaaa aaattaatta aaaaatgaaa tagtttccac atttcttgaa 240  
 gaatatactg ttaacagcag ttaacgaagt gtaagcagaa ggaacaagta caatgttatg 300  
 cattaagaat atgaatccct aatctcaatt tcattcagtg cagctgttca agttttttct 360  
 atagttcttt gccaaagaaa tattacgact tgccaaaaac caaaacccca accacaaaat 420  
 gtagactttg aagcgaagga cgtctctgct gataagtga aaataaatga ctgatagctc 480  
 aagtacaaac atgcacatag tgatatgcgt atatacatgt gcgtgcattt gtgtgtatat 540  
 acccttcagc tatctccaaa tttaaataac attttctctt ttatcgagc gaccgaagaa 600

atatctttat ctgcacactc cacaatttta atattatattt tgcctgcagt gcgtgacttg 660  
 aattttttgc tcaactcactc tttcgtatga ctcataaacc cgcataaaag caagacgagt 720  
 tcgaattatc tacggatttg ggattacggg tcttatcggc gagtgcatag ggggttctgg 780  
 ctgcgatggc aaccctgatt gttggacagt cgcccagctg actttgtttt tccaactttt 840  
 cttggtgact cacttgccct tttgctgttt ttctttttcg ccaactccag ctcaccttgt 900  
 aacaattata aaaagtcata ttgctcggtt tttttttttt ttttttcgga taaagttttt 960  
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<210> 704

<211> 431

<212> DNA

<213> *Drosophila melanogaster*

<400> 704

atctgtggtt cagctgctgg tgtttgtgga ctccgttcgt cattgattgg actccccctt 60  
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 acgtgtgttt gtaggggctt tgaatggctt aaaacgccta cgaaagcagg gattgtgttt 180  
 gtcacggtgt cattgcttgt taaatttatg caagagtctt ccctaatttg ctggatttgc 240  
 ttacacgttt gaattttgca aatacttcta aagagctcca tatcctaacg acattcattc 300  
 ccgttggaat ctgttttttt ggctagtttt gctcgcattt tgacccccctt ttatttagct 360  
 tgttggaact tttcagatga ctcacagat atggctacga gttaaaggga ataaaagagg 420  
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<210> 705

<211> 754

<212> DNA

<213> *Drosophila melanogaster*

<400> 705

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 gtcaagtaaa tggcactatt accataacta cgcgcaaagt ccttgatgaa aatctaaaat 180  
 ccttactgga tgagggaaag ggcgagggtga gtgtctagt aaccatctag tctcaaaagt 240  
 ttacggagac actaatacgt ttttgcttct agctgtttct ctctgtgata ccgaggaatc 300  
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 aacagcacta accctaataa tcccagtcgt ccaatgcatg tccgacagct ttgcatgtgc 540  
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 cttagaccat ggcaagtgtg ccaggagatg ttgaagatac atccctttac catcgttcga 660  
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<210> 706

<211> 156

<212> DNA

<213> *Drosophila melanogaster*

<400> 706

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 gcgacggcat ttcgagggct gttacgcacg gccgtggaaa cgtaagcagc tgaggtcaca 120  
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<210> 707

<211> 989

<212> DNA

<213> *Drosophila melanogaster*

<400> 707

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 taaaccacaca cgtagaaaaa ttttagtgga tcatgaaaat caatttagga taacattctc 120  
 agtaacaaac taaatgcttt cttttatttt gtaatcggtt ctatgaaatg aaaatgtaca 180  
 ttttaatttg aaagtatact ggtttatgat tagtaccttg actacgttaa taggctgaat 240  
 ttttctctgt gtaagaaaaa gagagataca aagcttatga gattgagaga gcggactaaa 300  
 acacttgatga gcgtgtgaaa atgcggcaat tgagcagttt gaatttgat gtgattattg 360  
 ttcattgccg tgctggttga tggtgtgtgt cctgttcttg tccctgtaca gagagaaaag 420  
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 agatagcggg tcatgctgca gaggccgaga aactatcgcg agcaaactcg ttacacaaac 540  
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 tgtaaaaatc tggataatca ttacatttt 989

<210> 708

<211> 183

<212> DNA

<213> *Drosophila melanogaster*

<400> 708

gtatgactct tatcacttgc actccgtgac gtcgacgatg acgtcgcggg ggcatecccta 60  
 tgattccatt tcttttttca tgtttttctc ttcttttttt aatggactat atattcacgt 120  
 ggccccagca aatccacaat tcagtctgat tcccaactct gagacaagcg gacgtacaag 180  
 tgg 183

<210> 709

<211> 304

<212> DNA

<213> *Drosophila melanogaster*

<400> 709

gattggatta ttcactaatg gtagtatcga taggtcgatt gtcacaatac cgatgcttca 60  
 gtttcgatat cgactgtttt tagtatggct gtattttgtc agtattttta cgттаататс 120  
 таатааттгт тагтаатааа тттсааагас сгсгататтс ааааттгтт тсаагттатт 180  
 стсаттттта тттсаааата атаааатсгт ттттсастт тгтттаааа тгаатттат 240  
 гтатгттстт тттсгтаас ааттагаттс атаасгатг ататттгтт тгсттсас 300  
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<210> 710

<211> 855

<212> DNA

<213> *Drosophila melanogaster*

<400> 710

acctcgccag ccactcgcac actaaccgat gtcgttggtg gctcaacgct tgccgttggt 60  
gctgcctgct cgctctctgg aaatttggtt gtggcaacga tgacgtcggt actgttatcg 120  
tcgttgctgt cgcgaatggt gctgatttga gtcgctttca ttgctatttc ggttggtgctg 180  
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cttgctcattg ctgataacgt atctgttgaa tttgccttag acatttcacc tgactctggt 480  
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tggaggtcca ttgaccagga tcaagggtgt gaaggcattg gtcgtgctgt ggtggacgtt 780  
atcctgttcc aatccactg gaatatcacc tttggaaatg gggttttcct ctaaccaagc 840  
tttcgggaat aacct 855

<210> 711

<211> 825

<212> DNA

<213> *Drosophila melanogaster*

<400> 711

ccccaaacca tgtacaacaa gtcgtgctct ttcgctgct ctctcgcttt ttctctcagc 60  
agccaagcag agacctacc cctcctcct cctactccta gcgggccact caactaaacc 120  
tcgtacaccc gtgcactcca accccccacc actccccgcc tatgtacaat ggcataagat 180  
ataagatatg cgcatttctt ataatgtcga accgaaacgt ggcgaaataa atgtttgttt 240  
gctaagctgc gtcttgcttg ctttttgata atttaaaacg tttttattct gtcccaaagt 300  
acttttaggt gtattaaagc ctataggcgg ttttttaata aacattcaga ctttcttggg 360  
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cagagcaaca actttttact actattccat gactgcatga aaataaatat acaaactaa 480  
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ttctcaaagt agtttagata tgtgtaaata tgtatatact atgtatgtat gtacgtatga 600  
aatcagctaa cgggtgtgcgc gatgagtctt gaaagttata attctaatag aatcatagat 660

taaagatatt tatgattctt taatgtaatc aaagtatgac tggtttgtaa tgcgcaatat 720  
aaagaaagta tttagttaag tctttatctg caaggctgat aacaaactaa tatgcaaate 780  
gatgggtggg gagattgggt ggggtgtaac ccgtgggtgat gtggg 825

<210> 712

<211> 798

<212> DNA

<213> *Drosophila melanogaster*

<400> 712

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gcgcactctc actggctggc cctcacgatg aaacatttaa ctagagggct acaatttcga 120  
catggctctt aaaagtaaaa gcatttgaaa gctgtgtacg tagatggatg gagattagaa 180  
cacaaaggcg aggctgaaaa caaaattaat acccaaatgc tattttgctc acatttatat 240  
ggctgcagta atttttttgt ttacgagcaa aagaacatgt gtgataattt gttagatttc 300  
gttgctaaca acagcgaagt aaagcaaaaa aaaagggtac aaaatgtgaa gctcagataa 360  
agcagagtat ctttgagtta atttatatat atatatatag attatatatg tgtgtatgta 420  
atgctaaata ttgcagagta ctaaacaagt ttaacatag tacctgagta cttacaaatt 480  
attttccaca aactgaagag ctattgaaaa ctgggcatct tataggaaat aacatcggaa 540  
tatctatctg catgcaaact atttgtgttg agcaacattt ttcgtattgt tacaccgatg 600  
taaacctgcc cttttatgat gtctaccact catgttgggt ttttctttta aatcttcgtg 660  
ttgtgtgtat accagcaagt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt ctttatgtgt 720  
ttgtgtgtgg tggcgatgag gggggcgttg ccattgggaa gtggaagtgt tgtggtgtct 780  
gaaaggcgtg actgcate 798

<210> 713

<211> 797

<212> DNA

<213> *Drosophila melanogaster*

<400> 713

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ccgcatacat aaccggatca tgttcacggt cacgtcggag atctacggac agaacaacta 120  
ccagacgacc cgcgatggag gtaaggcggt gtccaagtgc cgtttcgtct atccggagga 180  
gaagctggcg gggattagga cggataaaga cggcgacctt gaggtgccaa ggccgaaacg 240

tggcgtgac gaattggaac attccgaggc cacggagctc cggctggtgg gcttgcaggt 300  
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 gaaaacccta atggaactgg gagctggtgt cggcctgacc agcattgccg ccggaataca 420  
 caataacgga aggatctatt gcacggatgt ggacctggga tgcatactga agctgatccg 480  
 cggcaatgtc caaagaaatt caaaactcct cgcgcctacg atatcagttc tggagtttga 540  
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 cttggataac ctcttgatc gaggtcgcca aactgggaga cccaaaacga tatacatggc 720  
 actggagaag cgctatgtgt tcacactgga ggattgcgat tcggtggctc ccatgtatga 780  
 gtaccttate cggcaga 797

<210> 714

<211> 491

<212> DNA

<213> *Drosophila melanogaster*

<400> 714

gaatggcttt ttactatect ttcactgtcc atttttaggat ttatttataa caaacgaagt 60  
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 cgccaacgat tttttgttga ctacggtcac actaaggaaa ttttaaagta ttcgaaaaat 180  
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 ttttaagtgg tacaattatc ttttagtatt atttcaattt tcaagtattt aattattctt 360  
 gtggcttttg gcggcaatct taaagttttc tcacacagct tactcgctgg tattttccaa 420  
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 cacgtccaaa g 491

<210> 715

<211> 1013

<212> DNA

<213> *Drosophila melanogaster*

<400> 715

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cagcacgcat aatctcttgg ccccggttgc cgcctaata gtagtattag ttttatatat 180  
 attggggggg acttaactat ttaaatttaa gtgcgtgagc gtcggtgacg tggctgataa 240  
 caccgttcgt attgcggggc aaaaataaaa tcgtaatgtg caaaaaccgc caagtttggg 300  
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 tccatcattt tgcgtttgcc gaatgcaatt ccaaaaagcc acacgcaaag cactcaagtt 420  
 gctagacaga cagctaagac gtagtgcgca aaataatagc aactaaatta ttgataatcg 480  
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 tctgctcaaa atatctacga cttttttaa acaattttaa tgccatactt ctgcataaca 780  
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 cgaccccgac tgtgcccaga ggcgactgtc gatttggcgt tgagtgtggt cagtgcggc 900  
 ggggcagcga ggtgcaagag aaaagcgcg ctaacagcag caaccagcag tgggccaatg 960  
 acgccttcca ccggccgccc aagctcccct cgacgcccc cccactcggg ggc  
 1013

<210> 716

<211> 902

<212> DNA

<213> *Drosophila melanogaster*

<400> 716

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 gtggcagttc ataataattt ttcaataacc ccaaagttag gctctaattt ccaatttcga 180  
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 caaccacca ctgaaaatgt caattactaa gcgttttttt tttgttttc cattttcgac 300  
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 cagcgagctt ttgaaaggaa ggggccccga gttaatagtg ataaggagcg tataaatcaa 420  
 gtggaaccaa cagaaactaa gcgaaagcga tttagattcc gccagactg agataagctt 480  
 agtgggagac aattggcaac agttttttgt acctacagta cggcttctat atatagcagc 540  
 atatatttcc ttaatagtaa actaaactac gtttttagaa tacatgatct ttgaaacaaa 600  
 gtaattaatc tagataggtc caggttttca attttataac atggccttaa atttgattat 660  
 gtttaatcta cgaaatccgt acgataagcg aataataaaa gcgaaaaaga aatgttctaa 720  
 tcaaacattt agggaaaata aacaaatcc aaaaagtgt gaaactgggt gatttcaatt 780



agaggaagta cgactgtttt ttcgttttca tgttttatatt atttctttgt ttgtattttt 840  
 tcgtttttaca tttegactcc atgagtctgg tcgtctgact tgcggacgag gaaggagata 900  
 aa 902

<210> 717

<211> 64

<212> DNA

<213> Drosophila melanogaster

<400> 717

gtttgggtgcc tcgcgagtca catttgtttg ttcgccgcat tcgagcgtac gacgaagcga 60  
 attc 64

<210> 718

<211> 526

<212> DNA

<213> Drosophila melanogaster

<400> 718

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 tataactgtt tggcgtgagg gagcacgaaa ctccagtga gacttctccg catcgccagc 120  
 gaaacaaacg atcaaaatga atactctgat aacgtgtgaa ggtgagcaac aaaataaagt 180  
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 atggcaattg ttgcttttgt tttcgagagg ggggtggtgaa actcataaat atcagctatg 480  
 gcgaggggggt ggggggcagt ctttgctgac gtaccgactt ttaatt 526

<210> 719

<211> 143

<212> DNA

<213> Drosophila melanogaster

<400> 719

gatcagcact cagagtcagt tacttttttt cgctccatac gtgactcaca attcgcgtgt 60  
ctttcaaaaa taaaagcaaa agaagcggtt ggattcggtt ctgatggctg gataaatgaa 120  
aaaaaatcag tcagagccaa caa 143

<210> 720

<211> 110

<212> DNA

<213> *Drosophila melanogaster*

<400> 720

ttctggcgaa tgcaatgaac tcggcttggt tatttaaaaa taaaatatac atttgcaaag 60  
aaataaaaag atcgcagaac aaaaatcgaa tcaacaaaca aaaggaattc 110

<210> 721

<211> 1070

<212> DNA

<213> *Drosophila melanogaster*

<400> 721

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accccagccg tattgccaga gatcgggtatt gccagatcgt accacccgac tcggccagaa 120  
tcggatcgta acgactaccg actaccgaca tcgacgacat cacgcacga gggcatgac 180  
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tttctgaaat ttttaagcaaa gtccaatagt aagagactga aaatagtttt aactcggaaa  
1020

atctgtcgtg gatttggttt tcttaatatc tgcacgttcc aataatataa  
1070

<210> 722

<211> 765

<212> DNA

<213> *Drosophila melanogaster*

<400> 722

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acacacacac acacatatat atgatgtgcg aggcggacag aagctgaaac tgatgcgac 120  
cggacacggg tcttgtgttt cagttctctg tgtggcatgg ccaccgtggc caggttggac 180  
atcgtggcct aaaaggacac acacgaagcc cttttggccc tatgctaatt tgcacgccat 240  
aaatgagacg aatgtgccga gtggtggcat gtgaagtgtg gttgcagttg ccgtcgtgca 300  
cttagagaaa aaaatgttat cgatcaagtc catttgaat ttaatttatg taaaacgtat 360  
atataacaga ccaattctca aatccataat tacctctttc aaggatttta agaattaatt 420  
tttaaaactga aattactcta taaatctaaa ctatttttcc ctgtgcattt gagtagtggt 480  
tgctgttgca gttgcaattg ttgcaagtgg ataactgctg cggcccgtca tggatcgagt 540  
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aacgccggct gaaagaacaa atctgcaacc tggggtggcc ccgcccagag tttctgtgat 660  
gatggggccg actgccagag acatgtgttg ctggttecta tatggctccg tagttgggat 720  
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<210> 723

<211> 568

<212> DNA

<213> *Drosophila melanogaster*

<400> 723

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aagagagaac ggctaagaga aggtagacgt gcgcaagtat tggataaaaa agtatctgtg 120  
tgccgatgat tttgatttcg ttacttttagc cagcgtccgc gtcagttcgc tctatgtgat 180  
tcagtgttaa ttttcataat attatgtaat agcatgtgcc gccgcctggg tgcgattcta 240  
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 cgctttttgg gcctgggtgat gtgggaaatg catttcgagt gcgtgatatc tgtggcgtct 480  
 ccagtgggta agtaatagat actgtagttc ttcttcctct tcttctctggc ccacccagta 540  
 atcccaagac cgcgaagaag agagggtt 568

<210> 724

<211> 580

<212> DNA

<213> *Drosophila melanogaster*

<400> 724

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 ttcaattaaa tgcgcttcac ctacaaagtc tgcgacagtg acgtcaatat cgaaaataat 180  
 tgataacctt cgatcacgat cgggaagaga ttgtaacaga cttgctttga tggctcgcat 240  
 ttgtgtaaca agttttacca ccacaccacc taaactaata atacacgcaa ttgggggcaat 300  
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 gttctctgtc attgccgttt tttatcgctc cggegccttc taccctcttt tatacataat 480  
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<210> 725

<211> 403

<212> DNA

<213> *Drosophila melanogaster*

<400> 725

ggcacaacaa accggttaact ctgaagaaat ttcgtgcgtg ttaaacagaa tctaacgaaa 60  
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 caaaaagttg taaggaatgt ctcataaaaa agttaaatata ttacacact cgaagctgaa 180  
 gcgcacaata gagcacaaaa tattcagaat cgcaaaatat tccatgattt tttttgcctt 240  
 tgttccagag ccataattac aagaccgcga aggacagcaa taaaccaaac aaaaatattt 300  
 attgaaaata aattcattct acattcaact tcaacgactt tgactcgaca cttaattggt 360

aataagagca aattatcggt aaaaacttat gtccattgtg ttt

403

<210> 726

<211> 465

<212> DNA

<213> *Drosophila melanogaster*

<400> 726

gacagttcgt gtcgcccgat ttgttttagga tgttgatatct gacaactgag tatttgcact 60  
ttatctaatt tgacaaatag actttaactg ccaaactagt tcgccgcttg aacaaactgt 120  
agctcagcaa gaggacaaa tgatttctcg caaattcgaa gcacttaatt tgcaatttaa 180  
gcgtatccat gcataattgc agtcaaagtt tattcaccgt aaaaaaagag ggaacgcca 240  
gcttagttaa aatgcacgaa agaagtaatt aattcatatg ataaatcaaa tagagcacgg 300  
aagcagtga tgcgtcgggt acagaacttc gattgccctt gcaaagtga ttggatgtta 360  
attgggcatt aaagtacaaa acttgaacat ccaaattgagt tgggcatatc aatatatcgc 420  
atattctggt acaatgccct acattttgcg caccttaatc gaatt 465

<210> 727

<211> 52

<212> DNA

<213> *Drosophila melanogaster*

<400> 727

cgcggcagtg tctcattgat cgctgaaacg atgatggttaa ttcttggat tc 52

<210> 728

<211> 490

<212> DNA

<213> *Drosophila melanogaster*

<400> 728

tatacgccat gcatattcac agacaaatgt acaagtactt ggactagact gcatatattg 60  
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tgtcaaatac ccaatcttga gattggcggg gatacttata gttatagcga ccctatgcag 180  
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agtgggctgga cgataaatgg aaaggggggtt ggttgcttag atgggtcttt ataaaatata 300  
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 gattcattat taaaatgtaa ttttctcatt tgggtggtact aaaccttctt tatcgcatgt 420  
 tcttagtgcc ttcccgctat atcaacctcc gtgggaaatg aagtagatac gtagatatatt 480  
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<210> 729

<211> 1153

<212> DNA

<213> *Drosophila melanogaster*

<400> 729

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 atttgttcat tcatcgggct ctttttccga tttcagtggtg tggcatttaa caataatccc 180  
 tgcgttcgct gtccacgtcc acattacgat acgttttagtg cacggaaaga aataagcgtg 240  
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 aatttaaaaa ttctcatctt accgtacctt gaaccactac caatcatctc agtacaagca 420  
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 cgcatttgcc attttcccgc ggttcgcaac atcagcgaca tttgtcacag tttcttaaag 660  
 aacatttgaa tatccaaagt ttacttgccg aacttgactg cggcattgag atgatgatgc 720  
 tgcccgttgt ttgtcattca gctccattaa ttcgatacca atcagtattt cgtgcattgt 780  
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 gagcagatga cccattgagc ccataatatg tactttattg aatttgaaaa atttgtattt 960  
 ccccaagcaa taaaaacaca gaactccata taaatcatcc cttctctggg gaattatgat 1020  
 attaaataag tgggcgggaca atgagctaatt cttctttagg gtaaaaaaag tccctcatta 1080  
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 atgacaacca ggg 1153

<210> 730

<211> 1144

<212> DNA

<213> *Drosophila melanogaster*

<400> 730

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aatttgccgc tgcttttgcc aatttcttgc gcgaaggga tggacatcgt gggagcttac 180  
acaagagcga acgagagcga tagtaagcgc taagagcaag atggaacgag agtagtttta 240  
attttgttat tgttggtgcc cgttatcacg ttgcaagagc gtgatgcttc actaagatat 300  
tacacgctga gaaaactgga gcgcgttctt aaagttcaga tgaactgaat gatctgtaat 360  
ttaaacaaaa ctaatagaac tgctatatc aaaattcgga atgtaaataa aagagttctt 420  
ctgtctttaa acttcatttt gtaataataa taagttttta acgttgtaga taatcaagta 480  
atattatgtc ataaatttgc aagtgaata aaaacggtaa tacttgatt ttcttcgacc 540  
tagtacggtg atacaggga attaactatg ccgcttacga aatatatgat ttgtttgcac 600  
aatgcattgc tagaatggt cctaacaatt aagcatgcca ccaattctgg caattatttt 660  
ttaaagtaca gttegtgtcg cccgatttgt ttaggatggt gtatctgaca actgagtatt 720  
tgcactttat ctaatttgac aaatagactt taactgccaa actagttcgc cgcttgaaca 780  
aactgtagct cagcaagagt gacaaatgat ttctcgcaaa ttcgaagcac ttaatttgca 840  
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cgcccagctt agttaaaatg cacgaaagaa gtaattaatt catatgataa atcaaataga 960  
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gatgttaatt ggggcattaa agtcaaaact tgaacatcca aatgagttgg gcatatcaat  
1080  
atatcgata ttctggtcaa tgccctacat ttccgcacc ttaatcgaat tccgcggaat  
1140  
taat  
1144

<210> 731

<211> 858

<212> DNA

<213> *Drosophila melanogaster*

<400> 731

ttctgcacat aaacaaaaca aagccgacca gataacagtg tgaccagaac acgagagggga 60  
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 aagatatcat tcgaaaatat ttttagaaaa agaataatta tccaaaaaga atcacatttc 180  
 aaagaacatt ttacgcattt gaattaattt attaagttct atctcgaatt atgatctaaa 240  
 agtactttta attcgcttgc ttgccaatcc gaccatttca ttttgaagt actcctttgg 300  
 cagaggcaag caattctcgt gcaactcgat ggcgtccttg tccatgtgcc acaccataaa 360  
 gttcctgcca caggcgatct gcttgtggag cgccaggtgc acccggtcca caaagtggga 420  
 ttgacactgg cggcactcaa acaccgatc gtgggtatcc acgcgcagga actttcttat 480  
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 ggggtgtgtt tcgacatcat cgcctcggag caaatatggt actgcaaata attccttggg 600  
 aagtgtgtca gacccgaaaa gtgtacaggt ttatttttag agttgccgga aatgtgttga 660  
 ttttggtcct tttgatttat attaagttta gaaagttgtg ctaaactcga ggaatgctta 720  
 ttacttccat ttccaatgac ttctggttgc gttttacttc ggtactgcaa agggaagttt 780  
 aggaaaattg ctcttaggcg aaaccaaact ctttgaccg gcaccttcat cttctgatga 840  
 ccacgccttc catggaac 858

<210> 732

<211> 882

<212> DNA

<213> *Drosophila melanogaster*

<400> 732

atgcgatcga attactcgcc gaattgtgag tcataaccaa agaaagagcg tgctttcgcg 60  
 caagtgccgt ttttctgtct tgctttcttt aatcgaatat atttcggtct cttcttttgc 120  
 agcagttctg tttttttagt gtgcgcggaa gtacgttctg tttgtatact attacctcct 180  
 ttacttatta aactaacttt aaacagttat tttaatagtt agattctaca caacggcaac 240  
 gtagaatgat tttttacata cataggtcag cttaaaacaa ttgtgaaata ctacttaata 300  
 gcgaatgaat gaataaagca aagctttggt ttcggttatt attatttttt tttttgtttt 360  
 ttctttatgt gttttgtgtg tgtttgatat atacatgtac atacatatgt atgtacatgc 420  
 atacataagt atgtatgtat aaaaatagtg aatgcttat acaggaagcc tgtattctta 480  
 aaagataaat atgattaata tgtataaata cagagaaagt aaggtaagta agttttaatt 540  
 ttttacctaa ttaaaataat tggtttgaaa ataattgtac gcataattta gtgtgttgtg 600  
 tacactaatg tacatgtaca actttatatt gcaatttcaa tctgaacatc cactatctaa 660  
 tggtagactt tataccgcgt atttccctta aatgtattga ggcccccgga tttatcccta 720  
 tttttatgcc agttaatacc gagccacag aaacctcaac ttgacacaga tgttctaggc 780



agtgatttaa ttaaaaaact ttgcaatta aatgcataaa ctgtaaaaaa caaagcggag 840  
tgcaggccat taagcccca aaaaaggctt gatgaaggaa at 882

<210> 733

<211> 532

<212> DNA

<213> *Drosophila melanogaster*

<400> 733

ggcccgagca gctgacagtt gcgcttcagc attagaccaa agtagtttga ctttttagtt 60  
tttagccgcg aagcgaatag tatatacgtg gctctgtgtg tgtgtgcggt gtgtgttgtg 120  
gcagctgcac ttgcagcgag agacagaaat acatttcgta caaaattccg cctgcattt 180  
agtatatattc accttagagc gtctttgcc aacacacact tgttaccact cacacactgg 240  
caagcgagaa caagacacac acgtggccat caaagcggta tcggttcgcg tcgcgtttgg 300  
cctaaaattg taaacagttt tccttttaca acaacgaaga ataccagaag aagcaaagcc 360  
aaaaacgcag cttgcagttt gacgtcgacc gccaaagtgtt agctgctgcc atcgctgctg 420  
cagtcgcccc gacggtccgt tttctgtttg ggcccatttg ccgttggcca gctttcagtg 480  
gttcatttcc cattcgagtc ggcaacaacg agccggggaa gtcgcagagg cc 532

<210> 734

<211> 113

<212> DNA

<213> *Drosophila melanogaster*

<400> 734

ctgtggcaca agctaaagag agaggatgag agcgagcgcg atcgaagaga gagcgccagc 60  
tgctcccatt ggagcagcta acgtttccaa ttggaccagc tcaaagggaa ttc 113

<210> 735

<211> 1145

<212> DNA

<213> *Drosophila melanogaster*

<400> 735

ggctgatgca acacttgcca cacgttgcaa cagctgtttt agtctggccc agctgattcg 60

tattgttggc ttgttgccag agactgcgaa aatctcttgg caacatgtag ccacaacttt 120  
 tggaaaactc atagtgttgc taaacatgtt gggcgaaatt ttcacaccga tgcagggcaa 180  
 aaaggggtgg cttaaactgt agctggctgg ctggctaaaa ttagccgaac gatgattcat 240  
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 ttagatgtat aatttttctt catacattca aaacatacaa tcgcattgca ctttgcgatt 420  
 ggccttgaca ccctgacgtg gttccatttg gcgacactgt tcctgctttt atcttctcca 480  
 tggcgcaaga taaaatcaga aagtcaacgt gttgatcacc taatggccag agtcatgcaa 540  
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 tggtttataa atgtaaagtg tttttaagc attttaaatt ttaaataaaa catttttttt 780  
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 agcatttggt gtgttgatga gattaaaact gggaactggg gaatgggaat tgaatgccgt  
 1020

cttaaacaga gaacggagaa atgagaggct ttgtggacac ttaaaagtat gcggctctct  
 1080

tgaccgactt cagtcgctga cgtcgctgga aaatgcttgg tttgcggccc aaattattga  
 1140

attgg  
 1145

<210> 736

<211> 447

<212> DNA

<213> *Drosophila melanogaster*

<400> 736

gactagcgcg tctacgaaat gccgaaatca gtgttggtta atcctgcgaa tagtcacgta 60  
 caatggtaat gggatcagtt tcaatttcaa ctgtaactac aaattaatca taatttactg 120  
 tataacaatg tattttttcc ttgttaatgt aattgtaaat ctacaagggc atttaaatat 180  
 tacacaatta aaatctttgt tctggatatc acttcgaaaa actattgtat attacgaaac 240  
 accggtacat acgtgttatg atctgagtca tttaacacaa caattttaag ggtagatcaa 300  
 gaaaacgatg cttcaatttg aaaattttgt aatcgaagca atcaagttgt acatttttgt 360  
 gactgaatta gtagttatat tgttatcaca ttctatttat attagctaaa atgttaaate 420

gataaatatt aagttttcgg ggaattc

447

<210> 737

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<400> 737

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cttggcattg gcagcgaagt tggagttttc ctccactccg attttccgca cttcttcatt 120  
ccgtttttcg gggttggtgg gtggtggttg gctgggtttc actttccacc accgccgcca 180  
accgctcgct tttcattcgg tggaaaactg aacagatttt tggcgctaaa atgagaaatg 240  
gtgggggaaa attgcggaag gggctacaaa aaaagtgtct aattcactag aattttccac 300  
tgtaggccag aatttggtac attttccac tttacaacgg aacttttgat agcagttaca 360  
tacttgatta gattaaatgt cttaaaaata tatgtaggag tttagacttt tgtaataaag 420  
cttcatttcc atagaaaatg tttctatcaa gccgtatttt ctttaaacta ataagaataa 480  
taataacatg tttctaactt tatagccaaa aaggaatata tattctccta ggctttgggt 540  
ccaaaattaa a 551

<210> 738

<211> 885

<212> DNA

<213> *Drosophila melanogaster*

<400> 738

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cggcgctgcc acatccgccg atttttcagc tgtatggccc ggcgggttta atcttgataa 120  
atttcttggc tgtctatcga tatgatagac aaaacaagaa atgcgcccat atcgggtgtt 180  
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taataatctt tcaatgatct ggcactcact ccacgtactt tttgtaaatt tacatgtaga 420  
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taactagaac cgcagttcgg acagcttttt ggtgacccaa attctgttca aatctttaat 600

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 ttgaccggct ttatcttggt gtttttgag tgctgataat cgttatttgt ttgaatagtt 840  
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<210> 739

<211> 1083

<212> DNA

<213> *Drosophila melanogaster*

<400> 739

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 cctgtacgtt tttattttgc agtactcgac tttattgtta ttattatttt tcgcgactct 180  
 cctctccgct ttattttcta ctcatcgct accgtgtgta tttgcttttg cgcgactca 240  
 gctcgctgc ctgatttttt ttttggtgtg ctcttttcga ttactttatg tcatagcata 300  
 gcgacaacaa caactacaaa taccgatgac aatgataaca gcagcgaaag caacaacaaa 360  
 tgacaaggac ggcagtggtt aaaaggggac agacaatgtg ttgtgggggg tagggactct 420  
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 catacaataa ataccacatc aatttctgaa aaacacctcg atgcattaat tttgaaattc 1080

cgg  
 1083

<210> 740

<211> 1796

<212> DNA

<213> *Drosophila melanogaster*

<400> 740

gaattccctg caatacaagt acatttacct tcatattgtg gtaggatgaa cactcataag 60  
gcccactgta ccatgtagta gcatcaaaga cactagaata ttctagggtc tttggtagca 120  
tagtcttagg tatgaagccc atagtggcag agagaagcat atgatcatat ccccgtagg 180  
aataagaata ttattgttat ctgctctta cttataagct agcgtaaga gataagaatg 240  
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catttaaagg tcgagatctt tgggtactatg aacgctagaa agttcagatt atgtctgcag 600  
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1080  
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1200  
aatgggagga ccaaggacag acttttgtga cagctgctcg ccatacatc tgcactctcg  
1260  
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1320  
tcacacgaca actctctctt ttccattttc acgaatgtgc aactgtgcgt gcaatcgttt  
1380  
aattaacacc ccaatcatca aaatgccagc atcgatgtgg gcaattgcac ttagaaaagt  
1440  
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1500  
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1560

gagggtattat agtttttgcca tatacatttc cccagtgtga catagttggg aatgtaggta  
1620

aaaatccata taaatataat ccaatttggt tgacaggagt gtacggcaaa cagttcacca  
1680

atcgaccaat cagtaatgaa tggcaatgac cccacttctt aggtagtact ctcattaate  
1740

gaaatatgac tgttcgtttc tgccataaat atcccctagg ctggccttggtg gcatgg  
1796

<210> 741

<211> 819

<212> DNA

<213> *Drosophila melanogaster*

<400> 741

gctcagcagc tgacaaagga gagcggcgcg ctctcccgtg cgccgtcgtc ctccggcgat 60  
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aatcacatca gcggagcagg agaaggattc agagagagtc actgcgaagc cctcacttga 240  
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gccttcactt ttacttttcg gtctctgggt tttgtgtgct cattttcgtt atggcggttt 360  
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acgtgtttta agtttcgccc gccagcttag ccaagtcagg cggagtcgga tcgcactcgg 480  
attggagtag gattcgaaaa cgggctgttg tcgcactcga tggagttgcc tttagcctgg 540  
gggcaatgca gttccacttt cccgcttcgc gcatcctgca gtccttcat tgccaattag 600  
cggcgcagta attgtatatt gctgcaaata cgcaaatcaa ttgaatattg tctcagcatg 660  
cacatgtcta ctatctactt gtgtatztat accgtataca acttaaatgg aaattttggg 720  
ggaattaaaa tttaaatgaa acccaattgg cttggtaact gttgataaat aaattagata 780  
ggaaaacggg taaacaatat taatcgaata aaaagcctt 819

<210> 742

<211> 1003

<212> DNA

<213> *Drosophila melanogaster*

<400> 742

ctctcactct tegtctctg atcatagttg ttctggaact tttccgcagc caaatacctt 60  
 tgttggtgtc gccgctattc taaccgaaaa ttctcaagag gctgagtttg gaaataaagc 120  
 gaccaaagg ctggtcagca tggataagag cgcacgcaaa attataagat gatgtaaacc 180  
 actagtcagc ggagatcacc ccgtaccggg gttctggaaa gcctctaact agagtttcca 240  
 ctttatttaa ccacttacat agatacatat gtatgtatat tttgtgggtg tttgtaccac 300  
 taggggtgca aaataggagt tgcctaagtc ccaaactgac gtttcgcact tcgtttatta 360  
 gaataaatta ttttttata taaaggggga actaaatcgg agttgtatag tcttcacacc 420  
 gaacatcaat ttcattgtca tacggacgag attttagtaa taaaattatt atttttatac 480  
 attttaaatt gaaattatag atataataaa tcatacaatt tttaggtaaa acatttgtat 540  
 aaaatttcag atgcgtagta ttaaaaaaaaa ctgaaaaatc ataatccttt ccttaacttg 600  
 ctgtagctct ttgggtgtac taactttttc taaatgcacc cgatccaacc caatgagaag 660  
 atattttctt cgacacactc aagaaatcgc gcaaaaagac aatatatata aatatatacg 720  
 tatgtatatg tatgtatata acagcaaaca tttataagcc ctaaataaag agaaactata 780  
 taaattttgc atttgaaagt tgaactttgc ccacgtgcaa atcgatgata aaggctttgc 840  
 aggttcgca accaaagtcc acaattgaac aacatacatt taaaattttc accaacctct 900  
 cagttttctt tccaaagacc atcaattttc attcccaaag cctgggaaat tgcttagaag 960  
 ctggcaaact taacggccta ataagcgcaa ctttacttac ttt  
 1003

<210> 743

<211> 384

<212> DNA

<213> *Drosophila melanogaster*

<400> 743

gatcggggcg tcgcgataat ggcaatcgat cgatagtgtg atcgatagaa atactggata 60  
 agcacggatg cgcaaatgcg gccacactgt gggcagcgat cggcacgcga cggcagcgcc 120  
 ggaatatcgg tagtggcaac gccgttacga acggagaacg gagaaggata tgtgaagggt 180  
 caagatgccc cgtcgagatg cctaacgaca ggctgagacg ccaaggctga gaccagaagg 240  
 atgcaggaca aggagcggaa gaagttggaa ggagcggagg accttcaagg atcatcaagt 300  
 cttaaaactc cccacaaatc ttctgtagg gggagccggc ctaacataag ccgcgggtgc 360  
 agggcaaagc ggagagaacc gtga 384

<210> 744

<211> 1040

<212> DNA

<213> *Drosophila melanogaster*

<400> 744

cgtctgactg agctggagtt acagtcctac ctggataagt cttccacaaa agttatactt 60  
atacatttcc cagctatgaa tttcatttga tttttactaa atcacaattg tcaaattgca 120  
atgagatcgg ttttgctctt tttcgtctaa tatactatga agtgtctcat ggtaattcgt 180  
tcgctaagaa cttccaatca ccgaagtcgc actgtgggtc gttgggctct taaaatgagt 240  
gagcgagtga gcagcagcag cagaagaaga gcagtccaat aggagcgggt gtggtgtgtg 300  
tgtgtgtgaa gcgtgagaag gggtcggtt gccaaagcaac ggagacacaa ccaatgttgc 360  
cagagacggg atacagcgaa gtatgaagag agatagtcgt acagagaaca ctggcgatga 420  
gcaacaaaca caggagact acgtatttag cctaagggca tgaaatgtat tgcaggtttg 480  
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gcaacttcaa caacaccaac acccgaata ggcaaagcca acaaaccac aaaacgcaga 660  
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atttaaaagt taaaactttt aattaacatt aaatgtgtaa atgtgcagtt tatgactcta 960  
gacttcagtt aggcattctaa aaattgttaa accattgggc aaagaaccag tgagacttgg  
1020  
aatgataat tctattgcag  
1040

<210> 745

<211> 519

<212> DNA

<213> *Drosophila melanogaster*

<400> 745

ctgtgtccgt ttctatttac gtttcttttt tcaacggcta cctcgtgtg cgcgcgcttt 60  
ttgctttttc ctgtccactt tccaactccc cttcccccg cctgctgagg aagccagcag 120  
catgtgtgcg tgtgtgtata cgtgtgtagc tactcgccga agaagaagag aagaggagat 180  
gacgagagaa gcagggaat cggcgattcc ctttcaggct cacgttttgc cgctgccgcc 240  
gcgtctcgtt tgtttttatt tttgcttggt cctttttcga ctttttgttg tttgctgtac 300  
tttgtcatat aaggcggcac gaacacttgc atccgctccg cgggtgtgtg catgtgtatg 360



tatgcgatac gttgcgctct agattcggtt ccatttttta gcggcgactt tactaataga 420  
 tatacgtacg tacacatcga tgtctaactc aactcctccg atcgacagct attatgtggg 480  
 gggttcattt ggggtctggt tgggtgaatt ccgcggaat 519

<210> 746

<211> 597

<212> DNA

<213> *Drosophila melanogaster*

<400> 746

gtgcgggtct ttggagaatg tctgtgtgta tctctttggg tgtggaacgt atctgtggat 60  
 taaagaaaag ggctatgac cggtttaatg tctggaactt ctgctgagga tcaaaggaga 120  
 tgtgccacat caaacaaaagg gaggaatttc atcatgaatt gaaaatgaat ggggagaaat 180  
 acaaatgtag aataactaaa aaaaacgaaa tctgcaattg ctgcaaagaa tcaaacactt 240  
 cctcaatcga tgcaataagt ctccacctat tcaaagattt tctcactttt gaagtgtgta 300  
 aaagttgaaa agttcataac ttgagaaagg caacttcaat tcaattacct ctctctctct 360  
 ctctctatct ctttcgttct gcccgctctg aaaccaatcc gaaagatcat gtgcagccgg 420  
 tcaacaatgg catattaatt caatcaagag atcgcttatt aaacgtttaa acgtttaaaag 480  
 tgacaaacat gagaccccg agcgaaagt ccacagagat cactccatta tgcgactact 540  
 ggactgaact gactgaactg cactgaagtc ccgagtgacc caagaatatt ccgtgaa 597

<210> 747

<211> 99

<212> DNA

<213> *Drosophila melanogaster*

<400> 747

cgttatccca ccacgctagc aaccttcgca aaaacgagcg cgccgtactt accacttacc 60  
 atactacaac tgaaagtggg ggggtttttg gtggaattc 99

<210> 748

<211> 580

<212> DNA

<213> *Drosophila melanogaster*

<400> 748

cctcaaccgg tctgctgctg cggcgtctcg tatgcatgtc gcccatctgt ggcctcctt 60  
gtgtgcgtgt ggttgtgtgt ttgaacaatc gaggtcaatg caatagtggc aattaagaaa 120  
agtcataaaa cccaaaagtt ggttggttaa actatcttac aaaacaaact ataaaatgta 180  
caatagctta atgattggca ctagaattaa atacttatat gtattgttat caaaacatat 240  
gtattacaat gaaagtaata tgaattacta ctaaacgcca aacacttcaa tagtttttta 300  
aggtaatat taacacacat ttttcatttg aatttattaa ttttctcaat gtttacgctc 360  
tgatcttact gcttatgggt tcgccctcaa ctgtatgcat ctgcataagt gccgttgtgt 420  
gtggttgggtg tttctgtttg tgtgcgcttg tcattcggct cgttaaaaat gctctgccga 480  
cgttcgcagt tggcgttggc ggcttcttct ttaactctcg cgcattattt cgcaaagctc 540  
aagcctgctg cttcttcttc tgcaccccc cccctctg 580

<210> 749

<211> 1036

<212> DNA

<213> *Drosophila melanogaster*

<400> 749

atttgccgga tttgcttcga aatttattag ttcccggtgg gctggccaaa aaaaaaaaaa 60  
agaaaaaaaa gtggaaacaa taaatcgctg gatctttctc gccatacgcg catattccat 120  
atatattgta tttattttgt gtcgccgtgc ttttccttac gagccgaggc acatgcacat 180  
gcacacatgc tggcttttaa ttgaaatgaa cttaaattag cgcgagggtta ggcaaattga 240  
aagtaaatat gcgacacgaa cgagtatcgc gataaagccc gcgaaaaaaaa gaggggtggg 300  
agggtccgatc gaaatatgct tggagattag cccgaatagc aaatataact aactagctat 360  
gctactgtat tttatatctc tagtacatat atctccccga tcaaactcgt gcctggcact 420  
aaagcgtgaa gcacatagat aaccgcacct agccgtcca acatgcacag cagcaccatt 480  
tagttgctgg tgtgtccgtc gtcccaaagg cacataaaat aatcaaaca ttgtcaatta 540  
tcgaaggcat agcatttttt ccatatagac acacataaat atatacatat atatataagc 600  
gagcaactac gacacgctcg ttgttgcgtg tgttgctgca atcattatta ttttgaggct 660  
acacacacac acacacacac acagcagcaa tggcaacagc atgcatgtag atttcgcctt 720  
gcctcgtcgc tgcgagtgtt ttgaacttta ttcagggtcaa ttacaaatac attaaagtgc 780  
cagtgtaca cacagatact catggcaagc tgttgactaa aataatattg gaggtacac 840  
aaaatttaca ataacaacga gaacaaggcg gacaaggaga ccagagacta gatactagag 900  
accagagacc gaaaggcaag ggggtgggag gggggcttct ggggttgggc ctttggtagg 960  
agttaaacac ttggaccagt tcaaggagcc ttcgacttcg ctcatgagag tgggcgcgtt

1020

agtgggcccgc gcttgg  
1036

<210> 750

<211> 1091

<212> DNA

<213> *Drosophila melanogaster*

<400> 750

gttgccgtgc agccttttgt tggtattgtt ttgcggcggc aagtgccggt tctctgctgt 60  
ccgtctccct cactctcacc cggcttcgcc cagtaacaac aactaaagca caacaacacc 120  
cggcacttaa acagcgaatt ttcaagggga tgggggtatc tacaggagga ggaggagcag 180  
ggaactaagt gggaggggcg ggcgaaaaag gcgcggaatc tgagtacaat gtttttacgt 240  
tatgtgtgtc agtgtgtctg ccgcttctgc ccctttttta tattctttcc ttcgagtggg 300  
acttgacaaa tcctcagtga actgaatgaa gtgcgaccaa gacgaaaccc taaaaagtaa 360  
cagtaaatat tgcagcctcc ctcccacgca cacacacata cacacacact cccaaacgaa 420  
tacatgtgca caaacgtga cgagccctc tccatggaat gagtgggcag tgggtgtgtg 480  
gaatgcggtg gggtaggaga ttgggggagg gagatagcta gcacaaagcc accagcgaca 540  
accgcaccaa caacagcatg aaacacatgc cgtggaggcc tgcacatgga aatactccag 600  
taagtaagtg tgtgtgggtt tggggtcgat ggaatcaaaa tcagtgtcaa tgtcaagaca 660  
gctctaaaat aaaaaaaaaa tacataagga aaccctggc gataagattc ttggtattca 720  
gtctttaaga ggttgccttt aggcacaatg acaccatttc tggtgcaaca actagatcat 780  
ttaatattct tttcgaaaaa tgggtatttt gttacagaat acacaacatt tattgtgtcc 840  
ttttcattaa gtttctatcc tggaaggcgt ttaagctacc atccagtttt tcgttacttt 900  
aaagccgaag gttgcccccg caatattgag aataaatatg aaataagata ctataacttg 960  
aaaagacaac cgcattttct attttcggaa gctgtgaatt aaaacgaatc ataaaaacac  
1020  
tgcttttggg aaataacttca aggcattcta aacaacgtat tacaccggaa caaagtatta  
1080

caactatttc a  
1091

<210> 751

<211> 495

<212> DNA

<213> *Drosophila melanogaster*

<400> 751

ggcgtgagtt tgtgtgcatg tgtgtgagtg agcacgaggt gtggcgaggg tgaaaaaac 60  
taaaaagaga ggacggggag caggaggtgg agttggggtg ggagggccta tttattcgta 120  
tgtaggttgt gcctctccag ggaaaattct agaaaatgca tttccttttc gaatgagtct 180  
tagatttgat acagaaacag aaaaatgttt ctttttttca agtttttaaa agtgtttcac 240  
ttaccaagtg cgtgaaaaga ttaacattgt atttaattgg aattaaaaac atttccttgt 300  
atTTTTtaga aacaatatat ttaagtttgc aaactaaca tattatttat ttaaagggaac 360  
atacattaat aaaggggtat atggacaatt tctttagtca ttttgcttaa attttcaacc 420  
acataactgg gctaattttt tccacacatt tccattttac acctatttca aaccaacact 480  
tgcccaaat taccg 495

<210> 752

<211> 466

<212> DNA

<213> *Drosophila melanogaster*

<400> 752

gcctgcgctg tgacatgtaa acaacttctg cccggagagc ggccctctct ctttgcctct 60  
cagctgtttg gcgtcgcccg cgatttcggt cagctgactg ccgccgcacg cagcgcggcc 120  
gctgcgctgc tgccgcgatg ccagcgccga cattgacgtc tgcgtctgtt tgcattgcca 180  
ccacttggtg ctgtctgccg cattgttttc gcatttccca cgcattgtgac tgagcccgaa 240  
gcttttcccta tggcttgacc gccgaacgct ggtctacgca ccggttagtc cgataactga 300  
tggctttcag agccgtttgc aatcgtctga ctaacttaaa tcgcccaaat tgacaggccc 360  
gatatcgagc gatcccgct aagaccataa atgtgactac gaaagtgagc taggtcagtc 420  
catgctatat gctgacaatg aaattataat ggtaaattgg aaaaaa 466

<210> 753

<211> 556

<212> DNA

<213> *Drosophila melanogaster*

<400> 753

acggaaacca aaaaaatttg tgcaaactta gtgctggaac aaaaaacgat gactacgct 60  
tttcatcgat gggggcgaat atatcgcttc accgatgttt gaatgactat agcaactatc 120

gattgctacg atttttttttc gaacaaacaa ataattataa gggattttaat aaataaatta 180  
 aagaagggttc aagaataata taaaacttat gatagtttaa cgaaattatg aaatataaat 240  
 atagaaatag agtgtagatc aatgatattc ttctgataaa tcttttttat atcatatatt 300  
 ttatattcctt ttatttatta ttcatacaat tttatataaa ttacttcatt tgcactttcc 360  
 agaagaagca gtttcctatc ggaaaccgc agttaatgta cggcaatcgg ctgggtgcca 420  
 gggccattcc cccataggat ttcaggggag gcctccagca gaggaaccgg tgcacttggc 480  
 tgcgaacact ttggagagtc agcccgatga ccatgggcga taccatctcg gagctgctgg 540  
 cgcgaaaccgc accacc 556

<210> 754

<211> 925

<212> DNA

<213> *Drosophila melanogaster*

<400> 754

agctagagca catgttctgt cgattcaata tttttctoga tagctcgacg tttctcttga 60  
 tatcgatgtt gggcgatgtt ttgcaaaaca tcgcctgtag cgcttaacag cagtgggtgag 120  
 tatgtgagtt agcagctgct aacaactgtt gtattgggcg caaatttcaa aatatgctat 180  
 tgtactgtag ggcacttccc aaaaatgaaa caaattgccg ccttggtttt taaaccacat 240  
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 cgcaacacct ttgcctgggc gcgctgttca aattggtttg ggaatggggt ttctgattgg 480  
 gcttacacag gcgtaattag taataattaa cttaattgcg tagcgtattc attagtgggg 540  
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 attttgctgc gttcccgctg gctctctcct ttaaagtaat tatggccagt tgtatcggat 840  
 atttggtatg tatatatata tatatatata gttaatatat atgcaccggg 900  
 cctactggag ccgaatggcc atggc 925

<210> 755

<211> 1125

<212> DNA

<213> *Drosophila melanogaster*

<400> 755

gtggagagag aaataaattc tgctgacagc tggatgatga cgtcggccga ttggcttcga 60  
taaggttatc gaaaagtatc gatgcgccgc caggggtact agatccaaat gaaatacaat 120  
ttaaaattcg aatgtataat aataattaca gtgttgccca actaataagt ccagtaccct 180  
cattgttcat aaaaagcatg accattgaaa atgtatttaa aatttgtatt ttaagcttat 240  
atatttaggt agctatttat ttagtaagga aaagcagccg gttaataaaa caattttatt 300  
gagtacgtat gccttaaaat gtcatatcta accggtaaat tgtaacgggt tccagttcta 360  
actgttggtt aaagtgttca attttgagat ttagagattg gaatagaaga actaggatgt 420  
gtggacgggc tgtgcgcgat tgggttggtgc tattgaccat ggagaagtac attggtaaat 480  
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tggccaacgc acccgagcag ttcattctga aggagccgtg tgagctgcat gaggagattg 660  
aactgaaatt agaccgcatg gttgagttgt ttgcttcgct aaagtgcctg gaaaatgttg 720  
atttcctaga aacacctgtt ccatattcgc taacatctcc acaaagacg ctcacaactc 780  
gggactcttg caaatggaat gtcaaagggt tggatcagtt accttcgat aacatattta 840  
actaaatata aacaaagcaa aaaataatgc gtgtgataag gatctttata tatttttaag 900  
aaccaataaa acgacaattg aaaagctgtt ttacaacact atcataatca accaatataa 960  
tttcgtaaat acctttcagt ttaaataaat acatcatatg tatgtattgg attatagtaa  
1020  
aaaaaaatgg ggtgagcaga ttaccaggaa ctcatactcc tgtgggtttg aattaatgaa  
1080  
aataacttaa tgtaattaaa ggatcacaac gcgtcacaaa tcttt  
1125

<210> 756

<211> 1475

<212> DNA

<213> *Drosophila melanogaster*

<400> 756

gcgtgtgctt aaagggaaaa gtcgaataaa ggcattgtga aattatttaa aggattgagt 60  
acatatattc atttttcggc gtccacaata ttaaactgta atcttatagt aaatgttcgg 120  
cataatgtat gtatgtaacc ggtataagga agcctttccg actccatgaa gcatataaat 180  
taatgagcag gtctagacga tctggccttg tcagactgtc catttaaagg tcgagatctt 240  
tgggtactatg aacgctagaa agttcagatt atgtctgcag attatagagg tctacgccgc 300

gcaagaatgt tttgaacttt acataccag actaacgact accagccgcc caaatctgtc 360  
gcaaacacaa ctttcaaagc ttaccctatt ttattatttg ttttgccatt accttaacgg 420  
aacaggatat caacagggat attaatcggg catgaaacag tgacaggccc agtctgtcag 480  
gataataaac caggatacgg actttccgcc tcagcctact atggccacat atgccaacac 540  
aacgatgtca caactgtcct ttcgaaatcc gttgaatagt ggaaaaaatt catttccatt 600  
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gaataatgca tgcgtgggtg gtgcctgtgc tttcacttcc ccaattttctg ccaccccacg 720  
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1020  
ttccattttc acgaatgtgc aactgtgcgt gcaatcgttt aattaacacc ccaatcatca  
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aaatgccagc atcgatgtgg gcaattgcac ttagaaaagt gcacctactg aaacaagaaa  
1140  
taattttgga tcagaggagt agattcgtgc tgagaaattg gtattacctc atgaatttta  
1200  
aagaatatca cgcagaactt tgtagtatat atggaaacac gaggtattat agttttgcca  
1260  
tatacatttc ccagtgatga catagttggg aatgtaggta aaaatccata taaatataat  
1320  
ccaatttggg tgacaggagt gtacggcaaa cagttcacca atcgaccaat cagtaatgaa  
1380  
tggcaatgac ccacttctt aggtagtact ctcatatc gaaatatgac tgttcgtttc  
1440  
tgccataaat atcccctagg ctggottgtg gcatg  
1475

<210> 757

<211> 848

<212> DNA

<213> *Drosophila melanogaster*

<400> 757

cctcgtgcta attcatttta attcatttga ccgaagggtga atttgctgcg ggtgggagcg 60  
agagcgcgag aggaagaaga agcagggcgc acatgtgcac tatagtaatt cctctctcac 120  
tttgtttatg ttttgttttt gtaacgggtt atttcaattg ttgtagctta agctattttt 180

ttctaattgt ctatgaggaa gtgtgtgcaa gctcttttga gttgttttgt acttaggttt 240  
 ttttttttca atttttctat tttgtgcgaa ggtgtttcca tttgtaatta caattacatg 300  
 cctctgcctt cgagtgtgtt tgtatgtgtg ccccgtttgt ttgatgtaat catgggttac 360  
 aaaagcgttt tgctattgct attgctgttt caatttgtgc gataaggteg ttttgcctta 420  
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 ccacatatct tgaagttata aaagccatgg aaatgcatag cttaaacata ggaactgtag 720  
 atacatcgaa aatcataatt gtttcagttt gctgaagaag actgcccata gaatatgcta 780  
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<210> 758

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<400> 758

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 cgccagccgt tcgccaagcg cgcgtaattc aaagttatca actcgaaaca ctgtttcccg 180  
 gaaaaagtgc acaccgttaa atgtgaaata ttcaatcaag tcaactggag aatataaaaa 240  
 aatattaaaa aaaattaaag tgaactgcat tatacacaga ttgatcagtt taagtagtgc 300  
 cagccatggt cgtccaagtt ctgtgatgcc gcttttgggt cgtcctacg cctgggtcgt 360  
 cccgctttcc ttcgggacac ctgtggcca ccctctgat ccgcccacgc cgcccagtga 420  
 ctgactgaaa ggggatcgta ccgccctgaa caaaaactca aacgcgttac cttttttttt 480  
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<210> 759

<211> 646

<212> DNA

<213> *Drosophila melanogaster*

<400> 759



gttcaaacta gactgattga gagacggaga gagagagaga gagagagagg agtgagtga 60  
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 ccccaaatg ggccaagctt tgtggacccc tcgtctcac tcctcctgcc tcgtcactc 180  
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 ttttgcatc caacattttg taaaaattac gattggcact cctctgtatt ataacgaacg 540  
 agaaaatgat ttgcatcaga gaacaacgtt ttgggaagta cagaaacgta atttggttcc 600  
 ataaataata aagttaaaat ttaatccata accgatgtca gtttaa 646

<210> 760

<211> 93

<212> DNA

<213> *Drosophila melanogaster*

<400> 760

gggcgtggat tgaaatttgg caacgatcgc gtgagcagga gtaagtgaga gagggcataa 60  
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<210> 761

<211> 1064

<212> DNA

<213> *Drosophila melanogaster*

<400> 761

atccagctc atccttttcc ttcttgcgtt ttttgcctt tctacaaatc gagaatttca 60  
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 ttcttaatgc gtgcatgac gtagtctgac atcgtcacaa aataggtaaa ttgttgatat 180  
 agttttgggt tacaacacaa taaacaaaca tgcgatacaa catcgcagat gagctggctc 240  
 atcggttatc gatattctac caataaatac tgtaagcgta cattttaaaa agtacggact 300  
 caaaccattc attaacttgg taaaaaaatt aaaatcaaat gatttttgat ctgtgagaga 360  
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 tgcttacaaa aaggaaatac aatcacggct gctggatttg ttaaactaaa caaaagactt 480

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 ccttcgacag agacattttg ccattggccc tgaaatggag agggattttt ttttttaatt 780  
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 cctgcaggat tttcctctgt aattccgcag cgctgcaaa tgataccatt gagggagatg 900  
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 ggcacattgg cggcattggg ccagaactgc cagtgggagc cctcagggaa agtcctcgaa  
 1020

atctccttac gcacagccaa acgttgctgg ttgtccagcg ccca  
 1064

<210> 762

<211> 1345

<212> DNA

<213> *Drosophila melanogaster*

<400> 762

ggctaataa tgaatgaacg aggcggaatg cggaagagc gcagagagc gcaatgacaa 60  
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 acccacaccc ctagtccacc ggaaaaagaa aattcgtttg cggcggggggt gtatttttca 180  
 ccaaaaagag agtggtgca aaacgctaga gagagagaga gagagagaaa gaactgacgt 240  
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 cgagaagaag cagaacaaac acacacaaaa attcgacag tggagcagaa atcaagcttg 360  
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 tgccaatttt ggtgatcacc attttagcat attttttctc atttaataag tttgcaaaaa 480  
 aacctaggta cagtgaatg gttataatta ataaaggat ttacattgat cctttttttt 540  
 acataacatt tattaagaaa gtaacaaaaa atacatcaa actttataaa atgcactctt 600  
 aacaacacaa aaccatatat acatacatat gtacatatgt atggcccact ttactgatca 660  
 ttactgtgc atataagtag tttttaacaa gtggttttct tttgcttttt ggcaccgtga 720  
 gaaaaaaatt cagaactgcg gctgtctggc atccactgtc ttctattagc ccggtccga 780  
 atttttcacc accccaact caaaagtcac cagctgatga gctggtcac aatttctgtc 840  
 tctctctcat tttttggcgg cttttgggccc gaattttgtt tgtttgctcg taaaaataaa 900  
 tcatcgaccg tggaggaaac acgagcgatg agtgaaaaac tattaaattg gcaccatcgc 960  
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 1020

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1080

ggtaaaaatg agtgtcgagt tgaaggaatc cccttggtcg ccttaaactt ttggctaacc  
1140

cactttttat aataatgaaa aatttaacat tgttttgaac tcacgaagtt ttagacaaaa  
1200

acctgtttat agatgggatg ttcgttcata ctggaattgc ccataactca ccgcaaatga  
1260

atctttgact ttttgagaat gcttctactg attgattgac aattacttaa ttgataaatt  
1320

ggaaaagaat acaggggagg aattc  
1345

<210> 763

<211> 597

<212> DNA

<213> *Drosophila melanogaster*

<400> 763

ggcgttccca tgtgttggtc tgtatgccgt agtgtgcccg tcgcagcggg tttcacgcca 60  
aatctggcctt gtttcagagg tcaggaacta acttagtctg caggtgtagt tagcatgttc 120  
ccgcctacac aggttcactg aacaaaagta tttaaacata aaaatatcta ttttatagat 180  
acaatttttc ttgttcttat agtttttact aagaaaacga ttagttataa aaaatattat 240  
gtaagtgatg tcaaaaaaga aagtagcatg tcgttggtat tcttttcata attgagttca 300  
aggctaaaact ttttctattc catatatattt taataaattt atatcattac ccgaattata 360  
tttcaaagga aaaaacaggtt aggtaaaactt tcttctatta tatttttact ctttaaaaaac 420  
tttcctatgc attgtagtaa acgtttttaga ttgttttttg cctatttatt taaacataaa 480  
tcagcaaatt ctattttatt cataaatgtc ccaccaacca atgttcttca agacaatagc 540  
ctacagcact agtattccgt cagcatgtct gccacaatg ttggcgcagc agaattc 597

<210> 764

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<400> 764

atcgtgccca actcccggcc atcggttatg gcgtgtcctc gaaaacgggg aaaaaagtta 60  
caactagcag taaacgtgaa aaaggaccag caaggacgag aaaatctcgg cgaggcgaaa 120

gcgctgtggtt ttcattgtcg tcgtcggtcg cctttggctc atcaataaaa atttccttga 180  
cattttatga gccaaaggat tctgagctca ctttacttac tccattcgcc attcagccat 240  
tcgccgggat ggccaatata ttaaatacga caacggatta aacgctcggt tgcccttttt 300  
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gtttgcacac atttatggte tgtgaatgct ttatataatc gccatgggtga tcgaatccca 420  
caaagaagtt ctacttcate ggcaggggaat gaggggggaa aatttaatta agcctcttcg 480  
cgattgttta taaattcatg ttaatgatat ttggacagcc ccctttttcg gatgccgaaa 540  
gtatctgcaa ttacgtcgaa tcgttgggag cgaattc 577

<210> 765

<211> 940

<212> DNA

<213> *Drosophila melanogaster*

<400> 765

gtttgggcac agggttgtat ttcatttatt tttgggggga gtcgatacgc tctcttggcg 60  
tggtcgaacg gtcacactgg ccgagagata acggaaaatg tttcaaagggt aagtaaagat 120  
tataaacgta ttaagcttaa tactataatt agcttactat tccaagtatg tataattatt 180  
acacgtttta aaggcataac gttaagtgtg accaaattat atcaatggat tttgaatacc 240  
aatattattht attttatatt ttgagcttaa tatattaaat cacatatatt taagcctctt 300  
tatatatgta aatattttta ttttattaaa ataaattata tattgttttg taatatgate 360  
gagggctgcc acctgtgat aaatgcttac caacactttt aggtacgccg tttagtgtac 420  
gtaagttgag tacctagata tccagcgaaa tcaaaacatt gagtaaactg tggaaaatgg 480  
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gagagagcaa cgatgtgtgc ttcttcatag ccaccaactc cttgaagccc accaatcagg 600  
ttcacttaat ccagtacgag gaggagcagg gatccgtgca atcaaagggt aatatctggg 660  
atgatcaaag tatgagctaa acatacaact ttgaacaggt ctttgagcac gccctgggtg 720  
aagtttgga actaaatagt tgtccgcgta atcctcgctt gctggcctcc gtctacaatg 780  
tacaaaaggg agcacaagtg ctgaccaaag cggctctgtt tacgctgccc gagaatctca 840  
atcccgatcc ggagcagctg aagtcagagt acctgccgtg ggagcaggtt gaggtcctgg 900  
ataccgaagc actgggcgaa cgtgtgaagc catcgaattc 940

<210> 766

<211> 1131

<212> DNA

<213> *Drosophila melanogaster*

<400> 766

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actagtacct aaatatgtat acctgaagtg cgtaattgaa accgaaatag gcgctgaagt 180  
tttggagtca attaccatga gggcatgtca acaatacaat taccgaaagt taataatggg 240  
gatagccaac gcagctgttg gggtagcct tcgcactttg gaaccagctg caggctcgga 300  
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gcccgggtcca aaaccagttg gccagatca gcctcctaga cccatgattt tacatatgta 480  
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aatattaact aaacttttaa ggtacataac tcagaaaatt ttcttaaaca gcaataattc 780  
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tttaattctca tcaccagagc caccatatat gtatggtaat ctggggagcg aatatataga  
1080  
cagaatcgta gtttcaaagt catcctgact tcagcgacct aatgggatta c  
1131

<210> 767

<211> 687

<212> DNA

<213> *Drosophila melanogaster*

<400> 767

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ttcgacagcc gtctctcgt ctccactta tgctttttgt ttgtcatgtt ggctttggcc 180  
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caccgcgcga caaagtaacg agcaccagca agggcccaat gcaatttggt tatttgcaaa 300  
 tacaatttcg atttggcgcc agataacggg atccaagggc tcccgttacg gatgtcagtg 360  
 ccttggaag tcgaaaagga ggaacggaga gcggagaaat accggcaaaa catgcgttcc 420  
 cctgttgagg ttaaattgga agcgcggcct aaccttaatg ggtttacaag tttgccgcaa 480  
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 aattggaata taaacttgaa aagatgtggc tcgggaaagt tccacttatt agatggagca 600  
 cttttaaaaa accgattaga ataccgggtt aagcaaaaaa ggtagcttat tgcattgaaa 660  
 aattaaaatt aaaagttaatt ttgggaa 687

<210> 768

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<400> 768

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 acaatatttg ctttattcag ccaaacgttt tcacttaaac caacttggtt gaaattagct 480  
 ttgattattt gcattgagtg attactgac 510

<210> 769

<211> 1144

<212> DNA

<213> *Drosophila melanogaster*

<400> 769

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 agtgcccaga ggcacgctgg gtatatcggt tgggaggtat tcgcacccct tttcctcgt 120  
 tatggtttag atggttttta gtttttatat ttcgttagag ggctaattggc actcgttttc 180  
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atcgtttaat tagtttttca aattatttaa tacatataat aaatagaatg tttttaaatc 300  
 aaccgattgc taatgataat tttacacccc ttttagcgct cctcttggtta aatatatttt 360  
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 1140  
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 1144

<210> 770

<211> 113

<212> DNA

<213> *Drosophila melanogaster*

<400> 770

gatcatagta ttgtcaacat taatgctcgt catttaaata atggagatgt ataaggaaat 60  
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<210> 771

<211> 1166

<212> DNA

<213> *Drosophila melanogaster*

<400> 771

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ggaatgcaaa caagacgacg cgtgtcgagt gtttgtgata gaaacaaatt gtttttgaat 120  
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 gagctaacaa ttatttttgg tagccacgct tcgcgaagct gggcgcaaac aaaaaagaac 720  
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 caaaaaggag aatcaaatca caaacg 1166

<210> 772

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<400> 772

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 cgccggagcg tgcgcataaa ccatatattc ctctcgcttg cactcgctga gttatggcca 120  
 agagcgagtt aatggcacia ttgttgcatc tgaacagagc ggggcagctg catgattgac 180  
 aatcatgccg caccgcttgc acccgttgac tttgctgttg tttgtcgctc agcgtctctc 240  
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 actgcgaagc gcgtacgacg tgtgtctgtg ttgcgttgcg ttccaataaa aaagagaaga 420



aaagcgaaaa agtggtgccc tcggtgaagt ttattattat tatgattatt attattggcc 480  
 gttaccacgc gttttggcat caatcaacaa ataaacacac aagaaacatt tggaaatcgc 540  
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<210> 773

<211> 727

<212> DNA

<213> *Drosophila melanogaster*

<400> 773

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 gcccgcgacg aggaggcgt gatggtgttc tccacactgg gcggcgact gacagccatc 600  
 gatccggtga ccagcgaaat acgctggaca atagcagatg gtaattacgc gggcactccg 660  
 ctgtcttcac actcactgca cccctatttt ccggccacaa gtgtgggact cgaacatatg 720  
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<210> 774

<211> 1010

<212> DNA

<213> *Drosophila melanogaster*

<400> 774

atccgcatag aactccggac gacagtgaag taagtcagtg gaacggagag gcgctggacg 60  
 cccagacnnc tatatataaa ttaattgccg cacagaatat tcgtggcagt ttcgtttaag 120  
 cttgagccgt gcttaacggg ttttttttcg gggctaagaa cactggttgt gcacacagaa 180  
 aatgttgaaa atcgtattcg tagtcgcggt tctgtcgcta gtgaagtgtg cacaatocca 240  
 aattgcttgt gagttgattg aacaaatgtg acgaaaagag taataagtca aatataatat 300

gaaaaataaaa ataattatag ttcttaaatt aggattcctg ggaactacct ttttaactttt 360  
 aacttgtgtt taatattcca ttcatTTTTg cagtccttaa tatttttaggt tagtttatat 420  
 caattaagaa agcatgatct ttttagcattg tggatttata tgctaaattc actggataaa 480  
 tctaacatct aatgtttcaa ttgcaacagt ttatgcttcc ctatttgata agaactcaac 540  
 ctacaaatat ttcaagattc tatcaaaact tgtataatca taaaacgtgc ataaggaaaa 600  
 gtttactaga ttatgagaaa tataaataaa tgcgttctgc ttatattaac taattatttt 660  
 caacactcct tatcatgaac tcacgcaaatt tgaaattcct ctgactccca tgacagtttag 720  
 caaccagcca tgctcgggtc gaaatccaaa aatcgtggga ggtagtgagg cggagcgcaa 780  
 cgaaatgcc tacatgggtca gtctgatgcg tcgtgggtgg cacttttgtg gcggcactat 840  
 catctcggag cgatggatcc tcacggcggg acattgcac tgcaatgggc tgcagcagtt 900  
 catgaaacca gctcaaatca aggagttggg ggggtgcata gcatcagga gtacctcacg 960  
 ggattggcaa cgggtccggat gcctgagggt ggactcaaga acattgtgcc  
 1010

<210> 775

<211> 1426

<212> DNA

<213> *Drosophila melanogaster*

<400> 775

gtctggcggc tttttgcatt tgetgetgcg ctctatttga cttttacttt tcatttgcct 60  
 gcctgccacc gcgaagagct caattttgta gctttttgtt tgtttctcaa acgccttccg 120  
 tccataatat aaccactcac atttccgcct ctatgtctgc atatgcgatt tgccacgctt 180  
 gtacgtacat gcgattgtat togagtattg aagtattcaa gtattcgaat actgaagtat 240  
 tcaagcattc gagttgttcg agtatctgcg tattcgagt gaaaaacatc ggagaaagaa 300  
 gtgaattatt atcagggcgt attgttacat ttttttttta tcccattatt actcgagctc 360  
 ttgaaaaaga aaaaaaaaaa agatttttact tctatgccac agcgattgtt aggattgcaa 420  
 ttactctcga ttaatgtaaa ccccgctgat ctaccaatt tctgcagaag agaaattggg 480  
 ccaactttat tgtgaatcta gccagccaac cgagcagcac aatctgcgtt gtattacatc 540  
 tcagccaagc gttaaccgaa atcctaatta atttgttatg gcctggcgta taaaaatcag 600  
 gcgtaaatgt atatatatat atacatatgt acgtatctac tccctcgact tgaacgacct 660  
 caagtgaac agcgggatat aaatacatat atacatacat atgtacatac atatagaagc 720  
 cgaaatcggc ggtgcaagat aaagcgggct aattacataa cgtagcacc gcgtactggg 780  
 taagtgtaga aaccactgct ttccggccat ttctatacag ctattaaatt ggtcaattac 840  
 gtgtgtgtgc tcccatttgt tgtttttttt tcttttcgcc ttagccttta attttgattt 900  
 cccgaaaaat taagttttta ttgaatttgg ccatttcttc ggcgatacat ttcacaatca 960

tcatcaagtt atgtgtaata tggttattat atacaaatgg cgctatttgc tcatattatc  
1020

acactttaaag ttgcaaaaat atatatgctg cagttttgag ataacttttt tttctttgtc  
1080

gcttatttct gcatttgaca atgcaactgt aacagttttt gtgcataaga taacaattaa  
1140

atgttgtagt tccgtaaaaa aaactgctgc atagccatat ttatttgtga cttttaatta  
1200

ctgcaaaatg tagcgggttt catttctttt tttcgggtggg ttggtgaacg gggggcagag  
1260

ggcagggcgg aagagagcaa ttcgtggcgc tatcattaaa caaataataa atgcttactt  
1320

tggcataata tttattttgc gcgcctcgtt gtctgcgccg tcagaaattg taagccgttt  
1380

tttgagtgat aacaatgggg caaaaagcaa atggcaaatt gaattc  
1426

<210> 776

<211> 403

<212> DNA

<213> *Drosophila melanogaster*

<400> 776

tgccagcgtt tctctcgggtg tttgcttaat taactttttc acattttgca ccttaatttt 60  
tttttttttt tgggagttgg tgacaacgtc acccaggctg gtaatggtct gctcctccaa 120  
ggctgggctc ttatcttctg tagagaatgc aaagatgttc gtggaagcgg aaccaatgcc 180  
agggccacgt cagccgcagc tataggcaaa tcgcaagaag ccggcgataa ggcggcattc 240  
aatatgtata atacgacaat cccgattgtg aacgttgtca agccgggcat tatgtcatct 300  
tcaactgctg gtgcccccca gttctcattc aaattcgagt gcgtggatgc gtacctaatt 360  
gcagtcgtgg ctccgaggag ctgcacttgg gcaatgggaa ttc 403

<210> 777

<211> 1111

<212> DNA

<213> *Drosophila melanogaster*

<400> 777

gactcgctc tcagcgatgc ctctcgtct gaacgacttc tcgtctgctg gcgttggtgtg 60  
tcggtgtctt tcctcttact ctttctcttt tactgcctct gtgcctattc atgtgcctgt 120

ttgagtgtgc gggagcagag cgcgtattta gaatgggagt cgccaaccgt gagaggacag 180  
 gggcccatct cggagagcct ctctaagctt ttttagccaa aacattcgcg aattttttca 240  
 actttttgcc ggcgagtgag cctgcgtgag tgtgggttcc gcgcgtctta cacaaccgcc 300  
 ttggtgttag tgcagtctct cgaaaagctc gctcttcagc tctattgtca tattccaagt 360  
 gttggagcag cgaagcccg cagtcgcagc ggcgtcgcag tccttctatg ccgccacaat 420  
 ttctaataat ttcgaacttg atgcactaaa gactcactct aaccaacagc atatatatgt 480  
 tcttattagg tggggctgca attaacgcaa gtgttacaca ttttactcag ttacaaaaaa 540  
 ttattcagga tcagctttgc tttctaagct tgaaatgtgc ttggacttga tctacatatc 600  
 tatgtatgta ctatgcatgg aatctttaat aatttttgtt cccactatag attcttgtgc 660  
 ccacaaattg aatttcacct atacgaaaat atacctatag aatatacata ttactctacc 720  
 ctaggaatcg gtggccctga tataccacga cactaaggac tgcagtcaac gtagtaacga 780  
 agcgcgctag gaaagatcat atacataaat atatcataaa tcatatacat ataccgaacg 840  
 taatagcaca aaaaataaaa aattgcataa caaatctcaa aaacacctata tggtttaaaa 900  
 gaaaaagcat actaattgga aaagtacaat ctaaaaattg tgctgatatc ttcccattac 960  
 taaattttga tgggaatttc agtaaaatgt gttgctccag cttgtagtta gttggtcac 1020

ctaatttccg aactaaaata tcctattttc ccgaccttc cgaaatcacg tttactacaa 1080

atgacttttg gcagtggatg gcgtaagata a 1111

<210> 778

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<400> 778

ggttaagcag agaacgccg aaaataaaaag tgagggtgcaa tgtacagctg gattctcagg 60  
 caggcgaaca ttaccgaaca aacaatgcgt cctcgtcgag aaataaagca cgtcttaaat 120  
 taataataag cagcataaga acaacaaata ccagtatcct cagacgaaga tgaaccaagg 180  
 gagaaaagag agaacttaca aaagcacttg aaaaaaaagt aaacctgaaa accaccacaa 240  
 taaaattatt agacaacatg tgctgcgatc cttatacaat actttcaaga aagtatttgg 300  
 tattttgatt taagcataac agaaggaaat gcttatgtta tgttacttgt ttatactata 360  
 aatccagtgc aaacaattcg gttctctcag tgggtaaaag tgaaatgtat aggggtgctgg 420  
 catcatcatc tgctccccc tttgcaaagg gaatatctga gcacacctga gtgggctgga 480  
 caagcggatg acggaattc 499

<210> 779

<211> 371

<212> DNA

<213> *Drosophila melanogaster*

<400> 779

gggtcgttta tttggtttt ggagcgttga ctgcgtgttg tcggctgtgc atgatgatga 60  
tgacgatgat gatgcagaag agaattgatga tgatgatgac gacgacgaca acgatggaga 120  
ggagacgagg ctgcttgaat agatgctcaa tcgtttgggt tgaatgaaga aaagcatgtg 180  
gagtggcgag tggaatgaag tgaagtgcc atggagtccg tgtccatgtc cgtatccgtg 240  
tgtgtggcag agattggagc atgaatagga atgccaagaa ggagacgatg gaggaggagg 300  
aggaggagca gtagcaccag cgtgagtgcc acttgcggtg gcataatggt cttgttgatg 360  
tttgactaat g 371

<210> 780

<211> 1013

<212> DNA

<213> *Drosophila melanogaster*

<400> 780

atttggattt tcatattgtt ttttaagcttt tttttctgc acatcatgaa acgtgtcact 60  
ggcattaacg gttatcttta tggtttccgt tatgtcttgc gttcagttcg ttgctgataa 120  
ctctcctgca cagttacagt gcactatcga tatggaggac ccataaatac gagcattact 180  
gttatatttatt cgactagctt cggttaattga tattgcatat gtgaaacttg aagcaaagag 240  
cactatatta tgtttatgtc taaatataga tttcgtagtt gttaaagggt cataaaacgt 300  
tgctgtcgtt ataaagaaga gtgccccgta atcatatacg tgctcgtac caatgtatcg 360  
cattttgtca agtcatcaat gtttatgggt taagctttga ccttgccac agaggggtat 420  
aaatacacga gagcttgtcc caatcagctt acgaattgat ttgtctaatt aactgcaggc 480  
gcgcaataat gccagattgc acatggagat tgtgtttttg gttatactag aaaacaaaaa 540  
aaaaaatata tatatatgcc ccttgggcgt gtcgtttgtt ctccatttag actgtgatta 600  
gataccagg gggcagcaga tcggactcct tcttatcagc aggccgcggg gccagaaaaga 660  
tgtggaaagg tggccaggta tttggaaaca gcaaaaaata actgagagac gcacacgagc 720  
tcttccccac acacgcacac actcattcct tatcgcgca taagataagt ccagtgaat 780  
atggaaaatg actgcacagt ttttagtatt tctcctcatt ttgaacagcg aaactgaatg 840

ctagtcgtaa atttgtgctt tataatcgaa gctgcgagtg actcaagacg tgtcttgtga 900  
taagggcgat cctccctaata caagaccgtc tacttgaagt gggtcaggcc aaaagcagta 960  
gcaccagttg ggaaactagt tcgattttga tcaattggga ggatagcgta aaa  
1013

<210> 781

<211> 1063

<212> DNA

<213> *Drosophila melanogaster*

<400> 781

cactgggtggg tgggtgggtgc gcgcgcgaga gagagagaga gagaaagggtg agagtggcgc 60  
tttgcctcga ttggtcgaga aaaagcgaga aaaacgtcat gccgttctct tcgccgcaaa 120  
atcatcggaat catctcggcg gtcgccgttc gcctgtcgcc gttcgcagtt cgcagctcgc 180  
ctttcgcgga atcggattca caatcacatc cttctcgagag ttcgaggagt gcacaccggt 240  
ggtcgcatcc gcaaagtccg cgcttcgaaa ccgctatcgt aatcgcaatc gctattgcca 300  
gcgcaaccag aaatagaacc atggatatct ccgcctacca gcacatgaac atcccggatg 360  
agcacgcgcg gcaaagcgtc ctctgaggaa cctcacgccc aacgaccaag ggttgcggtgc 420  
catccagcgc atccacaatg ggtgaaacca agccagtgtg tcgcgggaca tcggagtgcc 480  
ggagtccacg ctgcggtggct ggtgcaagaa cgagcagaag ctgcgcttca tgtgccgcca 540  
gctgggcccc gatcacctgg gtctcgacac gccaccggaa aagcgcgcca agttcgagct 600  
gcagctccag ctgccaccga agttcgtggc actgcctcca aactacgagg agctgggctt 660  
cgggtgcactg ccctacagtc cagccgatta cccagtgcaa aatgaatccc tgctggagaa 720  
gcttagcctt gtggaatttg taaaaaagaa cgggtggattg catccggagg gtgcactgca 780  
tccgggtcag gccgcggtga tggactactc caacaacatg ctgcaccagc tgaatcttct 840  
ggccctgctc aactccaaac tcaccccaaca gactgcccga tgtcctggta gatgcacagc 900  
cgaaatcaga ggacaacaaa gtgattgatt cgcccgctgc ttccgaggat tacagcaaaa 960  
acaattaccc cttgcttgaa tggtaaaaac tgggcccaag gatccggcca agcgggtgaac  
1020  
ttcggcaatc agccggagca agtgaacgat aagacaacat gcc  
1063

<210> 782

<211> 118

<212> DNA

<213> *Drosophila melanogaster*

<400> 782

aattgacgct gccgctgcgg atcaacatgt gtgtgctgta agagagcggg agagcgaaat 60  
cagttctctc gttctcccg cgcacacat tcatgcaatg ggcattctgca gcgaattc 118

<210> 783

<211> 176

<212> DNA

<213> *Drosophila melanogaster*

<400> 783

cttttgtcat ttcaaattgg ctgtttaatt gcctaattgtt gctttgtttg ctcattaaac 60  
tgtaagtggc ccatatattt tctcatgaaa aacaaaaaat ccataaaagc ggataaaaaat 120  
gttcgccgcg cacattactt ttgttggttt ttggtggttg tgttcgtgtg gaattc 176

<210> 784

<211> 537

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(537))

<223> Area matching *Drosophila* Genomic sequence

AC006073.

<400> 784

ttaatthttgg acttaaactt accaatatta catttccttt tcagactgag aaataactta 60  
attcgattaa atgcgacttt attaattgaa actataattt atcagagggc gcacattttt 120  
atcgcaactta ccaccaatg aatcaaaaac tcggggctgt ctctttctac cgaaaacttt 180  
tggccaagaa agcgctggca attctgcaat tcaattggc ggccgtccgt ctttctttct 240  
tctcgggctc tctgcagtct tcaccttgcc actttgccc gttggaaaag taaacacaat 300  
ctgattgtat ggcttagata atagccccct tgtgcgccag tgtgtgtgtg tgtgtgtgtg 360  
tctgtgagtg tgttgccag ttggaggagg atggggctaa aaaaaacga gtgagaaacc 420  
accgacgcgc tgcattgaac atgttcgcc tcgaacgtca aacgacgagc atcgaacgtc 480  
gaacttcgaa catcgaacgt ggagccgacg aagagtgcgt cggattttac ttaccgc 537

<210> 785

<211> 720

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(720)

<223> Area matching *Drosophila* Genomic sequence

AC004299. Matches in area of ORF with sequence  
similarity to Human C-TAK1 gene.

<400> 785

gctgagcttg tgcaacagca gtagaaatag gagagagcaa tttagagaga gaccgaaaac 60  
aaacacacgc acaagagctc acctccacca caggtgtgta ggtgccactt cgctttttctc 120  
tctcgcgcac tctctttttgc tatgtatgta attgtgtggt taggtatatt gccctccctt 180  
tcacatcccc acatcgcttg ccgtgtgttt atttcagtgt caccggggag acagattagc 240  
tcttgtccgc ctgttgtcgt aaatatcacg cacacacgct tcccgccgc ccctctgtac 300  
atacatatgt acatacgtag aaatggaagt tgctagctgt gtgtttaatt cattttcgag 360  
gttttaaatgc gcaacaactg cgacttggtg tgtgttggtt agacgacaaa aaacaaacaa 420  
aagtaacgtt gagaatttag aaagcccaat gcaaacgaac gcacacacaa gcacttactc 480  
ctgtcgggtg gagctgcatt gtacttccga agccccaaga ccaatttaat aattttcccc 540  
aaactcacag tgtaagaaca ataaacacgc caagcgcact tgaaaaagaa ataagaaaaa 600  
agaaaaagtt gcgactttcg agcacaagta cttggcacca cacactcagg gaagagtgcc 660  
acgacaaaaa aatttagaga aaaaacccga aaaccgaatc acacaaacgg aggactatgg 720

<210> 786

<211> 599

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(599)



<223> Area matching Drosophila Genomic sequence  
AC004115.

<400> 786

ggcagaccgg taagtaagcc aaataactccg gaataaagtt atagcctccg atctctaact 60  
tccagcctga gactgcacga tgggtgtcctg agggacgttg agcagcaaca acggcgcaaa 120  
cacgagaata cctacacgct gcagcagcaa atagacatga ccaagcaact gaaagccagg 180  
gaggcgtcta gcaactcctc tgacacgccc gtacctccat cgacgcatcg cgcacagagt 240  
aatcttcaag cggagaagcc agcagtgcaa aatgaaggcg aggctttcag aggtgttcct 300  
caggggtggaa cgactaatca cgatggaagc ccgccaactg acatagcttg atcacaaata 360  
tgcccctaaa tatgcaccta ttaaaatcta agactaagtc ggggaaaaca agaatttcgt 420  
tgttcaaatg tacgcatttt tgaagatttt aagatttcgt cttaagaaca gttgacagca 480  
tctttacgct ggttgatcg ttttcaagtt ggtgaagcct tttgcgcatg ggaatataat 540  
taaacaacgt ggtaagaatc aatcttacca agcgaaataa gactgcaggc taacaaggg 599

<210> 787

<211> 581

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(581)

<223> Area matching Drosophila Genomic sequence  
AC004716.

<400> 787

ggcgaaggta aacgcgaagg cttccgaggc acgtaaaaaa aaagttcaaa cccgactagg 60  
acaacaacgc gaacaggaca ctcacacgca ggcaatcagc cgcacacgca cacagtcacg 120  
agtcggaaaa gcttgtaagg accacaattc gccgcactcc gaatgtgtgt taaagcttcg 180  
tgaaatcctg gggaaataat atcccgc aaa tacccttgca gcgcaatgtg aaagggaatg 240  
ggcattcata aatttataaa tttaaaaaaa aatcataata aaattagaaa aaatattttt 300  
atttataccc aactgcccta aaagtataat ttttgtatat ctttaatttt aaatatttat 360  
atttggttta gataatattt tcaaaaaatt aagagactta ttaccaattt tcatactatt 420  
tggtcttgca tattctttcc ctgctttaag tagaaagcag tctgcactgc tttttagttt 480

aagtagaatg atatattttt tcatagacca taagcaaaaa atcttttagc tgctaaatga 540  
atctacgtgt ggtaatgctc ctcttctcag ttcaaaccaa a 581

<210> 788

<211> 628

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(628)

<223> Area matching *Drosophila* Genomic sequence

AC005889.

<400> 788

caccaacgat tggctagttg ggagggggcg gtggatgtct aacattgcaa cgtgaccatc 60  
gcgcattgcc tttgcacttg taacatgttg ttggagtgcg gtttttttcg ttagcccggt 120  
ttttgttggc tttgttgctg ctgtaaactt gttcgcgttg catgccaatg aggcgcattc 180  
gacgtcaggc ggatttggtg acacagaaac tggattagag gcaacaacca atcaaccaa 240  
tgagtgaaaa aaaaaacaac ttggaacca aaactagaca ctaagccatg aaaattgtgg 300  
gaaactaagt atttacttta tgattcaata attatacctc ttaaataaac tggttttggc 360  
aacgtaaaaa aatttggttt cacacaaatt gtaatttgtg tacggtactt ttgaagcaaa 420  
gcaaaaattg ttcttttaggt atatctttt tctatttact aataaaataa ataaataact 480  
ttaaaaaaaaa atttgtgtgc taaaaccaa atatttactt attattatgg gtatgtaaat 540  
ttggtcagca cctgccact gtgcgcacgt catcggttgc atgccttgtg gttggtggtg 600  
cttctgcttt ggggggtttct tgggtttt 628

<210> 789

<211> 536

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(536)

<223> Area matching Drosophila Genomic sequence L4908.

Matches in area of 401AA predicted protein.

Sequence similarity to mammalian glia maturation factor.

<400> 789

```
ccccacagat acggtgagag aacgacaaga gagagagagg gagcgagagc agctgtgcga 60
tgccggcaga ccaatgttgt tgttattgtt gttgtttggc ttggccatct tttagttgtt 120
attattgctt tttagtagtg acctccgaca acaaaccgaa atcgaaacaa gttttaagca 180
acaacaacaa cagaaaaaaaa aagaactgca ttaaagcaga gatttatggt tctttaatca 240
aagtctgaag aatgcaaagg cattcctttg ccatgagtat tgcatttgta aaaaaggaaa 300
ctgaaaaaat ttgggattta tgtttttctt tttttgtcta acaaattttg tgctattata 360
atggaaatgt taatgatatt tgtggctctt ggggaaaatg ttttatatca attcatttca 420
cctgggtatc tacttgccgt agaaatcaaa tgcaataaaa aattacagtc aagatttagc 480
caattgttgc gtattttgag ccatttgtgc ttttagacac cggcttggtt gaattc 536
```

<210> 790

<211> 86

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(86))

<223> Area matching Drosophila Genomic sequence. Matches  
in area of ORF with sequence similarity to a mouse  
G protein.

<400> 790

```
ctatagtcgc tctagctccg ttctccgaag agagagagtg aacgaagaga ggcgaggaag 60
agagttccag gaaatcgcaa gaattc 86
```

<210> 791

<211> 573

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(537))

<223> Area matching *Drosophila* Genomic sequence

AC004306.

<400> 791

```
ggcgcaactt gttttcgatg ttgttggtgt cgttgctgct ggcttacgtt tttttttatg 60
cgccgctcgg gttggtaatg atcttcgtgc atgtgggttg gcgtcggttg tgttttttgtt 120
gctggtgatg tcggtggatg tagagaagga tgaggaggtg actgcgactg ttgcgttcatt 180
tagcggggca gaggcctttt tgggttttgt gtatggtata tggccagaag gagggcgtgc 240
gatacatggt ccaggtagac acatgacgaa gccacagtcg aactcccata acccgtcatt 300
ttactaattg aatacatttg tagtgaaaac gaacccttcg attcggtttt aaaatcattt 360
tttagagatt taattttgat ttttcagtta aactttgcac ataactgata agtggtacggt 420
tcatactttc ggagtttcac tgtattttata aacaaattca cccacatggc agcctcgatt 480
gggtggcggc atatcccgcc gatttcggcg tgggctgatt ttagccgcat tcgatttcca 540
tttcgggttc aagacttgcc cttcaacttt ggt 573
```

<210> 792

<211> 648

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(648)

<223> Area matching *Drosophila* genomic sequence AC006472

(71606-72257). NPS1077 lies in an intron of a  
gene at 62506-79351bp coding for a 1876AA protein  
similar to hypothetical genes from yeast and  
human.

<400> 792

ctccttacc c atgtaacgtt tcgccaacgt gtgcgagcga gagggcgcggt gtgtaatttg 60  
 ttgtggagca gctgcgacgg cggggccaaa gctgttgtct cgctcccccg ttcggagtga 120  
 ggccttgatt cgggactccg agctccggat caaatatttc aacagttttg gatccgtagg 180  
 gagggagggg gatattctagc ctcctagaaa agttttgcc ttcaaattag tatcataaca 240  
 aatacttggc ttagaatggc accatttgcc caacaatccc ctaaaaagta atcgtttggtg 300  
 ggacaaacta tgctacagat cccgttttct tgacagtaaa tggcatattc ctcaaaaatt 360  
 aaaaaaatg ataaaaaaaa aaatgataac aaaacagagt catatacttc agtattttga 420  
 aattctcaac aatctatatc tgccatttaa aaagcctgat aagttttcaa gttattcgaa 480  
 ctcagtagga ttaccaaatt ttcactgata ttcaatgttg gaatggaagt actaggataa 540  
 cccacggaat ttatagtaag aaaaggtcta ggaatttggt ggattcatgg agaaattatc 600  
 ggatagaaaa tccttactac ttaacgatag cccaattgag atatagct 648

<210> 793

<211> 463

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(463))

<223> Area matching *Drosophila* Genomic sequence

AC006092.

<400> 793

gtctgaggta ttaaatagtg aaaaaaatg tctgccgcgc cgaaaattga caaagcgacg 60  
 ccgccatgtc gcaacctata gccatctccc tctcgacgcg tgctcccagc accaccagtg 120  
 ttcattctatg tgtgtagtgc atatttcgag cgtaaatac tgttgaaaat ttaaaacat 180  
 tcaaacagtg gaaaatattg tgcacacatt atagggtttt cacatttccc ttgcggaaat 240  
 cggaaaagca agcgtatgtg tgccgaatgg aaaaaaccaa gacgcagggt tgcatttttc 300  
 ttgatttcga ggggtgcatt ctgtgtgata agcgtttttt tattctgtct ttaaaatgat 360  
 tgtagacttt tgtcccgta tgtttcgata atggatatta cgcagcggca aaattattat 420  
 ttaatgtctg ttattgagtc aatgaacttt ctgcggtttg gcc 463

<210> 794

<211> 519

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(519)

<223> Area matching *Drosophila* Genomic sequence

AC006073.

<400> 794

```
ggttcgagtt tgaaatgagg tctcaggagc ttcgtgttgc atcgaacctg ctcgatggca 60
tctattggtg agaggggCGT tctgtgttcg caataaccgg aaacggaaat catatttggT 120
caagttctaa tgccatcaac gattgcaatt aaatggccaa atgtcaattg tttcaagctg 180
actaagtgcg agaaggacaa aaaagtgttg tgcgaaaaga gacaggcgcc aaaagcctga 240
acctgccatt aaccgttaat gcacggatcg taaatcgaat tgaaaggaag ggtgtgtcat 300
gccggactta taaataaaat taacaaccag ccgggggaaag aggttaaggc ggaaatattt 360
gcgccactgc gactttcttg ctcgtcgtat tggTcccgTt gttttttgtt gcttgtaatt 420
aatgggcaaa caattacaaa aaaaaataa agggagtcgg ggcaagaaga atgaggcccc 480
cagtTgaatt taccagtatt aaaggcgag aagcaagTt                                     519
```

<210> 795

<211> 704

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(704))

<223> Area matching *Drosophila* Genomic sequence

AC007176.

<400> 795

```
atacacccta ttacgttta ctaagagagc gaccaacgCG agacgagTcc caaaatgagc 60
gctctttttg ccgaactgtt gaatgccggc tgcaaaagca acaatacaac tgcaacatc 120
accacccccca ttgcgcttat gtttttagcaa cccctaaaac aatatggcgg cgagtaaccc 180
```

acaacaaaat aaataaaaag aggaaacttc cccccagaaa gagcaacaat tttccacgcc 240  
 aaaatacact ttttttgcgc gcgctacagg ttgcgtgaga gaacgaaaga gagcgtggag 300  
 agagcagcgg agagcgagtg tcaagagaaa agcgcaacaa aagcaggaag cgataaacga 360  
 taaatacaca cagcaaaaac gtagcagact ttgcgaaaag aaatttcatt ccgtgtagat 420  
 aaaagataca ttaaaatagg agagtatatc ttaatgcaaa ttttttccca tactctaatac 480  
 aaaaatcaaa atattctcta tgccaaataa tatcgacttt tatttatatt acaaaacagg 540  
 ttcttttcag tgtactctgt gcgcatgttt ttttccaatt tgggcaacga ccgcatccaa 600  
 agcattacca ccaaacgttc tcttgggcac cagccttttt cctctgcttt gctattcttt 660  
 tacttagcat ttctctggtc tatgttgccg caaactttca gagg 704

<210> 796

<211> 307

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(307))

<223> Area matching *Drosophila* Genomic sequence

AC004423. Matches in area of 702AA predicted

protein. Sequence similarity to *Xenopus* DNA repair

protein XPGC

<400> 796

agttggctca gcaagaagtt ttttgcattt ttaggggttg taagtgggaa atgaaatgga 60  
 gaaggtgttg tgtgtgctcg tatgcagcta aaaaatggcg gcaaacacac acaccaaacc 120  
 cgaccacac agacaacaaa ggctaaaaga gcagctgttc cgacggcttt ctctagaccc 180  
 ggtgaatcaa cagcctccca catccgaacc atccacatgc ccgccccacc atccaattcc 240  
 acttccactt ttaacagaag cacacgcacc accggcacgt ggtgcgccat atgcaaatta 300  
 agaattc 307

<210> 797

<211> 412

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(412))

<223> Area matching Drosophila Genomic sequence. Matches  
in area of ORF with sequence similarity to Septin.

<400> 797

gtcgaaagtt aactgcggtt ttcgataacg atacgtgttt gctatcgcca ttgatgggtcc 60  
cgttcatggt atcgagccat atttgtccat tttatagcca aacgtttgat tcatttttat 120  
ataatgacat agtttataat catatataat ttcaatgtag tttttaatag gtttgctatt 180  
tctgtaatat atattcggcg aacttagata taacaataga acagttttta agttttaaga 240  
tcataaatct ttaaaacacg cgagattaag acaacgcgat atacgtttac gtaaaggatt 300  
tttttatgga ggtggagaac tttaagttgg cattactgtt caaaatcgcg accgacttaa 360  
catttgccga gttattgccc atatatgacc acaaagtgtg gaaaaagtca tc 412

<210> 798

<211> 478

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(478)

<223> Area matching Drosophila Genomic sequence  
AC004313. Matches in area of ORF with sequence  
similarity to potassium channel genes.

<400> 798

acagaagccg tcaactcagg cgaagtgtc gtagcggaac ggaatggaaa cggaacatgc 60  
acacgaatgc cagccgaagc aggagtacga agcatgccat cctgtcgtgt gtcagcgaaa 120  
gagaggcaga gagaaccaca actcgtctc aatgggaatg ggtctctccc tctctccctc 180  
tctctctctc tctccgcaca acgcctcctg tggctgttcc ctcttccatt tctacgagc 240  
gacaggatgt gcagctgccg actgcgactg catttgatt cgcgcccccg actccctgtt 300  
actggggatt ttgggatgca ttcccgtaga aagcatagcg atctgggcaa ttcgattccc 360



ggattgagca acaatccacg cggataacag gactacagga taataggaag tgggtgaaaa 420  
atatacactt tatgatttat gatccttaag cggaattta ccacattaaa catatttt 478

<210> 799

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(489))

<223> Area matching *Drosophila* Genomic sequence

AC004641. Matches area of 402AA predicted protein  
. Sequence similarity to *Xenopus* FLAP  
endonuclease.

<400> 799

atcgtgacgg tttgctcgcg ctctccgctg cgccgccttt tccgttgcac atgtgtgcgg 60  
gcgttattgt gcatgtttcc ggtggccgaa aaaaaatagn nntatagaaa acagaaacca 120  
agaataataa cagccatacg ataaacagtg tgccaatgtg tgtgtctgtg tgtgtgtgca 180  
tctcgcgtaa caacataatt gcatttatcg gatggcgcaa gcttcaattt aattataaat 240  
aacatgttca actttttata ctattttccc tgcgtcaaag tgggcgttgc aactgcccc 300  
ggaaaatcac gcgccccggt tcaaagttaa agtttgctgg gtaacgcaca cacacacaca 360  
cacaatcact cacacgcggc acacgcacat ttcaataaac taatggagcc tggctttggg 420  
tttggtntaa ttccaacca cttgagcaca cagcacacac agagaggaaa aatcaatact 480  
cgttatggg 489

<210> 800

<211> 558

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(558))

<223> Area matching Drosophila genomic sequence

AC004306(57408-57954). No good predicted exons in  
this area.

<400> 800

gcaagcacga tgaagaagga aagcgagagc gaccgaaccg cacaccacga gaaattccaa 60  
cagactgaga tggaaacaac aaacgatgac gccggcaatg ccgacgcaca aagcagcgca 120  
cagtggggcg atgtgcggtg gattcgttat ccattctaaa tagtaatacg ataggcatga 180  
acaatatttt caacaactct tttgcgaaca ctgtaagcag aatgacatgc atttttgcag 240  
aattgtaatt ataattaatt ccggcactaa aattaaatga tttttgttta gtttttaaac 300  
acgatttact tgattcgtaa atattatcaa gtattaatta attacttaag cgaatagtta 360  
aaactggtaa attagcccca aacaatattt taatggtttc aagcccacta tggccaagtg 420  
gccacacctta caaacgaaat ggatccgcac aaaagaagaa attgcaacaa acaggcggca 480  
aggcagccac cgctcatttc aagtcgcttt ggtgggtgctt ctgctggctc tctccgtttt 540  
tagtaattgg ggtgtggc 558

<210> 801

<211> 623

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(623)

<223> Area matching Drosophila Genomic sequence

AC001646. Matches in area of 724AA predicted  
protein. Sequence similarity to Mouse serine  
C-palmitoyltransferase.

<400> 801

ggccagttac tcggccagct gttatactga aaactgcgcg ccttcggtat ttttaaggtag 60  
ttatcgtatt ttcacatata atttaaaagg ccacattttg tggaacaacg cttccggttg 120  
tgttctctgc ttttagtact gccagctcct agcgaatacc tccaccatgc aagcagttca 180  
agccgcagtg ctgttttagta tactttctga gcgccagatg tcgcaaaaga gaagtcggtt 240  
tttgtattaa ttagattttc aaagaaattt atttaacta aaatggtttc tatttttagtc 300

acataggggt tcaacttaaa ttatttgaaa gcaattatta tgaaaaatat ataaattaat 360  
 atgtgatacg aagggttttta gtgcgagata agctaaaaaa aatgatgttt tatattccat 420  
 tacatattag aaactacaag ttttcagact taagacgtca agcattttcc ccttgagcat 480  
 taaaatctgg ccaaaactta cgcaaagaaa aattccgctc gccggcaata ataaattaga 540  
 ttaaaatgca caaagaaaag gagggaaaaca gaatttcagg ccacaggatt tcagataaaa 600  
 gtgccgtaag cggcaatgta gta 623

<210> 802

<211> 544

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(544)

<223> Area matching *Drosophila* Genomic sequence. Matches  
 in area of ORF with sequence similarity to U5  
 snRNP genes. *Drosophila* ESTs AA803646, AI518976  
 and AI108114 come from this gene.

<400> 802

ctcttggtg accgacacaa tgtggtcgca gcagtgtcct atgaaaatac acacacccta 60  
 agttaatacc aaaaatatac taaacattta tttgtccag caccctaaacc attaacatca 120  
 gtttttcaac agaactatgt taagcgcagg tgttaactta tttttatttt ataagtggac 180  
 tttgttgctc tgaaacttaa tcatcaccag aatcattatc atgctctcta gctttatttc 240  
 tcgtttaact tatgaaaacc acaaatatca aagaccaaca taacatagct ttacaccgga 300  
 aaagtatagt agatagtata gccaggagt cagctctagc tgtgttggtt atcgttatcg 360  
 cggctagcag cttgttttgt tttgcttaca cgacaaataa ataaatataa aagaagtatg 420  
 agtaatttaa aatcggacct ggatgaatac ttgctactgc agagtgatca gaagaaccaa 480  
 tttcaacgtc aagttgccac agctggaagt tccattttct cagcttcgac ccagaacaaa 540  
 tagt 544

<210> 803

<211> 201

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(201)

<223> Area matching Drosophila Genomic sequence

AC004154. In intron of predicted gene with  
sequence similarity to mammalian geranylgeranyl  
transferase genes.

<400> 803

gaatcaacta aaaacattta ttaccacct gctcatttat atgctgcagc cctatcagct 60  
gttcgctgcg gcgcccacta tcagcgcata cggccacact gcgggggcgg cagggatgcc 120  
aaaaattgat gtggataaca tagaaatatt taaaattgtg aaattattcg attttgataa 180  
gtatacttct taacggaatt c 201

<210> 804

<211> 524

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(524)

<223> Area matching Drosophila Genomic sequence

AC004766. Matches in area of 1442 AA predicted  
protein. Sequence similarity to C. elegans  
ZK1128.2 gene.

<400> 804

gtctggactg aaacggtccg ggaaacgagc cgaaagtagg tctgagtggg aaattaatcg 60  
aggcacattg agtgaagtgc acaaagcttc gccagctttc aggagctttc ccaacaattt 120  
ccccctatct tcccaaggcc aaaataaatt aaattttaaa atgttaaata cctgtttgtg 180  
ttgtgaatgt gttgctgttt ttggtaaagt attaaatgcc aatagttacc tgaaagtaca 240  
ataaattaaa ttcaaatcag tggaggtcaa cagtataacg aaacacactc aaagaaatca 300

caaataacga ttaactcact aataaaggga ctttatggat agacatataa actttttcaa 360  
gctttgttag ttatggtaag ttatggaaag gagcaaaagc tttataaaa gcttttcgat 420  
tagaaaaagt gttgccagct taaagtattt ataagaaatt tgaaaaagga tttggtagaa 480  
atcttttagag tgaaacatgc caattacggc taatacatgg tagt 524

<210> 805

<211> 621

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(621)

<223> Area matching *Drosophila* Genomic sequence

AC004361.

<400> 805

cacagcagac tgcgtcagg atcggtatctg tgtggatctt cagttcggt tagttttcaa 60  
taccaaacc aattccagcg gcattgaaag tgcgtgtggt ttgttgttgc cccatgggct 120  
ttttgtttta ggtcttggca aatgaaagt ttctcttcat cgatgctgca ggacattatg 180  
tttgattaac gaaacgcagg tcgagttttg gactgttgta aataaatttt acaaccttta 240  
atgctgccac ccagacaacg taaaaacgag aagcaattga aatgtctgaa ttatgtttgc 300  
tgaattattg aattatatag gtggtcggat actacatgct acatgcatgt aactgaatgc 360  
aagtacttaa ttacgtcagg agaaatttat tttcatttcg aaaaacgcaa taaatgttaa 420  
gcagaaactt caaggggatt taaggagcat tgcataaaca accaaaaatc ccttttagatt 480  
tcataaaatt tacaatatct ggtatgattt cgaagactga aatattgatt aaaagaattt 540  
gtacgatttt tcaatcgaac aatgggtcaag cccgatgcc aactcatttt ggcccggcag 600  
taccacacca ttataacaca t 621

<210> 806

<211> 569

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(569))

<223> Area matching Drosophila Genomic sequence

AC007185.

<400> 806

```
ctcaatgcga attgttttca agcgccggag agaatctata tagaggggct tctccgactc 60
gcttcgaata cgtttttctc agcgcgcgcg ttgcgcatcg aaaatcagaa aagctggcaa 120
gcgttttaaaa acaaattcgg caggtacaat tgttacatgt tttccctca gttgactatt 180
tcgtcgcagg tttttggcca gcggaaacca tcgtaataac cgttattttg ttatattcgc 240
gtaaatcggt gtttgttcaa ccacagaata cttgttggtta cgcatttcga aaatggaaat 300
gcaaaaattt ccaagcagtg aaaatcaaaa cgaataaaat atattggctt ctttcgtgtt 360
tagccgcgta cgtgtgtgtt tctgtgttag tgagtgcagc aagaaataaa accaaaaagc 420
aacaataaaa taaatagaaa acaaaagcaa aatcaaatec aaattcaaag gcaaatactt 480
gcaaagtaag ttgataatat caggagtggg ggggtgctagc atatgttgca ttattttgcc 540
cagcatttac atggttttca caatttctt                                     569
```

<210> 807

<211> 462

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(462)

<223> Area matching Drosophila Genomic sequence L49408.

Matches in area of 401AA predicted protein.

Sequence similarity to mammalian glia maturation  
factor.

<400> 807

```
cggcagcacc aatgttggtg ttattgttgt tgtttggctt ggccatcttt tagttgttat 60
tattgctttt tagtagtgac ctccgacaac aaaccgaaat cgaacnnnca acaacaacag 120
aaaaaaaaag aactgcatta aagcagagat ttatggtttt ttaatcaaag tctgaagaat 180
gcaaaggcat tcctttgccca tgagtattgc atttgtaaaa aagtaaactg aaaaaatttg 240
```

ggatttatgt ttttcttttt ttgtctaaca aattttgtgc tattataatg gaaatgtaa 300  
 tgatatttgt ggttcttggg gaaaatgttt tatattaatt catttcacct gggatatctac 360  
 ttgcgtagaa atcaaatgca ataaaaaatt acagtcaaga tttaccaatt gttgcgtatt 420  
 ttgagccatt tgtgctttta gacaaccggc ttggttgaat tc 462

<210> 808

<211> 233

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(233))

<223> Area matching *Drosophila* Genomic sequence

AC005750. Matches in area of 1813AA predicted

protein. Sequence similarity to Rat CPG2 protein.

<400> 808

ctctgagctt tactacgatt actatacagc tcttctctcg cgactttttg gactggacaa 60  
 ggcgtagcac attgaacggc agtggggtttg ggttttagtat cgaaccggct ttctacgaca 120  
 gcggattgga agcgcgagc gacaaagtcg ccgggtaata atgtgatata gccggctatg 180  
 ttcagcaggc aaaactgaaa taaaagtaat aaacaccgaa agcccccgaa ttc 233

<210> 809

<211> 525

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(525)

<223> Area matching *Drosophila* Genomic sequence

AC005269.

<400> 809

```

ccccagccgc gtgcacagcg cacaccaacc gacacactca cagacacacc ccaaagccgt 60
gtctgagtag ctgacgtagt tgttgcaccg gaagtctgtg aacnnngaaa tacttttaaaa 120
ctggctcgaa acctggcaga cgcacctcaa gctgaaatct aagacctggc cgcatatatt 180
tgcattaact ttggaagtct gactttaagc agacacggat ttcattaata aacgaaaggc 240
atagtgcgaa agcaggagag tatgggagct caacagttga cggggagcat tgccaggccc 300
aagaaactgg gagataacaa agatgagtca cgaaaagcag gcatttcaaa atcctcttaa 360
tcaccaccag tgaatgcatg taactcaatt aaagtcgtca attgattaca tttatttttg 420
gttgaaaacc cttctaggac acgggtaaat tctacctggc aatgcttcgc gtttcgcctg 480
taacaggttt caaagcaaaa aggggcttcg acacagagca cacac 525

```

<210> 810

<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(531)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence  
similarity to Rat fatty acid synthase gene.

<400> 810

```

gtcggggatc atcatgtctc gatttttctc ttcagttgtg gagcgagagc ttacgcaatg 60
gagcggagtg atgagcacat tatccgaggc aattttttan nngccgaaat gccgccgggc 120
cgttagaaat gaatatgaaa ccatctactt taaatatgat tgtaatgtaa aaacttgcac 180
caacactaaa aggatctatg gactccccga gcgtatggcc aaaatgaagg actccgatct 240
ggagaagttc gacgacaagt tottttagcgt ccaccagaag caggcggagc tgatggaccc 300
ctgcatgcgg atgctgctgg agctgaccca cgaggcgatc atcgatgcgg gcatcaatcc 360
cgtacagctg cgcggcagtc ggacggggccg tctacatagg cctgtccttt gtggagacgg 420
acaccgagat cccaacatg gagccgaacc agtatcaacg gctactggct gacgggctgt 480
gcgcgtgcca tgttcgccaa tcgcattctc acacgttcga ctttcagggg c 531

```

<210> 811

<211> 443



<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(443))

<223> Area matching *Drosophila* Genomic sequence

AC004758.

<400> 811

```
ggctcgcccg aagagagccg agtgaaaccg agcgcgccacc cgaatgccga aaatcaagta 60
tacgtcgcta cgatcggtgc tcaccgcctt tcagtgtctt nnncaataac aaaaataata 120
gcactgctaa acggaaaaca gaaacgttcc tcttctaacy gtctcactga gttttgtaaa 180
ttgggtcattg gctgtgcgaa aaggagagac agagagagaa ccagagaact gtcgcagcga 240
ttgcgattac ggttacgcgg cgcagtgaaa aagtgaacaaa gtttaggcgg aaaacacttg 300
cctctgggtcg atttgcgtgt ttggacgcgc gactccctca gaacttgaaa aataaaggaa 360
aaatcggaac ttaagcaaaa aagtgatcac acatcaagaa gccaaacttg attacgattt 420
gcggtcgaga aggacttata aac                                     443
```

<210> 812

<211> 498

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(498))

<223> Area matching *Drosophila* Genomic sequence

AC005894. Matches in area of ORF with sequence  
similarity to metalloprotease genes.

<400> 812

```
gtccagcctt tcgaagggag tgcgtgggtg ggtgtgtgtc ttttttatta aatgtttgcc 60
gtggtgggcy tggccatcac tcgagccgct agctggcaca tcctttttat taaaattcgc 120
agtctataaa ttgctaagga gcccatgtgg gatggggcggg cgtgggattc caatggccat 180
```

gggactgcga tgagcggagg aaatggggta tgactggcgt acatgtttca aaagacgtgt 240  
 gtgtacccaa gacttttatg agacagcaac aggaaatgca tggaaatggt ctgggctggg 300  
 ccgcccgcg agaaagggga acgtgtgttt ctccaaatgg agcaggtcaa aaaacgaatg 360  
 tgggaagtcc gaagaatgat tcagaaactg aaaatatacg aataattatt acaaaatctg 420  
 ccttgcataa aattacttat aactttgcac tagttgcatt aaaaaatgaa agatagtcga 480  
 ccgaagtttt taagcttc 498

<210> 813

<211> 320

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(320)

<223> Area matching *Drosophila* Genomic sequence

AC004564. Matches in area of ORF with sequence  
similarity to Immunophilin genes.

<400> 813

ttgtaaata agcgaaaagt caaagaagaa gcagaaacca gcataaaaaa tgtttgtgcg 60  
 ctggcggctt gtaaaagtat gtgtgagtc gtgcgtgtgt gtgtaggcag cagacaactt 120  
 tgaagaagaa gagacagaat acaaaaacgt acggagttcg aaaactccgc cagagaagtt 180  
 tgtctacact gtgcaacaaa ttaggtggga atgggatgtt atcttatcag gttgggtgta 240  
 ttggttataa ttggcggcca aattgggtta ccaaaaaatg tgtttaacaa tcaggttaca 300  
 tctgaaaatt ataataaatt 320

<210> 814

<211> 429

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(429)

<223> Area matching Drosophila Genomic sequence

AC005716. Matches in area of ORF with sequence  
similarity to follistatin genes.

<400> 814

```
ctccagactg tctgtttggc agtgcgagtg tattggtgta cctcctctgg tgtgtgagtg 60
tgtgtgtgtg tggaccctga gtttggcaat gcagttgccg aggnntgcc ttgttgttgc 120
tgcggcgctc cttgcatttt ttcgcgctgc tgctcctgta ctcttgctgc cccctttgt 180
tatttgtgct gtgccccaaa gacatttcag cgagcctcga ggaatccaaa gcatttggat 240
acgaaaactt tgggtacagt aaaggctgct gggttcccg caaacagtgg aatgttatgc 300
cttagccgga tcattcgca tcggtgctga aatctgcggc tcattatcta agtatggcca 360
gggtgaatta acactttcac cgcactgaca gaaaaacatt ggccttttta aggggaacca 420
aataataat
```

429

<210> 815

<211> 71

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(71))

<223> Area matching Drosophila Genomic sequence

AC007180. Matches in area of 217AA predicted  
protein.

<400> 815

```
ttccaacggc tcgagacagt ccgagcggca cttgcaacat gttgcaagtt cgtgtgtgac 60
ttcgggaatt c
```

71

<210> 816

<211> 75

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(75)

<223> Area matching Drosophila genomic sequence

AC004758(92123-92197). In intron of gene at

87648-113518 coding for 945AA protein similar to

Human retinoblastoma binding protein 2.

<400> 816

aaactataca cacacacaca tacgcacgca ccgccagtca gtcaggcagg cacacattgc 60

ccacccactt ttact

75

<210> 817

<211> 116

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(116))

<223> Area matching Drosophila Genomic sequence

AC001661. Matches in intron of Drosophila wing

blister gene.

<400> 817

atctgggtctg aagtgcagcg cttgcgatca gtctgtgttt gacggtcggt tgcgtaggaa 60

gcaagacacg cgacgggtct cgagtgtctgt gctttgcctg tgcgatggct gaattc 116

<210> 818

<211> 512

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(512))

<223> Area matching Drosophila Genomic sequence

AC004758. Matches in area of ORF with sequence  
similarity to Human Retinoblastoma binding  
protein.

<400> 818

cacagtttct tatcggcgga ggtcgacgaa tcggatctcg tcttatcgcc gaccccccg 60  
ttattgtttc gtttctgtat tagattcaaa atcagttcgg tgataggcgt tactcagtct 120  
agccggcgcc gcgtttaaca ctatgccggt tcaggacag gacttgaaac atccatagga 180  
tccatcgagc atatacgcaa ggttttctaa gtacgctttt ttaattaatt ttatgaaatg 240  
tggttcaatg cagtgcgaga tgggtttttc aagacttcgg taagctaaaa aaggaaagt 300  
tggcattcta aaagagtggc ctagaattat attctaagtt attaataataa ggtaagtga 360  
ctcttttatt gtttttagaa tactgggtgtg tgaaattaaa ccttggcttt aagaatttga 420  
atttgataaa tatatttaaa ataactagta gacataagta tttagttaac ggtaatgcct 480  
atgaaatggt gctgctcact caacaaccac ag 512

<210> 819

<211> 54

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(54)

<223> Area matching Drosophila Genomic sequence

AC004334. Matches in area of 433AA predicted  
protein.

<400> 819

gtctgatgca gctgatctga tttattacca gtttactgga tcactcgtga attc 54

<210> 820

<211> 557

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(557))

<223> Area matching Drosophila Genomic sequence

AC005149. Matches in area of 424AA predicted  
protein.

<400> 820

```
cacgaaccca agaaacaggg cccgaatgga aaaagagaga atcgagagaa tcgcgggctg 60
agaaatgcgt agaaagagac aagcgacgag tagcgagcag tggcactaaa accagcttag 120
tgcactgtgg aaaaagtttt aacaattctt aaatatctga agagtaaggc tctaattttc 180
tgtaaataac aacagtataa agctatgtgt ttaaataatac tagataaata atggatgcat 240
ttacatatct atctgaattg gctagttact tatattcggg ttgaaaatag tacaaaattt 300
ctttcagtgaggagaggaa ttaaaccgaa ctcaacccaa acccaaccgg ccgccagtcg 360
cacgctgcta aatggacgga tgggcccgtg gacggactta tatggagact ggcactggcg 420
gaagcgtggg aacgtgcatt cgtacgacga gttattggca gttagagcgc tacctgttta 480
ccgacccgac taccgacta ccaccgactg cttttttttt ttggcccatc gaaaaggtag 540
ggtacaattg gcccggg                                     557
```

<210> 821

<211> 202

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(202)

<223> Area matching Drosophila Genomic sequence

AC005333.

<400> 821

```
tggcaggcct ttgcatttcc acttgtgcgt cacgtgctcc tggctgttgt tgttgcattg 60
aacttgaact agtggcaaag ttgttgcgt cgttgtgggt gctattgcac ttttgctgtt 120
```

cttccgacat tggcgccctat tttgccggct gtttttggct ggcattcggc gcgttttctc 180  
accgcgcacg cgctctgaat tc 202

<210> 822

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(534))

<223> Area matching *Drosophila* Genomic sequence

AC005334. Matches in area of 309AA predicted  
protein.

<400> 822

ctttgtgcgc tgaagcagca acaacagctg gctatctcgc tctagcaacc acgtcagacg 60  
gcaaacgtca attataagca aacaaagcga cgttgcctca tttcacgaaa gccgcagcga 120  
ggcagagcga gagcaagcga aatggcgctt cgcggaacg ttgccaaact tcagcgtcga 180  
ctgcgtgttg ttctttagt ttccatgctt ctttagtgca tggaatttta acatgctgta 240  
ccaccaaccc tctttacggg ggatggggga ttataataac gcgctgctga cgtcgctgct 300  
cgcattttcc accttctcgc attcgtattg ttgcaaagga aatgggccct atacaagaag 360  
tttatctttg aatatacata catacatatg tatatttaag tacatgccgt attccgtgct 420  
taaattgagg cacaggagga gaacatatct tgggggccat tgaaattcaa taaattaaat 480  
gctctagtga ataaataaaa gcgtatttta agtgggaaat aagcaatgcc attt 534

<210> 823

<211> 438

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(438)

<223> Area matching *Drosophila* Genomic sequence

AC006421.

<400> 823

cttgtccttc tcagaacaac agttataagc tcagtctgcg ccggcagcgc tgtcgacgtc 60  
gactgcagca gcagcgccgc tcatttgtgc gcttaatgac gtcattatTT ttattttaaC 120  
agtgccaaagc aaattgcata tataccgttg ctgctcctgc gcagtcggcg ctctgccggc 180  
gtcgctgcac cgccagtggg gcttgggcta ggggggtggg gagagagcga cagagagaga 240  
gccagagcga gagagaacga gaggcagtga gtgagagaga ccccggtcgc tttctcgctc 300  
gcacccgctg agctgggcct gcggettcgg gttcctcgcc ttcgttctgg ttgcttcgtg 360  
tttgccgatg tgatgctgct gatgttgctg ctgctccttt tgctgtgcta cttatgctga 420  
tgattgcgat gctggggg 438

<210> 824

<211> 524

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(524))

<223> Area matching *Drosophila* Genomic sequence

AC005443.

<400> 824

ggcacggcat cctttggcgc gagagaatgc gacatccgga gagccggaga gcacgaccat 60  
tgagggctct gttcgggaga gctgacgcct ctgtgtctaa ctaaacggaa gaggctcaag 120  
gcgtcgcatg atacttcac agtcattca atttcaagac tagaaggta aatagatctt 180  
tatttatatt atgattcaat taaattatta attttatatt tcaaatttt aaaaaaagc 240  
cttatggta tgccttaaa atatattatt tttaatttaa gttataagat agaaaatctt 300  
atatggagtt cttaaattatt attcataaaa cgtaagtggg aacatgtgaa ttagttaaac 360  
aataagtggg actctctgtt aaataaatac attttgcct gaattggatt acaaaatcac 420  
tcgttcttca aaacacctca aaatcaattg aggtctccat ccttttcggt atgccgcctg 480  
aatcgatttt cggcaattcg cgccaaatac ccgcaccgac aatg 524

<210> 825



<211> 492

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(492)

<223> Area matching *Drosophila* Genomic sequence. Matches  
in area of ORF with sequence similarity uridine  
phosphorylase.

<400> 825

```
gtgcagttcg cgtaccagca cacacaacac acacacacat gcatgcgtac atacgcgcgc 60
gctaagtga tacatacata cgtatgtatg gacgtacagc gtgctgagac gtacagtcgc 120
cgctaattgg gaaaactggc tgtgcgaaaa agcaggcaga gagcaagagg aagagagagc 180
ggccccgggg tgggggtggc acttcaactt tgccggctgc acttggcaac aagtctgcaa 240
gcgactgcca ctccaattga ggggtcaagg cagcgctcgc gcatcagctg ctgcgcatgt 300
gtgacgacca cgacggcggc cgtgacgcca cggtggcttc gcgaaagctg cgctccgagt 360
ttctggagcc cgcagtcgga tgggcaagaa cagagaaccg gttgcaagcc cggtttggtc 420
actttttgcg cttctcatal ttaagtgcgg tgcgatcgcg ggtcgtccaa ttcgcccgat 480
ttagttaggc ta 492
```

<210> 826

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(535)

<223> Area matching *Drosophila* Genomic sequence  
AC005889.

<400> 826

```
gtccagtcta caaacagaaa gaatttcaac ggcagcgcgc gacaataaag taaacaaact 60
```

gaaattgttt tccttcgtca tattttcctt tctcttgtct cgtctgacac ttgttgaaac 120  
 tatttcaagc gcagaaatca acttaagccc cagctaccca gctcatcaat aacaacatcg 180  
 caacatctct ggcgctcaat taacatgggt ttgtgaaaat ttattgaatc ccttctttaa 240  
 tgaagtgccca tgtcccgaag gctgttgctt cccttcacagc caaacgtgct catcgattgg 300  
 aaacgggtcta tggccgttta gtttgggtgc tgataaacct agattcagaa tctttagata 360  
 tatatcttta gatttatact ttcttgtgta attgaatttt cttaaattctt attctactgc 420  
 ccaagtaatg aaaattccca acaaataacg aaggcaagga tatcatcgct ttcttggttt 480  
 aatcaatcaa acggcaaacg gactggaaag aagtgatatc agaaatctgt aagtt 535

<210> 827

<211> 47

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(47))

<223> Area matching *Drosophila* Genomic sequence

AC005130. Matches in area of 826AA predicted  
 protein. Sequence similarity to Helix-loop-helix  
 genes. *Drosophila* ESTs AA949050 and AA817663 come  
 from this gene

<400> 827

gcttagccat attacttggt tgtatttgca aaagttgtaa tagattc

47

<210> 828

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(551)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence  
similarity to Rat fatty acid synthase.

<400> 828

```
atacgcccgt tcaattgctg taaaaggata gttctcacca tcgcattgcg agttttattca 60
ccggtagatc aaccgatctg gagagactat gaaaataata cttcaatgaa cttgagaaat 120
cacgccacct tatctcacta aacaaatggg acacgcgtcg agctcgtgtg tctgtgtgtg 180
tgtgtgtgtg tatgtacaca cacatggcgg tggggacttt tggggctgcg tcttgactat 240
acgccgctct ctttggcacc cacctccgat ttggatgccg actacaatag caaaacataa 300
acatagaagt ctggccaagc caacggccat ttgatagata agcttgctgc tgagtcgccc 360
gatttttacc ggcaatttgt agtggctaca cgcggaaaaa taggggtatt atatgaaaat 420
ggttcctgta aatatggttc catatttata tgatcaataa catttgaatt tcaaagaact 480
ctacggctac acgattcgaa ttcgtttgtc tgagtggact ggttatttgc tctgtgtgtg 540
accgtcatgt c 551
```

<210> 829

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(100)

<223> Area matching *Drosophila Drongo* gene.

<220>

<221> intron

<222> (101)..(146)

<223> Intron in *Drosophila Drongo* gene.

<220>

<221> misc\_feature

<222> (146)..(499)

<223> Area matching *Drosophila Drongo* gene.

<400> 829

gtcgcgctat tttgtttcga gtgcgctgtg ctgtttgggt tcgttccgtt tcgtttcgtt 60  
gttcgttttc cattcgtctt cgaatccgca ctgcaaaca acaagaagag ggggaagcag 120  
caaaagtggc gagtgcattc gcagcgtcga aatttcaatt gaaatctgaa atctgtgtgg 180  
caattgcagc ggcactcggg gtaaatagat tgaattgaag cgaaattctg cgagtcgaag 240  
aagtgaaaag taaacaataa cacgggcaat cggaaaagtg gttttcgata aatcgcaccg 300  
cacacacaca cctgtcagtg tgagtgtcaa agtgagtggt tggagtggtc gtcgaaggag 360  
aggaaagggtc aagccaaaat ttgcgtaaag aaaaggaaag gaaagcttag aagaggggaa 420  
aggggaatta cgtcagttcg cattccgata aaaattttga ttccttaaac cgatcctgat 480  
agccagcatt acgatggca 499

<210> 830

<211> 580

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (580)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence  
similarity to Rat fatty acid synthase.

<400> 830

gcttaaaccg actccgccag ctccgctcat tatatagttt cccttctttt gttgaatcat 60  
tcgatttcgc acatcgtacg agtttctcgg cgaataagaa agcagcttgc cgttcgcgtt 120  
ggctcagtggt gagtgtgtgc ggcctatggt aacgcgaatg gtgttgact gttaacgcga 180  
ctgccacaag ttgctgttaa ctgtcaaccc agtcgctggc ttcaaagcag caagccgccc 240  
ataacaaata atgctgtgtg ccggtatatg cgcagtcaaa gctccgactg cgcgggcatca 300  
cctgatttgc aatttctaca ccaactttcc accagctgaa cattcaaaca aaaaacctaa 360  
tcgcccggca tcccgcgcca gagagcgaaa gctctgcgct tcggggtggt aaagagcttt 420  
tgcttaacag cgaaggggtg gcagacaagt tgcagatgcy gcagaatgat cacaatttta 480  
aaatatttaa tacacgaaat gagttatact aaccagactt tcgcatcctc ttctccaatt 540  
gcagccccta cactaaacct gtgcaagccg tggaccaccg 580

<210> 831  
<211> 256  
<212> DNA  
<213> Drosophila melanogaster

<220>  
<221> misc\_feature  
<222> Complement((1)..(256))  
<223> Area matching Drosophila Genomic sequence  
AC004722. matches area of 834AA predicted  
protein. Sequence similarity to bromodomain  
containing proteins

<400> 831  
gatgagatgc caccgagcgc gcgattggtg gaggtcacca tgttttgcgt cggtttctgc 60  
agggcggtcg acttcctgag actcgcttg ttggcggcac tgaatagggt gcgcgtcgag 120  
ttgaggctct gcagcgaggt gtccagcttg ttgcgaatcc tgtccagatc ggcaagcatt 180  
cgctggatat ccacgctat ggtgtgtcga tcgctttgca gcttcttggt ctgctgcaac 240  
atggtctcca gcaatt 256

<210> 832  
<211> 406  
<212> DNA  
<213> Drosophila melanogaster

<220>  
<221> misc\_feature  
<222> (1)..(406)  
<223> Area matching Drosophila Genomic sequence  
AC003054. Matches in area of 822AA predicted  
protein.

<400> 832  
atctggattg aggtcttgcc acagttagcc gagcaaagcg cagctatacc aattctccat 60  
ggcgcgtctcg gccacagtgg gtcaattctc catgctccac tctgggcaat caatttctcg 120

atattgttgt gcagtgcacg tagattgagt cactcctcct cgcattcggc attcccattt 180  
gtatatatat aactcatat tcgtaattat tgtaatgagc catttctcta gttactttcc 240  
tcgttggtg catgggctgg gtttttaatt aattttccat tgaccagcc tgacagctga 300  
gcctcagctt tttcctcttt tatttctgag ctgagctcag aggctctgcc agcccaagag 360  
catttcatat taattctcat ttttcgggc tccaattcgg ggcttc 406

<210> 833

<211> 460

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (460)

<223> Area matching *Drosophila* Genomic sequence

AC004280.

<400> 833

gcccattcgg agcgcattgt gattgatgag cggagagagc gagcgagagc gcggtacatt 60  
agcattaacg gcgcatgtgg cgcgaaaatg cggatggaat caccttgtgg ttgttgttgt 120  
tgccgcgtgc accaccctta aagaacttgt tttgcactga cagaaatttt gagccgcccg 180  
tggttggaat aatgcaattg caacagtgac cgtggataat tgggaactcg aactgcgggc 240  
cgggggtgcgc aggtaaaagg cgcaggtgca ccggagcgca gatacaggta aaaagtgaag 300  
cggttatcct gaggaagaaa caagtaatca tgcttggccg tggatcgtct atttgaagtg 360  
taaatatgta ttgtaatgca atatggtatg tattgaagtg tggttggtatg aaggaaagca 420  
ggccggaata ctgattactg ctaccgtatg taggcagatt 460

<210> 834

<211> 99

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (99)

<223> Area matching Drosophila Genomic sequence  
AC004722. Matches in area of 289AA predicted  
protein.

<400> 834

ctttgaatga aaacaccgaa tagcatataa aatgcatttg ctccttagta aaaaagttaa 60  
gaaggtttgc cgctgttttc gtattcgaat tacgaattc 99

<210> 835

<211> 178

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(178))

<223> Area matching Drosophila Genomic sequence  
AC001661. matches in area of ORF with sequence  
similarity to Mouse Surfeit gene.

<400> 835

gtccttactt gcaattcatt ttcgaaagaa tcaagttggt tgcttttatt gaaagtctgc 60  
agtctgaaat taattgaagt gaagaatata aaggccttgc ttactcttga ccaatctcag 120  
gtaagtataa accattatag acggactaag aaaaggcaaa gaatctgtag gtgaattc 178

<210> 836

<211> 602

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(602))

<223> Area matching Drosophila Genomic sequence  
AC005269.

<400> 836

gcctagccaa aagctaggca aacaggccaa gcccacccc ataaaacccat gtcacatttc 60  
tggctcgttt tttatctggc caagaaagaa acaaacaaac actgtcgcac attagagcgc 120  
aacgtgccga gcccataaaa agatttcgac gtcttcgcac gagtcataat acacccctcg 180  
cattcgccctt ccccatgaaa tcacccacct gaggcacgtc ataataatat tgggtggtgtg 240  
gctgcatttt ccttgcacgc ttttaggcgc aattttttaa tggttctaga atatgcgccg 300  
aaaacgcaac agttgctcat gttttcatcc ttaaaaatta agtagtgaaa tttgaaaagt 360  
ccatattaaa aacagttttt aaaattttta gacatttttt gtttctgtca ggagcacatc 420  
aatttaaaga cttttatggt ggtcatcaat acagtattca cttttaacat ttacattacg 480  
tctataattt aaagcacagc tggcagcaca gttaatgagt aatattctgg caccctaaac 540  
ggcttaaaaa agttcaaaac cgcaaaacaa ggtccttggc tttcaaggac atgacctggg 600  
tg 602

<210> 837

<211> 562

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(562)

<223> Area matching *Drosophila* Genomic sequence

AC004362.

<400> 837

cgacggacct ttcgaaaact tgacgaacac gaagcagagg ttcaaagcaa aatggagtaa 60  
acgagtgaag aacaaaataa tgaattatgt caaaagtggc gcaaatatct ttggtacacg 120  
aagaaaaaga ttggtagtgg catttagccc ttaccacaaa totacgtaca tacatatgta 180  
tgtatgttta catatgtaga attattaata gtattttaat tattgtaaaa tcgtggttat 240  
atattttttt gtgagtagtt actctatgta cgtgctccca accaatgagt gagcgagata 300  
gactgctaag tggagaatgg gagttcattg atatttctcg ggcgttttgc tttcgcttcc 360  
ccttcgtctc caccttgctt cgcgccatct tcgttctttc ctcttctcct ctgcttccat 420  
ttacctgcca cattcatttt gtggtggttc ttcgcaattt tgctttcttc ttaatttttg 480  
cattcttttg gacgtttttt agtttgcggg tcgcttttgc gccgttaact ttggaccgtc 540



tgcggggtgt ctggtgtgga tg

562

<210> 838

<211> 521

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(521)

<223> Area matching *Drosophila* Genomic sequence

AC004370. Matches area of 1277AA predicted  
protein. Sequence similarity to human nuclear  
transport receptor.

<400> 838

gggccgtcta tttaagcact gcctctcgag gagagagtaa ctttctttta acgctctcgc 60  
tgctctcttt ttcgctctcc ccgaaatcgt tacgacgctc actcgctctc tctctccac 120  
gccattggcc catacaatac actcaaaaaa tcgccgcggc atttgtacag ccgcagtcga 180  
taagacaaca acaacagccc agagcagagc gatcgttgga tttttggtat attattttgc 240  
ggtgattttc tgataatata gtatctatat agtaaggctt tagggaggtg ccatatatca 300  
ggcggcgcta cggcaggcaa aaggatttac tcgtaggccc cacttgatgt atggaataat 360  
cccgttttcc tttttggttt gctaaccacc ggatatgtgc ttcccgtcgg acgggttcgt 420  
acaagacttg actttgcccg gtccgttcga tggcttagaa attgccgctt gcttcttctt 480  
gcgccaaaat cgggtgcata cattttcgct atacttgata c 521

<210> 839

<211> 619

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(619)

<223> Area matching *Drosophila* Genomic sequence L49408.

<400> 839

gttgtgggtg tgcgcgagcg tgtgagctat agctctcatt ctataaaccg tatctctagt 60  
gcaaattgtgt gtgtgtaatt cgagtaaagc cggtagaagt cgcagctggt tttgcctatt 120  
tttacgctca cacatat tttt gcaacaaaga aaaacaacaa ttctctagcg gcgattttat 180  
ggctcgtgca attcgtctca ggttcogtta tgatcaaaaa tatttggatg ctaatttttag 240  
caggctgccg ttactaataa atacgaaatc gtgtttaata gttcatcata gcgatcctta 300  
aaatatattc aggaaataaa cggaaacaac aagtgaatat atgcataaat agttgttgat 360  
ttcatagctt agcataatgt ttttcaaatt tcattttatgt caagtatttg aactgaaatt 420  
tttttcggtg caccogaaca cagattttct gctatcttct actttggcgt ggccatagag 480  
ctcagccaaa aatttgcaca aaaattaatg tcagctgact tgctttgggt cacttctcat 540  
tttcgtggcg cttcacacac acctggcatc atctgcaggt gaagagtcga aagataagcc 600  
agaacgctac gttaatggt 619

<210> 840

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(535))

<223> Area matching *Drosophila* Genomic sequence

AC005447. Matches in area of 802AA predicted  
protein.

<400> 840

ttccgtgcca ttgccgagcg gtaagcggcg agcgtctaaa cgctcaactca ctcacacact 60  
caagttcata ttttgtatgg tacagtgggc ctggttgcca gatttcgtcg aggggcgcag 120  
tttggttttg caatttacca atttacaggc gttttgccgc ccaaactgcc caaactgccg 180  
aactaagctg ggagcgtgac caaatcaatc gactgttcag acacagcatc ttgagtggtc 240  
ttgtaagtaa gacatttacg ccaattttcc aatcaccaaa cctgttggtg agcaacagcc 300  
gccaacgggtg cgtatgatta atgcctatcg ctgtctgtca tctgagctga ggctgggaca 360  
atgggcagcg cagcactcga aaaagtacct ggcaggcgct gtatcataat gctctcgtg 420  
tcacggcac ttcaatagct aaaaaaacct tatcaaagct ttaaggcctt atcaccgaca 480

aactgactct ttggcgcttc ttatcaacca ccattggccg cgatttcagt gagtt

535

<210> 841

<211> 342

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(342)

<223> Area matching Drosophila Genomic sequence

AC004120.

<400> 841

ccaccaacca agccacctac ccgccatctc gacgatgaac tgtcgcgctg tttgctgcca 60  
tttctgtccg ggcttggtat tgtttaactg gcaatgatta atggcaatga ggcagggcag 120  
agcagagcaa aagcggagca agaaggtggg caccgagttt tgaactacac aaaacggaac 180  
atcatcacat cgctggcatt tctttttgcc agtgacccag aaacatttct tcgccagctg 240  
ccattcaaca cttgaggggtg attagaattt gcgccatcac tgaagcgggg gccgataaaa 300  
gcggagcatt ttattgattt gtctgactca ttggatgtgc cg 342

<210> 842

<211> 512

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(512)

<223> Area matching Drosophila Genomic sequence

AC005454. Matches in area of ORF with sequence  
similarity to mitochondrial translocase.

<400> 842

gtacacggtc gacaacaaca aatgcagtat agcgaacgaa tgtgacgatt ctattatgat 60

cgtttatggt cggttataag gcggtgaaaa gtgtcatcca ttcccagaca tctagacagc 120  
 caaacttaag atcatatggc tgcgttctag acattctgaa gaaagccaaa aacaaaagca 180  
 tgtattcagc aaaagtcgac aagacatgag taactccaat cgaaatattt gggctataaa 240  
 cccaaaaact ggggtgtattc acttgtgtac tattacctca tgtcttttta ttctttttca 300  
 gatactctac gcgttaatac accttctgta cacattgctt aagttggaaa atgtatgttt 360  
 atggagccta atataataat tccattgttg ttgttaaata acgattacat atttaattat 420  
 gtgcagcaag ataaataaat tattcatcac accattgtca ccgtcacaat atcttaaggt 480  
 tttggttaatt catataaatg gtaataccat ca 512

<210> 843

<211> 515

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(515))

<223> Area matching *Drosophila* Genomic sequence

AC005130.

<400> 843

ggctgcggga aaccaggaag agatatgatg gtggcggggg cgtaggggaa tggaaaagca 60  
 gtgtagaagc aaacgtcgag cgacgtcacg caaaagttgt ttgcgttggc gaatagagcg 120  
 caaaagtagg caacgttata tgttcattgc ggtgactgtg tgtgcggtaa agtgggtcgg 180  
 tgggtggaat gtttacacac atgacctgc catgggagta tgcgtgggtg tgagtatgtg 240  
 aggcattgct atgagttctg tatgttggtt ttcttgaaca aactttaatt gtttttgatt 300  
 ttcctaagga ttcaagtgc gcgagtttta ttacttggtt gtttactcat ctgaaggatg 360  
 atgcatagag gtgcggggac agtttgcctt ttagaagcct tttcaaacgc ccagttggta 420  
 aaaaaatgag aaagcggaaa ggggcataac agaaatgggt ctctcttggc taattagatg 480  
 agcgttggtg tgcttcctg aaaaaagggg aattc 515

<210> 844

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(499)

<223> Area matching Drosophila Genomic sequence

AC005439.

<400> 844

```
gcttggcggc aaaagaatga agcacgacgg ccgcagagag aacaaggcag cgaagagaga 60
gcccgcgctc tcttaggcgc tctctttcgg ccacaaggca ctcggctggt gcattgaccc 120
cacagctcgc tgaccactt acgaagctgc tttttgccac tgcgaatgcg agttgcgaat 180
tgcgaactgc cgacgctgcg agctcgtgcc tccgtcgacg ccgctgccgt catcgttgtc 240
ggtgtttctg tttcgacgaa cgagcaactt gtgcaatagt cgcagcagca acagcaaaa 300
gagcagcaac aacaacggct gcagcggcaa cagcaagcaa ttcgcagtcg cagcagaggc 360
gactgcgctg ccacatgggc aactcaaaat tggactgtgc ttcactcttt gctagcacag 420
tggttgaaag taaggcgttt aataatgata aataatatat atgcattatt gaatgaaatg 480
gaagaataga ctgcagggg                                     499
```

<210> 845

<211> 565

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(565)

<223> Area matching Drosophila Genomic sequence

AC005127.

<400> 845

```
ggtaccacgt ttgtgttggt gtgaccgacg gggggatgcg agaaaatacc accaattaat 60
acaaataggg ttaaaatacc aattagcgtg tacacaatcc acaattagcg tggacacgca 120
ccgaaactat ctttttagcca gtacaacctc caaagttatg acgattggta acgccgtttt 180
cgacttcgaa tatttgtagt tgccaacctt cttgaagatt gtatgcgtgc gtgaatttaa 240
atTTTTTTTaa atcgtgataa tgcgtcgagc aacaatctaa gctaaaatta gatggcaccg 300
```

gcgttttattg atgcgaaaca tatgcaatgc caacaatctt aatatgattc tatgcttttag 360  
ctcttttgaaac cttttaaagt tggccaagca cccaaagtgt tgaactatag catgtgtttt 420  
atttaaaatc tatttgtgat agagcttaaa acctaaacag tggggtgtgg gattaaggta 480  
tctacaactg cgtgattgga agagaccag ttgctttgtg acggtcacaa cccgatgctg 540  
tgtcaagctt tacgctttat gataa 565

<210> 846

<211> 586

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(568)

<223> Area matching *Drosophila* Genomic sequence

AC005889. Matches in area of predicted gene coding  
for 1365AA protein. ESTs AI106939 and AI296430  
come from this gene.

<400> 846

ctttgcaccg atgacgtatc ggctatttgc aatttcacat agttgcgatt gcgtttcggt 60  
ctatattggt ctaaattggt gtcgctgccc ccactcacac atacgccctc acaaaacagg 120  
tgcagaatgt gataacacac acacacacac acactctccc gccgagcaag ccggtaaaca 180  
aaactggaaa gagagagtgc cagagagcaa agcttccttt ttttggcaaa gagegcgaag 240  
aagcttcgtg ttgccattgg tggtcgacgc cgggtgggtg ttggtgggtg tgctggtgag 300  
cgttttttta cacaattgca ttcaaaaaat gtgtgcttag tatttcggca actttgtgac 360  
tgagcgaacg ttctgtgttc tctgcttttc attatttcgg agatttttcg agagtaactt 420  
gcgattttctg gcccgattg agtcacacat ttagagccta gaccgtgata agacccgaaa 480  
aaaatattaa acataaaacg caagtaagag gagccacgag aaaccaaaca aaagtgaaag 540  
ccattgacat ttgtcctgcc aagtttgaag tgatgacctt gaattc 586

<210> 847

<211> 503

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(503))

<223> Area matching Drosophila Genomic sequence

AC005558. Matches in area of 1277AA predicted  
protein. Sequence similarity to human nuclear  
transport receptor.

<400> 847

```
tctcagactg aaactcgaaa taaaaatgta cagtttaacg ggagcggttct ctgctctct 60
ctctctctct ctctctccca ggagaaagat agatacaaat agagagcgct gctaactctc 120
tccctcgtaa tttgtataca caccgttttg tctgtttgcg tatgtgctta catttatctt 180
tcaactttttt tctgctctgc cttatgcgta tttatttttag tacataaaac aagacggcta 240
aacaggggtgt cgcaaaagtt agttggggtt cttcgggatt caattgaata atgatcatta 300
tcccatgatc atgaattagt tgagatacgt ttggcacgga taattcttaa gtggtacagt 360
aacgaattgt atagatttca agaaatagtt ttgaaaataa ttcgttgctt tccatatctt 420
tcgattccaa ccaccagatt actttgtcct ataaaatgta tcttcaccct tagaaacaca 480
acctaaacct ttactaatca gaa 503
```

<210> 848

<211> 620

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(620)

<223> Area matching Drosophila Genomic sequence

AC004351. Matches in area of ORF with sequence  
similarity to LUN/Forkhead genes.

<400> 848

```
tgtctcttgc cgaccctacg tgggctggaa gaactcgggtg cgccacaatc tcagcctgaa 60
cgagtgcttc aagaagctgc caaagggcat gggcgtgggc aagccgggca agggcaacta 120
```

ctggaccatt gacgagaact cggctcatct cttcgaggac gagggcagcc tgaggcgccg 180  
 gccgcgtggc tategctcca agatcaaggt gaagccgtat gccggccatg ccaatggata 240  
 ctacgccagc ggctatggcg atgcgggaat ggtaagctcc atcgatttca taacaactta 300  
 agatcatata atatctatag tactttctctc tttgccacc aggacaatgg caactattac 360  
 gcctcgcttg cttttgctag ctacgattac agtgcagctg gagccacttg gcgtctcgcc 420  
 ggctgggtgg tcaaggattc gcccgatccc tggaacgccc atgccggcca cagtggctcg 480  
 tcgtccggtg gggccgtggg catggggccg tgggtcccct ggcccagtat acgaacatat 540  
 ctggctggca gccggaggca atggtgaatg gctcggctac acgccccgc tggcccactt 600  
 cgcactggga atgggcccac 620

<210> 849

<211> 519

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(519))

<223> Area matching *Drosophila* Genomic sequence

AC004766. Matches in area of ORF with sequence  
 similarity to Lipase 3 genes.

<400> 849

gcgtggatgt acctgctcga gttaaataaca tcgatgaaaa catcgataat atcggtttgg 60  
 gtattgtcgt gacacacgca cagtgggtgca ccacacatcg gttcggttaa atataaacia 120  
 atataaatca aatTTTTTgta tttaaaaaaa agtggttaacg taaactggtc aatTTTtatat 180  
 tctgctaata agaacaagaa taaaatTTTT ttacaattaa ggaatatcat aacaagaatt 240  
 gatttaacgt ataaataaat gccatgaata tatttttcca cctaaatata cattacagat 300  
 atTTTTtact atgatcagta tgttgcggac tatcgactac cacaaaaaac gctggaaagt 360  
 ctatcgatga ttttacaaga tgcttcatcc ctggaaagtt ggcgcgcaat tcaaactaag 420  
 agtgcaaaat atttctcaac agtcacaatc agcaaataaa ataaaaatat ctagtcgctt 480  
 atattttatt atattacact taatataatc cattgattt 519

<210> 850

<211> 80



<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(80))

<223> Area matching Drosophila Genomic sequence

AC006247. Matches in area of ORF with sequence  
similarity to mammalian Valyl tRNA genes

<400> 850

gactggagtc gcagaaaaac atatgaaaac gtgtgcagtt tgggaccagg gttgccaaca 60  
gatattatta ttttgaattc 80

<210> 851

<211> 370

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(370))

<223> Area matching Drosophila Genomic sequence

AC005129. Matches in area of 1208AA predicted  
protein.

<400> 851

ggtaaaagtgt tgagctgtcg ctgcggctct cggcaattta tactcgcagc tcggtacttc 60  
ggctccgaac atccacttcg gcttcggcac gggcttcggc ttcgtccgct ctccaaattc 120  
ttattttttt ttttattatt actgtgagtc gagtgaagct cgctcttttg tgctctttgc 180  
cacgatgact tgtgcacttg ccagtgtctc catttgtgaat gggcaacgag gggctgggtgc 240  
aaacgaaccg ccaccaccca ctgcacagtg ggacggatac ttaaatacatt agattcaata 300  
ttaaacagta gattaaaatt aatagttttc ccactttatg tattatagaa taagttttcc 360  
ttttgaattc 370

<210> 852

<211> 748

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(748))

<223> Area matching *Drosophila* Genomic sequence

AC005894.

<400> 852

tgtgagtcga ggtgagccaa atacgaacca tccggaccga gccgagccaa aacgagcccg 60  
actatgccag ccgaactcat taaaaagccg agcggcattt aaggatgcgc ctgcgagca 120  
atctcttata ctgcgcgaa agctctgcga aaaagctccg agatcgagcc gagcttggtg 180  
acacttttcg ttgaaatacg gcggcacact tggcacggag ctgagttact gccaagtggg 240  
cagtgtgagt ggtgctccca gggaaggaca agccttctgg agaattggaat ggaaagcctc 300  
agccggaaat ggagccctcc agtcagacca ccaagatcat ctcggcattg aaatggaaat 360  
ggatgtagag gtgaagggtg tagtggaatt ggtgatggag atggagatgg cagaggaagt 420  
gagccactct agacacgaat cgtgaatcag cggcgcattc aacgtcaaca cgtaatcccc 480  
gcaaggactg actcgttctc gtcgtctcc tcattctcgc cgaggtggag gcatcataat 540  
aatgcccccg attaaagaac aaaaagccag gctgaagtgc tgcaagtcatt ttgtgtgctc 600  
attgtgcaaa cagatcccg gtccttggtc ctggttctcg cgccggaaac gctttaagac 660  
cccgccagcc gagggcttag tgcgggcaca taatgtctgc taatatttga aaatgcgtcg 720  
cattaattga catgaaagag tcacgaaa 748

<210> 853

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(535))

<223> Area matching *Drosophila* Genomic sequence

AC005447. Matches in area of 239AA predicted  
protein. Sequence similarity to C.elegans gene  
AF002196.

<400> 853

gtgagagcca ttaaccaaga gaacagtaat agagcgcatt ctctctttcc atgacccctt 60  
ttagcttcat cactctcaca tacataaaca caactttgca tatgtgtaac ttctgtattt 120  
ttaacagttt caaactaaat gcatatgcca taaaccatta ggtttgaaca gaaagcatta 180  
aaagtataaa tcccataata aatgtctact tttggcagtt ttccaggaca aaccaccac 240  
tccgccatcc gccgaccagg aggcagccca gctcttgga agttccggag cggagcaagt 300  
cagcttcatg cagtcgctga agaacctgat gaccaaccgg aacttcatct tctgtctct 360  
ctcgtaaggc atcaatgtgg gcgtctttta cgccatttcc acgctcctca atccggtacg 420  
aacatacttc gcatacttcc actcgattaa tgagcggctg ctaatggggt cttattgctg 480  
ggatctgttt ccaggtgggc tgaagtatta tcccggcacg aagtggacgc cggac 535

<210> 854

<211> 581

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(581))

<223> Area matching *Drosophila* Genomic sequence

AC005643. Matches in area of 242AA protein.

<400> 854

gcaccagcca gatgggaaac tgtgcggcag tgggtcgaag agccaatgct ctcgaaaaat 60  
ctatttagtt agctattaat tatccacttg atttctaaat ataaacaatg gtgttcatta 120  
aagcagggaa gttttaatgg ggtagtagg tcagtcaagt atttattatt tagttttgtt 180  
ttttattaac tagctatgcc ttcataaata aaccaattgc aatagtttag ttattatata 240  
gattttttga tatttaatat atgtttctga ggtagggat ccaaacgact atgcttagcc 300  
atctgcaaat ccccttcacc ccatatgagg tcagtttgct gtccggcaca gctgggtatt 360  
tatttttagg catcgcaatt ggatttacia attaaatgtt tctgccccac gatttgtagc 420  
cgcacttggt ccaactgcct atagtattcc atatgcatgt gaatgggggt tgtctatagg 480

ccctcggggg cctctaagct tgctagcggg ggtggttccg ctataattct gggcacgtct 540  
tatgactgcc aggggtggtg aatagaccat ttcattacat c 581

<210> 855

<211> 342

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(342)

<223> Area matching Drosophila Genomic sequence

AC005554. Matches in area of ORF with sequence  
similarity to Rat fatty acid synthase.

<400> 855

ggtcagaatg ttcggatcgt agtgattcat cgtggaaatc atgcgagtac cacgcgagta 60  
aaactggaaa cacgacggaa cttctccgat cgtttataag ccaattactt tgtgagaaat 120  
gcctcgcgat agtatacatt tggaaaatta tcttgattga gacaatgttc tgattagtga 180  
agttcgaccg tactgaatgc gtgcattatt cttaaacaat caatgcgcga ttgctacgtg 240  
tattgatagg attagggat atgtacatta agttctacag gataattcat cagcataatc 300  
cgtacgaaac tacttccttt ccactaggga cgctttccgc aa 342

<210> 856

<211> 77

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(77))

<223> Area matching Drosophila Genomic sequence

AC004532. matches in area of 1145AA predicted  
protein. Sequence similarity to C. elegans gene  
AF067608.

<400> 856

agctggccca gtggctttta ttttcgaccc gctcgcagac atcagttgca gttcggaagc 60  
ggaatcggat gatgcgg 77

<210> 857

<211> 496

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(496))

<223> Area matching *Drosophila* Genomic sequence

AC007186. Matches in area of ORF with sequence  
similarity to Human YL gene.

<400> 857

gtctggctta gtacattacg tactctggtc acattgcttt agtgaaaaga aaaacgaagg 60  
tataaacttg tagaactgcc gtctaaaagt gaataattta ttgcaatcgg tgctaaaaag 120  
aatgatatga gcttattaca ctgcagctaa ctaatgtaaa actcttcacg tagaagtggc 180  
cgaactgtta gccgttaatg aagttagagt tctttaggag gacgctgcca acgcgacgtc 240  
gctgcgggaa agagatggaa agcgttagcc ggcgttcgtc cgaaatttct ccgctattca 300  
actggctttt gaagcctgga gtgagcataa attaatggtc cgcaccttaa ttatcgcggt 360  
gtcgcaatta ttgtgctgtt gcagtagtgc aaagtgcggt tcgtgcatat gtgtgccgtg 420  
tcaagtatta acgggttggtg tattccgccg ttctgcactg gtaattggtg gcagctatag 480  
ctgcactttt ccataa 496

<210> 858

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(582)

<223> Area matching Drosophila Genomic sequence

AC007176.

<400> 858

```
gcctgtttta tttacgccga aagcttaaac acaagaggcg aaaacaaaac cgaaaccaa 60
atctaaaaac gtgtttcaaa tgttcctatc tgtgttgtgt ctctgggtcc agtatttggg 120
gtttggcgta caagcatgtg gatatggata cgaacagaac ggaaagacga aacataacat 180
atcgaatgct atttactcca tgtgtcttgt ttcacgctcg atttgctcg ccagcagagc 240
taaaaaataa aaaactacgc ttactgatta aaaaagctgt cgccgggctt tatattttgc 300
gtcgaactga ttgtgtgcag tgattactcg gaagcgggaa ttagaaagga ccccgccag 360
atattttatt gattaaaaaa tgcaaaagca tgctgctagc aacagaaaag aagaattgtt 420
taaattaatc ataaaatagc actagttttt gactagttt acactttata ctttatecta 480
aacaccagct cgggcaacct ttttgaaaac tcgagaattt actggttata aaataggtcc 540
actggaccct aaacaaacag gaaggggtga acaattataa tt 582
```

<210> 859

<211> 483

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(483)

<223> Area matching Drosophila Genomic sequence

AC004423. Matches in area of 604AA predicted  
protein. Sequence similarity to C. elegans gene  
AL0214481.

<400> 859

```
gttccaacca ggcagcagta acaaaactgg atgatgccgg tgagcagaat gtagccgagg 60
tagatgtcca ccagcttcag tcttgggcgt attctgcacg tagtcgttgt agaacttgga 120
aatgacgctc gacagctcca ccattttgct attttatgtg atatttgtcc ggatatttaa 180
ggataaaggc gctttttaac aaattaatcg cagacacgct acaaattggg agagaactca 240
aaagtaggac cgttcgtcta gtttgaaaat aatactgata gctttatcga tgaaggcgca 300
```

```

agtacagtgg gcactcaata ccttgaagtt taataaagaa taggtttata tattaataaaa 360
tttttgtggt ttagttaaaa ctaaaacata acaaattctta tagattaatg accgctatcg 420
attttttttt aatgttgcatt atgtttgaga ggtaatggta taatttaatt tatataaaaa 480
gaa 483

```

<210> 860

<211> 560

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(560)

<223> Area matching *Drosophila* Genomic sequence

AC005811.

<400> 860

```

gtctgccccca tcttttgtgt gccggcagcg catgtgtacg tttactttg tgtatgtgtg 60
tctctagcgg gtgtgtgtgg agctgaacttc ggtgctgcgt cttcttcttc gtggtttgct 120
tcgccgcgcg tgctgcgct atggttggtt ttggtttggt caaggctgtt tgcgtacaaa 180
attcaacatt atttgaaggt cgtcctttgc ttattctgcg cgtcgctttt tactcgttcg 240
ctctctcttc ccagcggggc ttttttttga atgtccctct ctgctgctgt ctcgattttg 300
tctttgtgca gtgcgtgggt ttttgtcttc gctaaacaca tcgaatgggc ctagtgtgtc 360
ttaaagggga aagaatttat ttttaagtct ttgatttatt agaattgggt cctggaacac 420
acttcaccgg ttattaagct accaaacatt cattggctcc aaaatgggtgc tttccaaaca 480
aagaaggggt attcccaggg aaacataaaa ggtataaaaa aataaaagac cccaaataat 540
ttcttaaattg cccatgctga 560

```

<210> 861

<211> 596

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(596)

<223> Area matching Drosophila Genomic sequence

AC005653. Matches in area of 528AA predicted  
protein. Sequence similarity to C. elegans gene  
U40420.

<400> 861

gttgagacaa actgataagg ataagcaaag atcactctct tgatgctctc tttgcacaat 60  
tctcaatcgt tatgatatcc tttcgatatg ccattgctta tgctgtgacc ttgaacttgg 120  
ctggacgaga cgggcacgtg acaatcaaca gttccatctt ctgcatttta aaatgcattt 180  
aagcagctct tgcagcacat ttcgcctgcc acaaagtgcg ggcagcatcg caattttgtc 240  
gcgcttgggt ttcgtgtcca cacatataca tatgtatatg catgtatgta tgtacacaaa 300  
tacataccta gcactatagt gcaactagcc ctctggttct tctttctatg tggttgctgt 360  
tgctgctttt ttcttgtggg cggttaacgc tcaagcgggt cgaacgcca tgttgcgccc 420  
cttcctgcc ctcccacctt cgccagctct ctggtttttc gcatgatgag cttgcctggc 480  
tgctgcttg gtcttgggtct tctttacacg tcttcaacg acgttcgctg gtgggggccc 540  
cgctttgctg gtgctgggtgt cctggtgctg ctggtgctgt gctgggtgtg gtgggt 596

<210> 862

<211> 539

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(539)

<223> Area matching Drosophila Genomic sequence

AC004516. Matches in area of 17300AA predicted  
protein. Sequence similarity to C.elegans UNC89  
gene

<400> 862

atcatgcccc tcattttgtt ttaacaaaaa tttgagtaca agaagtagaa aattcgatgg 60  
tgtgctaaaa ataacattgg gccacagctg ctatcgatta tcgatatatt cttactcttg 120  
caagaatctg acaaaattag ccaagacact aatcaccact gcttggcaag cagtttaatg 180



ggcgccaatt tcgaaatgca atatttttta ctcagtcaaa gtgctaaagc atattatctt 240  
 tttttttcaa cagatatact caacaaaagc cgcattggata aagtgcacac gagacatggg 300  
 taagtccaag cttattatca agatatgttg tcattaacaa gctttaacaa tttatttagca 360  
 acatcgagac ccttccccga ttcgttcgca acttgcgaaa tctgcgctgt tgcgatgggg 420  
 atgcgatatc gctggaatgt cacgttgagg cccgatccgg agcccggttca tcatctggga 480  
 aaaggatggg catgttgtgc ccagcgatcg ggactacgtg atgtccttcg atgggacca 539

<210> 863

<211> 505

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(505))

<223> Area matching *Drosophila* Genomic sequence

AC005285. Matches in area of gene with sequence  
 similarity to guanine nucleotide exchange genes.

<400> 863

agctgaaaac taaaagtccg acgcgtctta cagtgtgacc acaccgctca gtgataaccag 60  
 gttttctata ctatctatga ctatcgctga attgcggtat ttaaataccg attgggttggg 120  
 atagattgtt cactaagttc ctttttaata cgctagtggc gccactgctg tttcaaaaaa 180  
 taccgctga tctgggaatc gggtatttct gctttatgtt ttttaaaaca tttatttata 240  
 gatggcgctt tgggtatttt tattattttc atacattacc gttatcaatt tataaattgc 300  
 aaacttttta aaacaaagtc aagtttgccc cagaaaatcg aaatgctgtg tttttaagga 360  
 tttttcttta tttataatct aatggcaatt tcttccattt caaaaagcgt acaattctga 420  
 gtttcatctt tagaggtctt ttataactgg gcaatgtgct caacgatttc tttottgctc 480  
 tacttttggc ttattatatt ttgag 505

<210> 864

<211> 504

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(504))

<223> Area matching Drosophila Genomic sequence

AC007137.

<400> 864

```
cgcggatcgc tcggctggcg gcccctcatt taccgttcga aactcgtcta ggccagagca 60
tctttgcatg tgttcgtgat tctgtgtgag caggttcgct ggatcgctct acattaagaa 120
agaagtgtat tagcttcgat ttattgcata gttgcctagg cccctgcttc tgcctcggtc 180
gctgcctctg ctggcgtcgc tgatgcagtt ggcgtcgtcg tcgacgctgt ggattgtgag 240
tctcgcgtgg aagtgggaat catcactggg ggatcgggga tcggtctttt atcgttgtgt 300
attcattcag agcaccata cactcgccga agacgtcgtc tattttgctg tttttccttc 360
tgttatgttt ctgagctgag ctgctgctct tttcttagct tttcgttatt aggaaatcga 420
aaactgaagc tgcgactgcg actgggggtct atcatcagtc ccgtagagacg gtctcaaact 480
attggtcgtg gtggcgcttt ttgc 504
```

<210> 865

<211> 191

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(191))

<223> Area matching Drosophila Genomic sequence

AC005643.

<400> 865

```
gtgcgagcgc ctttttgaga aaaaccaagc gaaaaaagtt aaatcgatag cgaaccgcgc 60
cactgaagcg ggattatcta acacggctta cagtccgttt cgcccagaat cgcgacttta 120
ctttccactc ttgcacttg tctcgatttt tccagctacc tttgcgctcg ctaaaaaaaaa 180
ctctcgaatt c 191
```

<210> 866

<211> 468

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(468)

<223> Area matching Drosophila Genomic sequence

AC004642. Matches in area of gene with sequence  
similarity to mouse lysophosphatidic acid  
acyltransferase gene.

<400> 866

```
caggagacgg aacggcttct tgttcactg ccaatcgttt tgaaagggtt gaatgaacgt 60
gcactgaaaa caaaaggcac atttacattc agattatatt gttattgggt atgtgttttt 120
gacagacctt tgcctgcact tattacttaa atcaacaagg cacatttaca atcagtttat 180
attgttattg ggtgtgtttt tgacagacct ttgcctgtac ttattttcac taaacaaaat 240
gttataaacc aataaataat aattgtagt ctaataattt atagtctgat attatggaac 300
acaagtgtgt gggctataca cacaccataa tttaatatct actttgggtt gtgccttatt 360
aattacaaaa tatagaataa atcttttagct atagctaaag ggaaatcgac aaaagtcgta 420
tcggtttgcg gaatacccct gggcattccg caagtgcagc cacgaaac 468
```

<210> 867

<211> 578

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(578))

<223> Area matching Drosophila Genomic sequence

AC005749. Matches in area of 1481AA predicted  
protein. Sequence similarity to Human KIAA0596  
gene.

<400> 867

ctctgggggtg gaccttggtg gtaagctcat gtttgaaacc atgtaagggt tcaagtttac 60  
tgtatacccg tgcccagtcg cccaaaaaat atgtcgtaa tttaacgttt agctttaagg 120  
aaagttcacc cttagctgga cttttggggg ggtggctgcc caactgattg tgtcccacat 180  
gttgggccgat tacgtcacct gctgcgcggg cattttcttcg taggctgtaa taaacaccga 240  
ttgccaaggc aatttttaac gatccgtaat tgactcacac accggggttt ccgaacttta 300  
tttttgttca gtaaagtgtg aattatgctt tattacatgg ctttcaatat ttcttaggtg 360  
taacaataca caattcctgc agttagtcgt tttagtcgct tatagatgag gatattat 420  
ggttctgaat gaagtcctac ccatacatat atatattata taggttggga gtcttggtat 480  
cctggggcat atgacgttgc atatgtgcag gactctgaag gttagatttc ttgacccaaa 540  
tctttgcgca acagaaaagt gaagccttag tcatgggc 578

<210> 868

<211> 598

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(598))

<223> Area matching *Drosophila* Genomic sequence

AC007185.

<400> 868

attttgctt tctgtctgtc tgggttggtg cgcctagaac tttccatcaa aatgctgcga 60  
caaagcaaat gggccccaac attttgaaa acccgaataa caatatgctc ttttttttac 120  
gaaattactt ttctatcggt atatggtatg tccacatgta tttaaacaca tagctgtcaa 180  
aagtgtcgat ctaagacttc cgacattgcc tattgaaaat taaaatgtat gattttgtac 240  
atatttttct ttttccattt tcgatttcca ttattttccg tcaaacgcct acaaagtgtca 300  
aaaatcgaat gttgcctatt ggggcatccc gagaataaga gttcaacctg ggttggttat 360  
tttttgttgc tcccgtgct gtttttaagt ttctcaact acgccgccca atccccctc 420  
cactatcact ccgccgctat cgccatctct tttccgtgc ttggtgctat tgggtgtgca 480  
gctgcttttg gtgggttacgc attcggagca aaatgggtgcc tgcgtgtgtg tgtgtgtggt 540  
gaaatgagtg cgctgtgtgc ctgtttgcat ggctggataa taatttggtg aggcgaat 598

<210> 869

<211> 634

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(634)

<223> Area matching Drosophila Genomic sequence

AC004340. Matches in area of predicted gene with  
sequence similarity to human sec24 homologue.

<400> 869

```
tttcgagcta aacgaacttc cacgtcagtt ccctaattcg atcttttttg ctctttttgc 60
cttgccacgt aagctatcgg taatcggcag tggaaaatcg aatgtcaatc gattgtgctc 120
tttcggctgc catcgccgaa tcgataatcg tgttgaactt aacagcgctg ctgttagcga 180
acagctgcga gttatgttat gtgtaagggtg gtgcaataga atgcagtgac gtcattaaat 240
acgttggggtt aaaataaata agtgaataag atataatcaa agtacattta aaataaatat 300
gtatattttc acaattttat caaaatattc cttacattca ggggtttata ttaaatttaa 360
tttctggctg ggaggaaatg ttaccaaagg ctacagaaatt tctccaacc tgccggccca 420
agccctgggt gtccaccgta aatgaagtcc ttccgaatt ggactaccgg gttgcatgat 480
cttggtaaat ccgcagtcct gtgtaacgct ctatttcgct actttgaccc gtgggcattc 540
aacttgccgc cacccttcgg ctgggttcga tgataaagct tcatgaaagg ttgggggatcc 600
cggaacttca ctctcagat aatccttaaa gaaa 634
```

<210> 870

<211> 415

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(415))

<223> Area matching Drosophila Genomic sequence AC5456.

Matches in area of gene with sequence similarity

to Human GMP synthase.

<400> 870

```
tttcggcttt aattcgcgaa aaaactgcag gaaatccaaa aggaaagtc ctggaagcgg 60
ccataataac gcagccgtga aaaccacagg gatttcatcg ccagctgtgt cgagcagccc 120
tggatactcg gaaaagaagc tgcagcagcc gaagaaattt tgagtgtgtg cgtgaggaag 180
gaaaacgggg gaccgcaaac aacggatcgc gaatttcgtc ttaagacaaa gtcttcgcgt 240
gcttgtcacg gtattccacg gccttgccga cggacttccc ggttctggaa aaccgcagcc 300
aggctaaaac gagagaaggt gagagtcgca atatggcgaa aaagatcccc gatcccagcc 360
aaatcgccat gcggtgctgc tccgccaca attccgaacc ccgcccgttg aattc      415
```

<210> 871

<211> 198

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(198)

<223> Area matching *Drosophila* Genomic sequence

AC004375.

<400> 871

```
attccaggga tacagatata cacagacaca cacaatacac tggcacacag gggcacccga 60
ttccgccgtt tgttttgcgg ctaattgttt atacagcgca gattattctt cgcactggat 120
gtatttgctc atccggctat ttctgtttgt ttttgctccg cagcagcaaa tttgcagcgc 180
acacgcagcc gagaattc      198
```

<210> 872

<211> 316

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(316)

<223> Area matching Drosophila Genomic sequence

AC005472. Matches in area of gene matching Human  
NAT1/death associated protein.

<400> 872

```
agtgaatca ataaaagtga ggagctcccc tagatgccat agtcgctcca tcgcggtaat 60
aattttcaag agcaagcagg gtcgaaattc gtcaatcaaa acgttaattt gcatgaatca 120
tttcgagaga aaaaaaaaca caaagaaagt ttacgcgtat gactgtgtgt ggtaggtaca 180
cctattttgcy ccacaaaatg gcgtcggcac cgtcggaaaa tctgaaatgc tgtgtttgga 240
ccgttgcccc ctgcctttgc ttggagttat ctacagtgcc ccctccccgg gggaaagaca 300
gccctctcat tgggaa                                     316
```

<210> 873

<211> 495

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(495))

<223> Area matching Drosophila Genomic sequence

AC004154. Matches in area of human rabt  
geranylgeranyl transferase.

<400> 873

```
agtgaatcca atcgagcaca gctgattcat ttgcgcgatg gttggcaacg cggcagtggc 60
ttatcaaaca gctgatcgac gcaggggtgt agtgttaggg ggttactata accccatcca 120
aaaataaaaa ttaaacttac ttaaatttca aatagctagt ttattttatt caaaacacat 180
gcacactatt gcaccagcag gctggactgc ggatccggct cgtcgatgct tagggagact 240
atgtgctggc cggaaccat gacgttgccc agcaggcgcg gtcctggcc ctccaccaag 300
tactcggcgc acatggacag cacgatgttg gcgtcgcggt ccgtgcagtt gaagaatccc 360
accagcacgc gtccgtccgt aatcacgac cgcagaactc gaccagccac ttctggagct 420
tctcgcgtcc cggcgtcaaa ctggcatcgt catctggtgc ggggccgtcg ttgtgatgcy 480
gaaggctccg ggggt                                     495
```

<210> 874

<211> 116

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(116))

<223> Area matching Drosophila Genomic sequence

AC004328. Matches in area of gene with sequence  
similarity to Mouse BOP1.

<400> 874

agtggggcga agagtcccgga gctttattct ctttttcgga ctgcgcaca tgtcttaccg 60  
tccgttctct cgcgtctctc gctgtcagt cctctctctg tgtgtaccag gaattc 116

<210> 875

<211> 581

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(581))

<223> Area matching Drosophila Genomic sequence

AC005112. Matches in area of 407AA predicted  
protein.

<400> 875

gtgcgtcttt ttctgcagcg agtttcgtgt tctggtttta tttctctga ttctgattgc 60  
gattgtgaat ctggttctgt gtgaatttcg tttttattaa taaaatgcac aacttccgtt 120  
attaattttg caacgacaac aattgctgcg tgtgtgtgtg tgtgagtgtt tgtgtgtttg 180  
tttgcgatt tgtgacagcc gctgacaggc gaaaagcaaa agcaacaaag tgacaagcat 240  
gagcgtgtgt cgcctaggag gaaaagcgga aaagcagacc gaaaaataat aacaacaaaa 300



agtgggcgac aaacgggcgg tgggcggaac tcgaacggta caacctgtcc gcttttttac 360  
 caccgccccca cttcccccggt tttcttcaac gatttctgtc ctgtgcacgc gactcgcgct 420  
 atctcgctct ttnngtgcgg ttttttttct tgetgntagc tgattcattc ataaaaatcg 480  
 ggttgtaaaa aaagaacagc ggnacagaaa aaacgcgctg atttatttat tatgccattg 540  
 ccgacgcgtc gcgctgagtc tgggtgntata gttccctaga c 581

<210> 876

<211> 506

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(506))

<223> Area matching *Drosophila* Genomic sequence

AC004367. Matches in area of 387AA predicted protein.

<400> 876

ttcctcatat tctgggtatt tatectaata cgaatataaa atctatctac tggcacacta 60  
 ggtgaggaaa ttatggacca caaaagatta cttcatatgt gcagtgagag tagtagaaac 120  
 catccgtcat taacaaaaag aacttaaatt taaaacgtta ttattttatg tatctgtata 180  
 catatatggc taaacttgat taagtcttga catggaaggc atttttggca gtgcggagac 240  
 acagcacttg atcaaagtgt atagctccca atgtggcatc cacagttggg acagtagtgc 300  
 tggacactct tgcagtagtt gatgaagtag ggaaggcaga tgaagggcca gcagctggag 360  
 aatcaggtta gcaaagttag taagcccgtt ggtatcctga cgccccactc accagcagat 420  
 ataccaggtc agacgcacat gtgggtcttg ccggtggggg acgtggcaga ctggtggtga 480  
 cctcgccctg caggacggac acttac 506

<210> 877

<211> 411

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(411)

<223> Area matching Drosophila Genomic sequence

AC005472. Matches in area of gene with sequence  
similarity to Human NAT1/ death associated  
protein.

<400> 877

```
gtgtgtgctt tgcgcactat cgatggggga aaaagaagag tgcgttttca tgggttttct 60
caagatattt gctcttgaag ccccgaaaaa ctagtaaaat aaatactgtt tgcaatgtgg 120
gtgtgccact tggccagtta aacatgcaga cagcgacaaa cacttgtgca caagagccga 180
gccgaacgct cgaattgagg tcaaaatcat ccacaactgg gtctgtgcgg aagcaggggg 240
ggctcatttc tcaggtcggg gtcgacgcct caatgcagca gaggggtggg ttttcgcatt 300
gggggggtgt taagtttttg cttatccctt cccgcacga aagactacat tattgcaggc 360
ccaaagtctg tatgtatgga tgtggtggta ctgcacaat gacaaatcgc a 411
```

<210> 878

<211> 492

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(492)

<223> Area matching Drosophila genomic sequence AC007121

(41693-21184). intron of gene at  
22511-56594bp(complement) coding for 365AA  
protein.

<400> 878

```
atgtaaataa ttataataga aagaccgaac tatgtcagta gtgtgtatgc acaaattgtt 60
ctcaaaataa agcgaaaaaa ttgtgaaata ttttcgtata aaaatactca ccccgaccg 120
agtctgattc tattcttgat taaaaacaaa aagtgaaaag agagtggaac agagagagag 180
agagtgcaga caaatggaag aaacaaacaa aacgcagaga aaaaaattac caaatattcc 240
gagaatactt ggcattaagc aatcgccaaa agactgggcc gaggggaaga gatcgcttg 300
```

gaactaggga ctccaatgcc gaccaactaa cacactggcc agccctggtc tgcaaccatc 360  
tctatctcgc ccgccgtcca attagtgcag cattcttaaa gcggccgagg caactttctt 420  
ctactcccca aacgagtttc agccacgcac caacacacca acaccaatac cagcaacaac 480  
atgacggatg gg 492

<210> 879

<211> 291

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(291)

<223> Area matching Drosophila Genomic sequence L49405.

Matches in area of 626AA predicted protein.

Sequence similarity to human NAT1/death associated  
protein.

<400> 879

gccactgcaa taatggcccc aaacgacgat gccaatcgt gacgccagtg acttcggctt 60  
tcggccgcct ttcgggtttt cgaaattcat ccgtttcaga gaaggaatga actctcggtg 120  
ccggagagtt gttcactgga aagtctact actataagct atttactctt ctcttacgct 180  
taagattata tggattatta acatctcatt atgcgttgaa ccaataagtg tgttatatct 240  
tcattaaatt aaatattatg tttaaaatca aataattgcg tgatttaata c 291

<210> 880

<211> 454

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(454)

<223> Area matching Drosophila Genomic sequence

AC004658. Matches in area of 394AA predicted

protein.

<400> 880

```
gttcccggtta tctgatccag acatataggt ctaaagcggt ctccggggcgc tgcctagagc 60
gcgactcgcc ggatggaaac cccgtttaat cgcaatcaca agccacagaa agtaaaagca 120
agcgaaaagc ggcgtcgcac acacacacac acacaacagg gagtaacgcg cagaacgaaa 180
caacagaaaa tgtgtgtaat acaaaaatcc gttgacgcgt tcgcatttgg ttttagcaga 240
ggaattgtcg agcgttcgta cgtacttgca tacatatggt atgttatggt actacatgaa 300
tgttaccata tacacatggt atgttacata catacatagc ttaccaaagt acttggaatg 360
cgtttccttg gcagaaatac gcctgcactt cggccatata agcttcaatt aatatagggg 420
gttcaatccc cgtatcggaa caatttcgaa gaat 454
```

<210> 881

<211> 376

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(376)

<223> Area matching drosophila genomic sequence AC007757

( 38974-39348bp). This sequence also matches

*Drosophila* EST AA951801 which has sequence

similarity to transcription factors.

<400> 881

```
ggttagggta aaattaaagc cgaatattat caatcccatt ccaaagttca attttgtgtc 60
ggaaccatag taaattaatt gttccttgct attaacaacg aaaaatgcat atttagctat 120
tgcagttgag acggcagcta ttgcttcttc accacgctgg gaagttgaga atcgcagaca 180
aataaatctt cctcctcctt cgtccgggcc gaccatcaac ttcgatttca atttcataca 240
tttcgtttgc gtgggacaag cgagcgacag cagtctctgg agtttagcgga tttatattgt 300
ctcgatttgc tgctgctggt gattttgatg atgtgtttgc tgctgtctgt tggtctcctg 360
aggggtgatt gactga 376
```

<210> 882

<211> 597

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(597))

<223> Area matching Drosophila Genomic sequence

AC006091. Matches in area of 564AA predicted  
protein. Sequence similarity to yeast YII3  
hypothetical protein.

<400> 882

accagacaa tacgaatttg ttttgctgcc accgctgcat tatcagtaga caatgaattt 60  
ggggttacgc tttctggcaa acaaagtaaa agcgtgttgt ggctcaaaaa agcagcatta 120  
attagcacag acgaggtcaa tgaaatagca atgatggcgt caataaaata tatgtaaata 180  
ttttaatata tttatttaaa ttggaataag taaatagcag cctgttttac tttccgaaac 240  
tcaataacta actttaacca ttccattcct actttaatca ctgccactgt acactttaag 300  
atttgtttga atacgtatgg tttttttttt tgcaaacctg tccgtttata catacatata 360  
tactatatag cagaactgaa acaataaaca catttctaata gccacaaacg aatcgccaat 420  
gccgatcgct tttgggattc gcataaacgc ctcacgaatc gcgtcaaaat cgcgcgtag 480  
ctgggtggagc ttccaaaaat tcccccaaac caaaagccaa tttaaattcg aaaaagccat 540  
gatttagcct gatgtcttgc aatttatgcc ttcgacattc gttagtcccc cattttg 597

<210> 883

<211> 498

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(498))

<223> Area matching Drosophila Genomic sequence

AC005720.

<400> 883

ctgcagacga agcgccgaag cagcgtcggt tgacgtttct ttttcacatt ctctcacttt 60  
tgctaagact ctcacgctgg cggtcgggg tgacaaaggc tcctttaact attccactat 120  
gctcaagttt ctggtaagtt ttccggtttc ctgattcaca cctgaaaatt actacactcg 180  
cctaagtata cggtatgcat atcagatagc agatacaact tttctgtggt ttttgtggtt 240  
gtgttgcttt tcgcggcgat gacgcgcccc tgcacagtgg tgaaatgtgt tgtctagggg 300  
ttcaaaatca aaaccaatta tttgattaaa tattaatgat taatataaat gacaaaataa 360  
aatacatTTg aaaatacctt cccaatatct aacttccaca aataaaaaaa tagttattaa 420  
aagttttaag caaaattcca aaatattctt gctcggataa aacaagagtt ggatggtaaa 480  
cggtagaagt gcgccaaa 498

<210> 884

<211> 375

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(375)

<223> Area matching *Drosophila* Genomic sequence

AC005814. Matches in area of gene with sequence  
similarity to Rat NAB1 transcriptional repressor.

<400> 884

tgaggaacct tttggaaccg gccgacgaca gcgaagccaa cgaagccacc cgaagtccac 60  
ccgatccggg cgctttcgtc tatcagccgg ggcaaaaaaa aaagggttaa aatcagggat 120  
aaaaacaaaa ccaaacaat tggtcggagg gttagggacg taggacattg gtttccagat 180  
ttgagggtta ctttttatct gccgatgtc aagattctct tattagagaa caatcgggtct 240  
ctctctctct tcgcaattga gcgactttga gtgagttttt gtgctccgcc tcttgagaag 300  
cactcaaaga tttggaatgt cttgggtgcc ggagagactt tccaaatgat ccttttaatg 360  
tttttttttg gtgaa 375

<210> 885

<211> 486

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(486)

<223> Area matching Drosophila Genomic sequence

AC004713. Matches in area of gene with sequence  
similarity to CD36 genes.

<400> 885

```
tgccgtactt tctgtgectg tgccctctct ctgcccttcc gctctctcca ctcttccttc 60
cgctctcttt tcacaacaat aaacaacaac aaacacgcgg aatgcgggat gagagccact 120
ttttagttgt tgttagtcaa ttgtttgcct attgaggaaa agcgcgcaat caatatcaat 180
tcgccaggcg tgcttgaata atttctcttc ttatttatatt tttctttgtg aatagggggg 240
tgtgtggtta aacaacaaac accaaccggt agcgtcatca ccgcacaacg cacatttcac 300
gagtgaatc aaaatcaaat gcgaaatgag cacaggctga aagcagcgac gtccgcagcg 360
cagtggctgc gcaagtttcg ctttttgccc agtctccatt ctctcttctt tctggctctt 420
cgcttcttga ttcttggat ttttcttgc gcgctctggt ttggtgccat ttttctgtgt 480
cttttc
```

486

<210> 886

<211> 544

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(544)

<223> Area matching Drosophila Genomic sequence

AC005813.

<400> 886

```
acaaaccttg gttaatcggt aacattgctt acattaagcg gtgtaagaga gcagcactta 60
gagaattgta cactctttat cttgctcaat tgaacttga agagagccgg caactttgtt 120
tgttgcgacg ccaaatttca atgtcgacgt cgcagtcggc agcgtaagct ttcgagcagc 180
```

gaaaacaaca aacggatgcg agtaaagcaa aagagacaca aaaatgcagt tgtgaatcta 240  
 gtactaagat taaattatta cagacaaacg taactttatt tgcactagaa aatattacat 300  
 attatattat tatcttgtgt atatatatat aatacttacc gaacaccaag tactttacag 360  
 tattcaagta tttcctttta acgtaattaa tgaaatattc attatcttta atcttaattt 420  
 aaatataact aaacttcac tc aaatagga aggcgcgat taaaatcgga atagagatgg 480  
 caaataaacg aatgggtgtgc tttactaaag gtgagttgcg cagttgctag tagtgtgacc 540  
 agac 544

<210> 887

<211> 549

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(549)

<223> Area matching *Drosophila* Genomic sequence

AC006936.

<400> 887

cgtttagctct tccgctcagc gaacccatcg ctggcacgcc cctcaacctg cagccaatga 60  
 gtgaaatctg cggcactcaa ttctattcaa catggccgcc aaacggaagt cactcgaaga 120  
 gcgagagagc gcgttgtgtg gcaagtgtaa atgtgtgtgc gtggctttcc cctgctgtgt 180  
 tggtcgtttt gcagactttt tgcaccttta tttgtcattt gtgtgtaatt tcggaaaatg 240  
 ttggcacatt atgacgctcg acgccagttg ggccgggggc gcgcgcttaa gtgtcctcca 300  
 gggtaacttac ttcgtttagca gaagtttctc gccctcatcg tccttcgtcc tttgcggggt 360  
 ccttggtgct gtggttttgt gctgtgctgt ggctgttgcc gtgcggtgcc gactgtgtc 420  
 gtttgcgat gtgtctctta tttcataaac tgtaaattgc ttagatatt aagtctgctg 480  
 tactagctgt ggatttccaa acggcactgt atgtgtgcgt gtgacagcaa aaggacgaag 540  
 gatgggtct 549

<210> 888

<211> 306

<212> DNA

<213> *Drosophila melanogaster*



<220>

<221> misc\_feature

<222> Complement((1)..(306))

<223> Area matching Drosophila Genomic sequence

AC005425.

<400> 888

```
agccagagag aacttgacag agctgcatcc ggcgcgaaca aatcgaaccg gttatgtcag 60
atagaaatTTt taaaaatttc ttgtaaataa ataaaaatcg aagtatctgt aaacatatac 120
attgaaatta cctgagctct agtaacaact ctttaaaaag tagagaacct tacaattgga 180
atatataacg aaatacacac attttgcgga aatgtatggc tttctttcag tttcagcttt 240
gtttgccttc ctttttttta atttcaccag gttctcaaaa caagtttacc atcgtgcaaa 300
gaattc                                           306
```

<210> 889

<211> 579

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(579))

<223> Area matching Drosophila Genomic sequence

AC005720. Matches in area of 394AA predicted  
protein.

<400> 889

```
cccacgacca ttagccagcc gcatcgcccg cgtcccggcc aaggggttgc tgagaccag 60
agtcgggggtc tggacgcttc tttcaggctg ccctggccca catgctttcg togttcagtc 120
ctctcttaat ggggggctct cgtaccctca ccctcacaca cagaggcca cttgggtgtg 180
aaagttctgc tgggctctgt ctgtgtcacg cttatgattt aataagcaaa tgtgctgcga 240
aattgctgaa attgtttggc tgtccgtcat cccacaatc cgaatctcgc cccacgccct 300
gaaatcactg tccgccgtat ttcgcattga aatgctttag ccaatgcgtc acggaagaag 360
aaaagtgggc ggtagtccgt gcttgccctt tgattctcgt acctttaaat gcctttgcat 420
```

ggagctagtt cttgcctaataaatcataat aaaaagttct aggtctgcaa aaatctaaaa 480  
tctcattcgg accattggaa tatttaatta tgttattatt atattaatat tcatagattg 540  
tttccaagtgcaggtgatag agatttagaa aacgaattc 579

<210> 890

<211> 191

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(191))

<223> Area matching *Drosophila* Genomic sequence

AC004266. Matches in area of 931AA predicted  
protein. Sequence similarity to *C. elegans* Zinc  
finger gene. *Drosophila* EST AI259457 comes from  
this gene.

<400> 890

gctcaaagtg agagacaggg agagagagag agtacacggc gtatgtgaaa gattcacttt 60  
tacacatcca aaaaagagat gtgagttatt ttaaattgtag tattaaatta atctgaattt 120  
ttgccatatt aggcaattat ttgatatcat tttttgatca tgatcttttg taaatattct 180  
ttttggaatt c 191

<210> 891

<211> 264

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(264))

<223> Area matching *Drosophila* Genomic sequence

AC006936.

<400> 891

```
ggaaagaccc cgacccacac tcgtgtggcg ccataaaaa cgtcatcgtt gcacataaaa 60
cccgacagca aacaatgcag cttgccattt ggetgccgcc gtaatagttc ttttaattgct 120
cacaaaagtc gtcaaagttc gactcctcca cccatataca taaatgtata tttaccacaa 180
gcataacccg tacaaggtaa agtcggttgc tcgttgctcg tttgggccca ttaatcactt 240
ggagtgtagg gaggaggctg gggg                                     264
```

<210> 892

<211> 537

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (488)..(536)

<223> Area matching *Drosophila* EST AI062190. This EST  
comes from the *Drosophila ferrochelata* gene.

<400> 892

```
ggcgcgcct tttattgcgt ttttacgaag caattgtgcc tgcattcgtt ggaaaaacta 60
caaaatatta tttgatcgga ggaaacgaaa cactcgcagc aagcgacgag agcgaaatgc 120
agcgtgcaag agcgagactg caccacagtc agcttttacc gttgcacgca gcggtgatga 180
caagggaaag aaataaggac gcatgcgcga aaaatttctg ttggtcgctt gaagaacagt 240
atatacaaaa tattggtttc ggtttcaata aagagaaatt aaatggtaaa tgtgtaacaa 300
aaggaaaaat ttttaaata ttagattact gttgagtaat agttggcagc tattttacac 360
acatagatgg cgtgacggtt actttttaca gaactctgtt acgtttggaa aaatcagatc 420
tgtgagatca tacattttgg tatttaaaact attttagcaa ctggtaacac tattcgacac 480
cggtgccatc aattttgggt caatttaaaa ggaactatgg tttgcatac acaaagt 537
```

<210> 893

<211> 1068

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((4)..(579))

<223> AF104256. Area showing translational sequence similarity to human CRSP150 transcriptional co-activator protein.

<400> 893

actgggcaca atgggaaccg ccgagggcgg catgcgcaaa catatctgca ccgccattt 60  
caactggctg ccaccagct ccggcttcaa atccaaacgc atgatctgta cgaaatcctt 120  
aagtacctgg gcgggcaggt tcaacagccg gcagatgctg tgcaggaat tgggtcggta 180  
tggtggagct gccactctgg tgtcaaagta ctgctctata accagcagat cgtcctggct 240  
aagctggaac ggcgccggat gcttgctggg catgggcggc agctgagaga ctttgagggtg 300  
cagcgtctgc atgtgcatct gattcagcac cacctggcac tgcagtcctat cgaccttgaa 360  
gagcaccact cctggttctg tactgttttag ggcggttaagc gtctcctcgc tctgaatgtt 420  
tctgtgcaat tgccttctca tataaacgca gcctagaaaa cgctctagag gactcatgtc 480  
cggcacattg atatccttgt tcggatacgg actgggacga cacagagtct ccaaagcttc 540  
atgggtgagg agagtaggaa ctgctccagc ccagggccga ttgagagtgc ctcgagagcc 600  
tcctctatcc gtgccaccgg ccactcctgc tccaccaccg gtgctcttgt gatcaggact 660  
ctgtccgggt cgtggagatg ggcgcggcat gctgggggat ccgggccaat tgttattcgc 720  
cggcgacatg gcggtgaagg gagagtcttg gtggctctgc atgtagagcg tgttggttcc 780  
aggactatgg accatgtggg gactgggctg aggatcttagc ggagacgacg gcatcaagcc 840  
gcttggcgac ggatgtggca tatgtggcgc tggcggtgac gtcaggttga agttgcccgt 900  
gtccctgggg tccactgccg ccacctgccg ccgcacttgg atgccgactg gcgggtgtgt 960  
gcggatttga actggaaggc ggagtgtggg gggcaggaaa acgcagccac tgctctcggc  
1020  
gattgcggtc ccgcatttca gtacccaaaa ttgtgaggat ccaccaca  
1068

<210> 894

<211> 597

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (101)..(597)

<223> Area matching Drosophila EST AI388606. This EST  
forms a 1294bp contig with ESTs AI258281 and  
AI258326.

<400> 894

```
gctgtggctg tagtcaagcg agcgcacatg agtcagattc gtagcttttg ttttgttcag 60
tcgagtgcga gttcttggcg attcagatac tcgctgccat ccgaaccgaa ctgaagtcca 120
agtcgaatct aatgtgcgta cttacgtgta gaacagttca agaaaatgtg cagacattca 180
acggtcgcat ttgtgtggat gtgtgggtgt agtgaagagt gccagcatta atcgcatttt 240
tcccctgcac gagcaccacg actagaaaat actcgacacg tctgtctgtt tttctgcttt 300
attgcttcta cgctattctg cttttccggt tcgggttttcc tccgcttggc ctagtgaaaa 360
acaacaaatt tgattatatt gtgtaagtta tgtctagcat tgaaaagatg aaaagtgtca 420
ttcctataaa tacaccacca cctcgggaaa ggcactcgca atagagaaac tggccaaaac 480
ccaacaacaa acataacaaa caaaggaacc gcttgaatat aaccaactt tcggagtaag 540
gggctgacta aaaaggtatt agtgcgcaac catcatgact aactcaccac ccaaaac 597
```

<210> 895

<211> 491

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(491)

<223> Area matching Drosophila genomic sequence L49408  
(58018-58506). No good predicted exons in this  
area.

<400> 895

```
gttgagcgcg acagtgggag agagaagagc gcgcaaaagt acagatgccg ccacacacac 60
attttttact accacacacg tttcattgaa aaaacatata cacaaaagct aaggccgtaa 120
accactgca aatttgcgaa aaaaaaacg aaatgaaatg aaaactaata ccaacacatg 180
gcttaaaatc tgctgcgcaa atttttgggc gatggctctg tgtgtttcgt tccgtatgcc 240
aaaacgtttc gcttggtttc gtttcatttc cacaccgctt tttttttttt ttttttgctt 300
tttcccatgc ggcatttatt ggcaacctgc gagcaaaaga gagggcgact aggggttgtg 360
```

tgcaagggga gatggagcgc tacggcttgt ttatgaaaaa cacatgattt tttgtgtcca 420  
acagtttttg ggggcatggg cgaagagagg aagcacagga gtgcgaaaac tactattccc 480  
catagtttac a 491

<210> 896

<211> 475

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(475))

<223> Area matching *Drosophila* genomic sequence AC005714

(161048-161518). In space before gene at

162294-163466bp coding for 390AA protein similar  
to human death associated protein 3.

<400> 896

gtccatccaa ggaatacggg gtttcggcac ctatgccgac gatcttcaga gtataaagtt 60  
ttcctcgccg gttaccctga ttctgggcca gaacggatgc ggaaagacga ccgtggtaga 120  
gtgtctcaag tacgccttga ccggcgagtg tccgccgggc agtgatcggg gcaagagttt 180  
cgtccatgac cctaagatct ttgggctaaa cgaggtgcta gcgcagatca agatgcaggt 240  
gcgggacagg ccgtggtgcc caagtgtcca tctgccgcac catgaagggtg tccaagaagc 300  
gcaacaaaat gtcctttgaa acaatggact ccaccatcaa cttcctgacc ggcgctggac 360  
agtcgaagcg cgaaaagcag gactctctaa gcggccgctc cgtggatatt cgacgtggcc 420  
atctcggact tcatgggggtg tctccaggct attatcaaca atggtcctgg ttttg 475

<210> 897

<211> 461

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(461)

<223> Area matching Drosophila genomic sequence AC004375

(31191-31647). No good predicted exons in this

area.

<400> 897

```
cggtcaacca tccacagtgc tgtcgactat cgattgtttg tgttcgacta agatatcgga 60
gtggaatgtg tttggtttaa gtgtgggcat aaatcgatca atcgatcaac ttctatttta 120
gtacatattc aaattcaaac tcttccgtta acgatctaaa cggaaattta tcttgcttgc 180
ttcttttaat aagtataatc ttgaatatat tggcttgaag ttttcataag aaacactttt 240
atttaaaaac attttggcta aatttcagcg cctaaattat catcgatttt cgccgccaca 300
cccaaaggc agttctccca atggccctca aacctaaact ggtgtttccg atgcaggcag 360
ctcctccagc ttcagctgac ttgcgcagaa tgaactggtg ccgtttaccg tgcgcacca 420
gaagaaaggt atccccagtg aagtcccttt gactcctctg g 461
```

<210> 898

<211> 507

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (12)..(419)

<223> AF000177. Area showing translational sequence similarity to human CaSm protein.

<400> 898

```
gcatggacga cttaaatecg ctggcgggca cggctcacct cctggaagag gttgacagtg 60
agtaaatecg aatgaaagga aggccagtgc ttaaaaaccg gcgcattgca gagaaactga 120
tggtactttt gagagacgga cggactctga ttggatacct gcggtccgtg gaccagttcg 180
ccaacctggt gctgcaacgc accatcgagc ggatacatgt gggcaacgaa tacggcgaca 240
ttcctcgtgg agtcttcac c attcgcggcg agaatgtggt gctactgggc gaaatagtaa 300
gctttactcg atacattttc aacatgactg attaacaccc tttaaatatg cgtaaaaggg 360
accgtgaaaa ggagcagaaa ctgccactca aagagatatc cgtcgatgaa atcctggacc 420
cccaacgtag ggaacaggag cagcggcagg agaaacaccg cctagtatcc aagcactaaa 480
ggacgagcct ggcccgtaga tgccaac 507
```

<210> 899

<211> 544

<212> DNA

<213> *Drosophila melanogaster*

<400> 899

```
tggatgtctc ttgccgacgg gaccacctta tgttatttca tcaaaacgct aaaagctgtg 60
aactggcaac ttataaaaaa aaaggtatth tttttaataa tttgggctac gcctactcta 120
acgtcaagaa atgtcaaaac ctcgtaggga aatacaaaact atttcttata catatattgc 180
atthattcag tcaaacatca gagcgtcgaa gctattattg aaactgtcgc tagatggcgc 240
acatgtgtca catgtgtctc catctccctt gcaactacctt gcaatgacta acgggtatct 300
gatagtcgaa aaggtgcaaa attgaaaaga tgtgcgcaag tatttaataa gctgcgtgaa 360
atctctgtac agcaattcat tttgggtaat caaataaaaa atataataat ttttcaaaga 420
tttttaatga cttttaattg acttcaggat gataagagag ttcataaagg caagcaaata 480
ttctgaattt gaccagagaa ttggtatgta ttataataac gtcattctca tcattaattc 540
gatt 544
```

<210> 900

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<400> 900

```
gtgttgccca tatcagagaa cctgtcagaa aagcgaaaag ggggttcgag ccacgaagg 60
ggctttcaca cgtcatgggc ataattgaaa attgacagtt tattgccata ggcacgcca 120
cttttggcct cctggccttg ttggccatga ttaaaataac aaaagcacgc aaatacacac 180
acacacacac aactcaacc acacacactc actccggcga tgcttgtcta catcgccgtg 240
aagacggacg tcttaaatca acgctgcgcg aaatactcga aaccatagta gttgtgtcgg 300
cccgtgtgac gcggaatct agcaaaacca cacggtggga gtcgcgcca tagttctgcg 360
ctgcaatcac gccgagttaa ttgtgcgcct gttccgggta aataggtaat ttattatctt 420
gcgattattg cagcggataa agcagctgat agcgtgcca acttgccgac ggggcgatct 480
ggaaaggaaa gcgttgacga caaccggtgt gatcagtggt tgtgttgc 528
```

<210> 901



<211> 521

<212> DNA

<213> *Drosophila melanogaster*

<400> 901

gtttggacat cacaaagtct ccgaaaggct aactttactt tctccacatc gcccaaggcg 60  
aagtagcaga gtaagagggt aatgctactt ctaatgtttg cccgctccgt catgatgaac 120  
tcaaagctag aagcagcatc tgaataagag cccatgcgaa taaaaaggat tccaatgttt 180  
tcacggatct ttagccttaa ctgacttaag ctctttggta cagaatcaag ggccatgcgg 240  
tacattttta cgccttttg gtaaataccc atgctgtagt agatgttacc catatttagt 300  
tttagctgat tgacgtgtgg aaacatcttg tttttggcca taatgctgta ggtattgagg 360  
gcttcgatgt gcatctcact ccgttcgtat tgctccgcga gattaaaaaa aacctatagt 420  
ccatatatat taaagtttta aattatcctt ctaatcgtgc ttaccgcata tgtcaaactg 480  
aaagttgtga taaacatttc accgtgctgg tctcaaattg g 521

<210> 902

<211> 378

<212> DNA

<213> *Drosophila melanogaster*

<400> 902

ggccgtaact aagttaacca ttcggattgc accaatacaa ttgcctcttg aatttcacca 60  
gagcggggaa ggttcgggaa tataatattg ccatttatgg aagtggatct gcctaagtag 120  
aactgcgttt cccggaaaga ggtgcaccaa tcgaccttaa gtttacaaga tcaccaaagt 180  
tgaaagaatt aattttttta tctaaaaaca aaagtgaaaa ctctcaaac aataaacaaa 240  
aacggcagtg aaataccact ttcaaacaaa caaaatttat aaaatatttc ttaaagctgt 300  
aaacagtggc gcattcgcaa tgcattttgc caaaaaacaa acgccacaca tggatatgtg 360  
tatggtatgg gaatatgt 378

PCT NO : G800 / 03444

Tracey Carter.